

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:02:32 ; Search time 4148.82 Seconds  
(without alignments)  
10259.034 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcggggaagtga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_ov.\*  
5: gb\_ov.\*  
6: gb\_ph.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vt.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_ov.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vt.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rnd.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	801	81.6	1102	8	MDO251116	AJ251116 Malus dom
2	337	34.3	473	8	AB081094	AB081094 Malus x d
3	116	11.8	1043	8	AB081093	AB081093 Malus x d
4	34	3.5	1014	8	AB055966	AB055966 Rosa rugo
5	30	3.1	17606	9	BX537160	BX537160 Human DNA
6	30	3.1	183353	10	AL935278	AL935278 Mouse DNA
7	29	3.0	1698	8	NTA319873	AJ719873 Nicotiana
8	28	2.9	1256	8	ATPRP8A	M96732 Arabidopsis
9	28	2.9	1410	8	ATPRX1GE	X98313 A.thaliana
10	28	2.9	68291	8	BX897675	BX897675 Neurospor
11	28	2.9	143793	2	AC099530	AC099530 Felis cat
12	28	2.9	153829	2	AC141671	AC141671 Apis mell
13	28	2.9	174010	2	AC129127	AC129127 Rattus no
14	28	2.9	217691	2	AC103052	AC103052 Rattus no
15	28	2.9	262093	2	AC095577	AC095577 Rattus no
16	28	2.9	292004	2	AC127118	AC127118 Rattus no
17	28	2.9	302156	3	AC116977	AC116977 Dictyoste
18	27	2.7	121	6	AX324459	AX324459 Sequence
19	27	2.7	121	6	AX324460	AX324460 Sequence
20	27	2.7	121	6	AX324463	AX324463 Sequence
21	27	2.7	121	6	AX324464	AX324464 Sequence
22	27	2.7	610	8	AB047923	AB047923 Oryza sat
23	27	2.7	698	8	AB089156	AB089156 Houttuyni
24	27	2.7	753	8	ATH245906	AJ245906 Arabidops
25	27	2.7	912	8	AF088912	AF088912 Petunia x
26	27	2.7	959	8	AB007506	AB007506 Triticum
27	27	2.7	980	6	AX146915	AX146915 Sequence
28	27	2.7	1167	6	AR032064	AR032064 Sequence
29	27	2.7	1167	6	AR060347	AR060347 Sequence
30	27	2.7	1167	6	AR351552	AR351552 Sequence
31	27	2.7	1204	9	BC034821	BC034821 Homo sapi
32	27	2.7	1313	9	BC007035	BC007035 Homo sapi
33	27	2.7	1341	9	BC005317	BC005317 Homo sapi
34	27	2.7	1482	5	BC045299	BC045299 Danio rer
35	27	2.7	1547	8	VVLSTSYM	X76892 V.vinifera
36	27	2.7	1648	9	AB055302	AB055302 Macaca fa
37	27	2.7	2031	10	MMU97675	U97675 Mus musculu
38	27	2.7	2131	9	BC009356	BC009356 Homo sapi
39	27	2.7	2580	10	BC046536	BC046536 Mus muscu
40	27	2.7	3629	3	BT010089	BT010089 Drosophil
41	27	2.7	3907	10	BC052708	BC052708 Mus muscu
42	27	2.7	20622	2	AC115609	AC115609 Dictyoste
43	27	2.7	57203	3	AC116989	AC116989 Dictyoste
44	27	2.7	110000	2	PFNAL13_07	Continuation (8 of
45	27	2.7	110000	2	PFNAL13_02	Continuation (3 of
46	27	2.7	110000	3	AC116984_2	Continuation (3 of
47	27	2.7	112752	9	AF030876	AF030876 Homo sapi
48	27	2.7	115499	2	AC130963	AC130963 Medicago
49	27	2.7	133095	2	AC146721	AC146721 Medicago
50	27	2.7	137414	2	AC144721	AC144721 Medicago
51	27	2.7	140544	2	AC011798	AC011798 Homo sapi
52	27	2.7	144571	2	BX842683	BX842683 Danio rer
53	27	2.7	149815	10	AC125089	AC125089 Mus muscu
54	27	2.7	170691	9	AC104643	AC104643 Homo sapi
55	27	2.7	173183	2	AC102742	AC102742 Mus muscu
56	27	2.7	174424	6	AX335950	AX335950 Sequence
57	27	2.7	176317	2	AL670857	AL670857 Mus muscu
58	27	2.7	181343	9	U52112	U52112 Homo sapien
59	27	2.7	181573	2	AC020559	AC020559 Mus muscu
60	27	2.7	183648	3	AC117076	AC117076 Dictyoste
61	27	2.7	184520	9	AC009220	AC009220 Homo sapi
62	27	2.7	190168	10	AC127036	AC127036 Mus muscu
63	27	2.7	190790	2	AC122042	AC122042 Mus muscu
64	27	2.7	192420	2	BX511119	BX511119 Danio rer
65	27	2.7	193643	9	AC018644	AC018644 Homo sapi

Pred. No. is the number of results predicted by chance to have a





212	25	2.5	1791	9	BC016867	BC016867 Homo sapi	285	25	2.5	110000	3	AC116984_0	AC116984 Dictyoste
213	25	2.5	1793	9	BC009048	BC009048 Homo sapi	286	25	2.5	110000	3	AC116984_3	Continuation (4 of
214	25	2.5	1836	3	AF333201	AF333201 Caenorhab	287	25	2.5	112733	8	AC124964	AC124964 Medicago
215	25	2.5	1837	17	AF116609	AF116609 Homo sapi	288	25	2.5	117391	8	AC124964	AC124964 Medicago
216	25	2.5	1907	5	BC044563	BC044563 Danio rer	289	25	2.5	119927	8	AC146705	AC146705 Medicago
217	25	2.5	1916	6	AX753502	AX753502 Sequence	290	25	2.5	121143	8	AC144484	AC144484 Medicago
218	25	2.5	1928	9	BC021121	BC021121 Homo sapi	291	25	2.5	121188	2	AC135605	AC135605 Medicago
219	25	2.5	1940	6	173247	Sequence 3	292	25	2.5	121488	8	AC137554	AC137554 Medicago
220	25	2.5	1954	5	BC063984	BC063984 Danio rer	293	25	2.5	124770	2	AC146992	AC146992 Dictyoste
221	25	2.5	1961	10	BC018539	BC018539 Mus muscu	294	25	2.5	125623	3	AC115599	AC115599 Dictyoste
222	25	2.5	1967	10	BC005738	BC005738 Mus muscu	295	25	2.5	125736	2	BC323795	BC323795 Danio rer
223	25	2.5	1973	5	AF378701	AF378701 Anas plat	296	25	2.5	126087	8	T3E15	AF147264 Arabidops
224	25	2.5	1981	6	BD270074	BD270074 Secrated	297	25	2.5	126345	2	BC324229	BC324229 Danio rer
225	25	2.5	2005	9	HSM801586	HSM801586 Homo sapi	298	25	2.5	131707	5	BC247948	BC247948 Zebrafish
226	25	2.5	2050	9	BC031567	BC031567 Homo sapi	299	25	2.5	132254	3	AC116330	AC116330 Dictyoste
227	25	2.5	2112	3	AY069331	AY069331 Drosophill	300	25	2.5	134615	2	AC129576	AC129576 Mus muscu
228	25	2.5	2149	6	AX018825	AX018825 Sequence	301	25	2.5	135506	9	AC009950	AC009950 Homo sapi
229	25	2.5	2149	6	BD134935	BD134935 Human cys	302	25	2.5	137625	9	AC104663	AC104663 Homo sapi
230	25	2.5	2174	5	BC064233	BC064233 Silurana	303	25	2.5	144041	8	AC135102	AC135102 Medicago
231	25	2.5	2325	9	AB070171	AB070171 Macaca fa	304	25	2.5	146386	8	AC138130	AC138130 Medicago
232	25	2.5	2369	10	RNGP56	X99338 R. norvegicu	305	25	2.5	146570	3	AC117072	AC117072 Dictyoste
233	25	2.5	2562	3	AF102263	AF102263 Helicover	306	25	2.5	146570	3	AC117072	AC117072 Dictyoste
234	25	2.5	2689	5	AB026130	AB026130 Cyprinus	307	25	2.5	147889	2	AC018534	AC018534 Homo sapi
235	25	2.5	2722	9	BC047373	BC047373 Homo sapi	308	25	2.5	148415	9	AC016670	AC016670 Homo sapi
236	25	2.5	2737	10	BC006676	BC006676 Mus muscu	309	25	2.5	149768	2	AC016239	AC016239 Homo sapi
237	25	2.5	2749	10	AF146344	AF146344 Mus muscu	310	25	2.5	150601	9	AC117426	AC117426 Homo sapi
238	25	2.5	2879	9	AF136972	AF136972 Homo sapi	311	25	2.5	150628	10	AC133213	AC133213 Mus muscu
239	25	2.5	2996	6	E17367	E17367 Oryza sativ	312	25	2.5	151094	2	AC091797	AC091797 Felis cat
240	25	2.5	2996	6	E30255	E30255 Disease-res	313	25	2.5	152409	2	BC511160	BC511160 Danio rer
241	25	2.5	2996	6	E30267	E30267 Disease-res	314	25	2.5	152412	2	AL135899	AL135899 Mus muscu
242	25	2.5	2996	6	E33921	E33921 Method for	315	25	2.5	154071	3	AC115598	AC115598 Dictyoste
243	25	2.5	2996	6	E33933	E33933 Method for	316	25	2.5	160345	2	AC067870	AC067870 Homo sapi
244	25	2.5	3110	9	HSM803101	AL713794 Homo sapi	317	25	2.5	160863	5	AL112795	AL112795 Mus muscu
245	25	2.5	3389	9	AK027071	AK027071 Homo sapi	318	25	2.5	163866	10	AL929590	AL929590 Zebrafish
246	25	2.5	3479	9	HSM807707	EX647561 Homo sapi	319	25	2.5	164900	2	EX571776	EX571776 Danio rer
247	25	2.5	3533	3	CEL276018	AJ276018 Caenorhab	320	25	2.5	165277	5	AL954184	AL954184 Zebrafish
248	25	2.5	3636	3	AY119446	AY119446 Drosophill	321	25	2.5	165373	2	EX990611	EX990611 Danio rer
249	25	2.5	4116	5	AF406649	AF406649 Squall a	322	25	2.5	166516	2	AC135510	AC135510 Mus muscu
250	25	2.5	4134	6	AR182343	AR182343 Sequence	323	25	2.5	166900	2	AC115924	AC115924 Mus muscu
251	25	2.5	4134	6	AR236221	AR236221 Sequence	324	25	2.5	169794	2	AC004688	AC004688 Plasmodiu
252	25	2.5	4134	6	AR243543	AR243543 Sequence	325	25	2.5	171032	2	AC091761	AC091761 Felis cat
253	25	2.5	4134	6	AR254415	AR254415 Sequence	326	25	2.5	171955	2	AL954354	AL954354 Mus muscu
254	25	2.5	4134	6	AR321738	AR321738 Sequence	327	25	2.5	172493	2	AC146888	AC146888 Bos tauru
255	25	2.5	4134	6	AR411424	AR411424 Sequence	328	25	2.5	174494	9	AL353140	AL353140 Human DNA
256	25	2.5	4134	6	AR432994	AR432994 Sequence	329	25	2.5	175010	10	EX247953	EX247953 Mouse DNA
257	25	2.5	4134	6	AX417770	AX417770 Sequence	330	25	2.5	175932	5	AL845359	AL845359 Zebrafish
258	25	2.5	4134	6	AX449101	AX449101 Sequence	331	25	2.5	176038	10	EX284634	EX284634 Mouse DNA
259	25	2.5	4134	6	AX743965	AX743965 Sequence	332	25	2.5	176713	9	AP000751	AP000751 Homo sapi
260	25	2.5	5273	9	HSM807780	EX647634 Homo sapi	333	25	2.5	181515	10	AC127234	AC127234 Mus muscu
261	25	2.5	5708	10	BC054808	BC054808 Mus muscu	334	25	2.5	182752	2	EX510936	EX510936 Danio rer
262	25	2.5	9765	3	AY160106	AY160106 Dictyoste	335	25	2.5	182752	2	EX510936	EX510936 Dictyoste
263	25	2.5	14603	3	AC116959	AC116959 Dictyoste	336	25	2.5	182871	3	AC117176	AC117176 Dictyoste
264	25	2.5	25769	3	AC115610	AC115610 Dictyoste	337	25	2.5	184831	2	AC016030	AC016030 Homo sapi
265	25	2.5	29150	3	AC115683	AC115683 Dictyoste	338	25	2.5	185472	2	AC137513	AC137513 Mus muscu
266	25	2.5	29176	8	AP001312	AP001312 Arabidops	339	25	2.5	187081	10	AC124421	AC124421 Mus muscu
267	25	2.5	77289	2	AC067975	AC067975 Homo sapi	340	25	2.5	191607	9	AL137186	AL137186 Human DNA
268	25	2.5	81954	10	AL731562	AL731562 Mouse DNA	341	25	2.5	191635	10	EX113996	EX113996 Mouse DNA
269	25	2.5	83552	9	AL157759	AL157759 Human DNA	342	25	2.5	191712	2	BC323582	BC323582 Danio rer
270	25	2.5	88549	3	AC116979	AC116979 Dictyoste	343	25	2.5	191931	2	AP001958	AP001958 Homo sapi
271	25	2.5	90596	8	T15B16	AF104919 Arabidops	344	25	2.5	192913	2	AP001265	AP001265 Homo sapi
272	25	2.5	109027	10	AL732566	AL732566 Mouse DNA	345	25	2.5	195339	2	AC124707	AC124707 Mus muscu
273	25	2.5	110000	2	PFMAL13_04	Continuation (5 of	346	25	2.5	196149	2	AC004709	AC004709 Plasmodiu
274	25	2.5	110000	2	PFMAL13_07	Continuation (8 of	347	25	2.5	197064	8	ATCHRIV18	ATCHRIV18 Arabidops
275	25	2.5	110000	2	PFMAL13_12	Continuation (13 o	348	25	2.5	198697	8	ATCHRIV4	ATCHRIV4 Arabidops
276	25	2.5	110000	2	PFMAL13_13	Continuation (14 o	349	25	2.5	200182	9	AC119037	AC119037 Homo sapi
277	25	2.5	110000	2	PFMAL6PI_10	Continuation (11 o	350	25	2.5	202487	2	AC138318	AC138318 Mus muscu
278	25	2.5	110000	2	PFMAL6PI_11	Continuation (12 o	351	25	2.5	205136	2	AC129583	AC129583 Mus muscu
279	25	2.5	110000	2	PFMAL6PI_11	Continuation (12 o	352	25	2.5	205429	2	AC005506	AC005506 Plasmodiu
280	25	2.5	110000	2	PFMAL7PI_06	Continuation (7 of	353	25	2.5	205843	2	AC141957	AC141957 Rattus no
281	25	2.5	110000	2	PFMAL7PI_07	Continuation (8 of	354	25	2.5	208491	2	BC324225	BC324225 Danio rer
282	25	2.5	110000	2	PFMAL8PI_05	Continuation (6 of	355	25	2.5	209037	2	AC134319	AC134319 Pan trogl
283	25	2.5	110000	3	AC116957_1	Continuation (2 of	356	25	2.5	211442	2	BC322617	BC322617 Danio rer
284	25	2.5	110000	3	AC116957_2	Continuation (3 of	357	25	2.5	212712	2	AC063940	AC063940 Homo sapi

358	25	2.5	213604	2	AC146006	AC146006 Pan trogl	431	24	2.4	608	5	AV138880	AV138880 Crocodylu
359	25	2.5	218112	2	AC140406	AC140406 Mus muscu	432	24	2.4	626	11	BV037178	BV037178 S20856749
360	25	2.5	218112	2	AC140406	AC140406 Mus muscu	433	24	2.4	651	3	AY060645	AY060645 Drosophil
361	25	2.5	222337	2	AC140368	AC140368 Mus muscu	434	24	2.4	651	10	BC018321	BC018321 Mus muscu
362	25	2.5	222887	2	AC015681	AC015681 Homo sapi	435	24	2.4	652	3	AF207542	AF207542 Drosophil
363	25	2.5	224370	2	AC097049	AC097049 Rattus no	436	24	2.4	657	9	BC061632	BC061632 Homo sapi
364	25	2.5	226006	10	AL603907	AL603907 Mouse DNA	437	24	2.4	662	9	HS0809205	HS0809205 Homo sapi
365	25	2.5	227741	10	AC126071	AC126071 Rattus no	438	24	2.4	669	5	AV138894	AV138894 Crocodylu
366	25	2.5	237320	2	AC141339	AC141339 Rattus no	439	24	2.4	669	5	AV138894	AV138894 Crocodylu
367	25	2.5	240049	5	BA129660	BA129660 Rattus no	440	24	2.4	677	9	BC018211	BC018211 Homo sapi
368	25	2.5	242408	5	BA129660	BA129660 Rattus no	441	24	2.4	680	5	AV138893	AV138893 Crocodylu
369	25	2.5	243954	10	AL669845	AL669845 Mouse DNA	442	24	2.4	685	6	AX0406856	AX0406856 Sequence
370	25	2.5	247150	2	AC135416	AC135416 Medicago	443	24	2.4	690	8	GMU38424	GMU38424 Glycine max
371	25	2.5	247527	2	AC107443	AC107443 Rattus no	444	24	2.4	716	5	AV138876	AV138876 Crocodylu
372	25	2.5	250195	3	AE014831	AE014831 Plasmodiu	445	24	2.4	716	10	BC028492	BC028492 Mus muscu
373	25	2.5	250748	2	AC094505	AC094505 Rattus no	446	24	2.4	722	9	BC062667	BC062667 Homo sapi
374	25	2.5	251448	3	AE014819	AE014819 Plasmodiu	447	24	2.4	723	9	HS0808728	HS0808728 Homo sapi
375	25	2.5	252650	3	AE014847	AE014847 Plasmodiu	448	24	2.4	733	5	AV138891	AV138891 Crocodylu
376	25	2.5	253132	3	AE014846	AE014846 Plasmodiu	449	24	2.4	749	9	HS0420433	HS0420433 Homo sapi
377	25	2.5	254202	2	AC126506	AC126506 Rattus no	450	24	2.4	750	6	AX781131	AX781131 Sequence
378	25	2.5	254436	3	AE014827	AE014827 Plasmodiu	451	24	2.4	765	6	BD260633	BD260633 49 human
379	25	2.5	257109	3	AC115577	AC115577 Dictyoste	452	24	2.4	772	9	HS0802528	HS0802528 Homo sapi
380	25	2.5	259289	2	AC096268	AC096268 Rattus no	453	24	2.4	792	10	BC048482	BC048482 Mus muscu
381	25	2.5	260277	2	AC114063	AC114063 Rattus no	454	24	2.4	796	10	BC038517	BC038517 Mus muscu
382	25	2.5	261553	2	AC137757	AC137757 Mus muscu	455	24	2.4	801	10	BC049657	BC049657 Mus muscu
383	25	2.5	272112	2	AC127940	AC127940 Rattus no	456	24	2.4	802	6	BD018631	BD018631 Novel gen
384	25	2.5	281723	3	PF0329359	PF0329359 Plasmodiu	457	24	2.4	802	6	BD098569	BD098569 Novel gen
385	25	2.5	293431	2	PF0329359	PF0329359 Plasmodiu	458	24	2.4	807	8	NTA005899	NTA005899 Nicotiana
386	25	2.5	293962	2	AC112303	AC112303 Rattus no	459	24	2.4	817	6	BD215985	BD215985 Novel hum
387	25	2.5	306299	2	AC095803	AC095803 Rattus no	460	24	2.4	822	8	AF325718	AF325718 Pennisetu
388	25	2.5	333321	3	AC116986	AC116986 Dictyoste	461	24	2.4	834	9	BC015821	BC015821 Homo sapi
389	25	2.5	335050	3	PF0329356	PF0329356 Plasmodiu	462	24	2.4	850	8	AF371268	AF371268 Zea mays
390	25	2.5	346257	2	AC114014	AC114014 Rattus no	463	24	2.4	852	3	AY246429	AY246429 Caenorhab
391	25	2.5	347888	2	AC125166	AC125166 Mus muscu	464	24	2.4	910	10	BC061146	BC061146 Mus muscu
392	24	2.4	47	6	BD234055	BD234055 DNA/prote	465	24	2.4	923	3	AF033913	AF033913 Ctenoceph
393	24	2.4	47	6	BD234061	BD234061 DNA/prote	466	24	2.4	923	6	AR125408	AR125408 Sequence
394	24	2.4	47	6	BD217378	BD217378 Sequence	467	24	2.4	923	6	AR144680	AR144680 Sequence
395	24	2.4	47	6	AR222450	AR222450 Sequence	468	24	2.4	923	6	AR214314	AR214314 Sequence
396	24	2.4	64	6	I18658	I18658 Sequence 10	469	24	2.4	923	6	BD022611	BD022611 Flea prot
397	24	2.4	93	6	E10247	E10247 Synthetic D	470	24	2.4	937	10	BC018362	BC018362 Mus muscu
398	24	2.4	101	6	E10248	E10248 Synthetic D	471	24	2.4	945	10	BC061019	BC061019 Mus muscu
399	24	2.4	121	6	AX324455	AX324455 Sequence	472	24	2.4	948	5	AY040528	AY040528 Gallus ga
400	24	2.4	121	6	AX324456	AX324456 Sequence	473	24	2.4	1004	6	AX247641	AX247641 Sequence
401	24	2.4	121	6	AX324483	AX324483 Sequence	474	24	2.4	1012	10	BC004052	BC004052 Mus muscu
402	24	2.4	121	6	AX324484	AX324484 Sequence	475	24	2.4	1030	8	AY227636	AY227636 Arabidops
403	24	2.4	121	6	AX324487	AX324487 Sequence	476	24	2.4	1053	10	BC052053	BC052053 Mus muscu
404	24	2.4	121	6	AX324488	AX324488 Sequence	477	24	2.4	1061	8	AF077760	AF077760 Oryza sat
405	24	2.4	121	6	AX324491	AX324491 Sequence	478	24	2.4	1065	3	AF429951	AF429951 Plasmodiu
406	24	2.4	121	6	AX324492	AX324492 Sequence	479	24	2.4	1068	9	BC035243	BC035243 Homo sapi
407	24	2.4	121	6	AX324495	AX324495 Sequence	480	24	2.4	1074	10	BC005740	BC005740 Mus muscu
408	24	2.4	121	6	AX324496	AX324496 Sequence	481	24	2.4	1084	8	AB003323	AB003323 Oryza sat
409	24	2.4	121	6	AX136231	AX136231 Sequence	482	24	2.4	1084	8	GSU50845	GSU50845 Gaideria
410	24	2.4	169	6	AX208855	AX208855 Sequence	483	24	2.4	1088	9	BC010944	BC010944 Homo sapi
411	24	2.4	253	3	AK114512	AK114512 Ciona int	484	24	2.4	1093	6	BD269781	BD269781 50 human
412	24	2.4	317	9	AK000656	AK000656 Homo sapi	485	24	2.4	1101	9	BC006305	BC006305 Homo sapi
413	24	2.4	338	9	AB028624	AB028624 Homo sapi	486	24	2.4	1106	3	DJYBOX	DJYBOX X99748 D. japonica
414	24	2.4	374	6	AX198829	AX198829 Sequence	487	24	2.4	1109	5	AF460215	AF460215 Crocodylu
415	24	2.4	374	6	AX209356	AX209356 Sequence	488	24	2.4	1115	5	AF460212	AF460212 Crocodylu
416	24	2.4	414	9	HS0800130	HS0800130 Homo sapi	489	24	2.4	1120	9	BC004117	BC004117 Homo sapi
417	24	2.4	431	3	AF483662	AF483662 Ixodes sc	490	24	2.4	1125	3	AY118732	AY118732 Drosophil
418	24	2.4	448	6	AX042185	AX042185 Sequence	491	24	2.4	1129	9	BC032788	BC032788 Homo sapi
419	24	2.4	465	6	AX040866	AX040866 Sequence	492	24	2.4	1133	6	AR225004	AR225004 Sequence
420	24	2.4	466	11	G21883	G21883 human STS	493	24	2.4	1133	6	AF236370	AF236370 Zea mays
421	24	2.4	474	6	AL4236	AL4236 D5 anonymou	494	24	2.4	1143	5	AF198357	AF198357 Anguilla
422	24	2.4	478	8	GMU47406	GMU47406 Glycine max	495	24	2.4	1150	9	BC005042	BC005042 Homo sapi
423	24	2.4	501	10	BC019810	BC019810 Mus muscu	496	24	2.4	1161	5	AF460211	AF460211 Crocodylu
424	24	2.4	506	3	AF072331	AF072331 Schistos	497	24	2.4	1174	9	BC009797	BC009797 Homo sapi
425	24	2.4	521	6	AX381487	AX381487 Sequence	498	24	2.4	1186	9	BC014339	BC014339 Homo sapi
426	24	2.4	530	8	BC022858	BC022858 Homo sapi	499	24	2.4	1191	8	AF261141	AF261141 Lycopersi
427	24	2.4	578	8	AY299269	AY299269 Arabidops	500	24	2.4	1196	8	GGN132217	GGN132217 Gnetum gn
428	24	2.4	595	6	BD229601	BD229601 Human gen	501	24	2.4	1201	10	AF223416	AF223416 Mus muscu
429	24	2.4	604	5	AV138892	AV138892 Crocodylu	502	24	2.4	1205	9	BC011653	BC011653 Homo sapi
430	24	2.4	604	8	BT009360	BT009360 Triticum	503	24	2.4	1205	9	BC044945	BC044945 Homo sapi

504	24	2.4	1210	8	AK0693317	AK0693317 Oryza sat	577	24	2.4	1872	8	AP315733	AP315733 Arabidops
505	24	2.4	1213	10	AB016226	AB016226 Mus muscu	578	24	2.4	1876	10	MUSIGU1	M1555 Mouse Ig ac
506	24	2.4	1217	3	AF520473	AF520473 Branchios	579	24	2.4	1889	9	AF202889	BC021889 Homo sapi
507	24	2.4	1225	10	BC010797	BC010797 Mus muscu	580	24	2.4	1895	9	BC051752	BC051752 Homo sapi
508	24	2.4	1231	3	AF273806	AF273806 Caenorhab	581	24	2.4	1917	5	BC049324	BC049324 Danio rer
509	24	2.4	1234	3	AY069742	AY069742 Drosophi	582	24	2.4	1917	9	BC009755	BC009755 Homo sapi
510	24	2.4	1234	8	AF208051	AF208051 Arabidops	583	24	2.4	1921	6	AR438047	AR438047 Sequence
511	24	2.4	1238	9	BC017817	BC017817 Homo sapi	584	24	2.4	1921	6	BD192848	BD192848 Plant fat
512	24	2.4	1271	3	AY089282	AY089282 Drosophi	585	24	2.4	1924	10	BC024840	BC024840 Mus muscu
513	24	2.4	1281	10	BC024504	BC024504 Mus muscu	586	24	2.4	1925	10	BC055947	BC055947 Mus muscu
514	24	2.4	1287	3	BT009948	BT009948 Drosophi	587	24	2.4	1939	9	BC041937	BC041937 Homo sapi
515	24	2.4	1288	8	AF464903	AF464903 Triticum	588	24	2.4	1941	5	AF117343	AF117343 Fundulus
516	24	2.4	1291	8	CAR291816	AJ291816 Cicer ari	589	24	2.4	1942	10	BC046293	BC046293 Mus muscu
517	24	2.4	1303	6	EO6716	EO6716 cDNA encodi	590	24	2.4	1959	9	AK027180	AK027180 Homo sapi
518	24	2.4	1305	6	AR275654	AR275654 Sequence	591	24	2.4	1968	5	PPUGTWRN	X74116 P. plateasa
519	24	2.4	1315	3	AY094690	AY094690 Drosophi	592	24	2.4	1971	6	AR078523	AR078523 Sequence
520	24	2.4	1323	6	BD091588	BD091588 Novel ser	593	24	2.4	1973	9	AB071133	AB071133 Macaca fa
521	24	2.4	1329	10	BC019428	BC019428 Mus muscu	594	24	2.4	2021	3	CEL345015	AF145015 Caenorhab
522	24	2.4	1330	8	AY030360	AY030360 Oryza sat	595	24	2.4	2031	9	AK025437	AK025437 Homo sapi
523	24	2.4	1341	9	BC016737	BC016737 Homo sapi	596	24	2.4	2049	9	AK027165	AK027165 Homo sapi
524	24	2.4	1350	8	AY035056	AY035056 Arabidops	597	24	2.4	2082	5	BC044459	BC044459 Danio rer
525	24	2.4	1363	8	AF284038	AF284038 Cucurbita	598	24	2.4	2095	5	BC055677	BC055677 Danio rer
526	24	2.4	1369	5	BC053222	BC053222 Danio rer	599	24	2.4	2096	5	BC044459	BC044459 Danio rer
527	24	2.4	1369	8	AF399920	AF399920 Camellia	600	24	2.4	2098	9	AF060866	AF060866 Homo sapi
528	24	2.4	1397	5	BC054127	BC054127 Danio rer	601	24	2.4	2099	10	AY195875	AY195875 Mus muscu
529	24	2.4	1398	8	BT009141	BT009141 Triticum	602	24	2.4	2099	10	BC023090	BC023090 Mus muscu
530	24	2.4	1407	3	AY069115	AY069115 Drosophi	603	24	2.4	2111	9	BC003160	BC003160 Homo sapi
531	24	2.4	1409	9	BC031002	BC031002 Homo sapi	604	24	2.4	2125	6	I08142	I08142 Sequence 3
532	24	2.4	1430	6	BD234682	BD234682 TNF-assoc	605	24	2.4	2125	6	I09588	I09588 Sequence 7
533	24	2.4	1430	6	AR224049	AR224049 Sequence	606	24	2.4	2137	9	BC033678	BC033678 Homo sapi
534	24	2.4	1439	6	AR403758	AR403758 Sequence	607	24	2.4	2168	10	BC057992	BC057992 Mus muscu
535	24	2.4	1448	10	BC052344	BC052344 Mus muscu	608	24	2.4	2174	3	AK116693	AK116693 Clona int
536	24	2.4	1462	9	AK024565	AK024565 Homo sapi	609	24	2.4	2179	10	MMTNFRES	X57796 Mouse mrna
537	24	2.4	1465	9	BC008042	BC008042 Homo sapi	610	24	2.4	2180	9	AF106697	AF106697 Homo sapi
538	24	2.4	1478	9	BC011645	BC011645 Homo sapi	611	24	2.4	2183	6	AK027227	AK027227 Homo sapi
539	24	2.4	1488	6	MTY10268	Y10268 M. truncatul	612	24	2.4	2185	6	BD249339	BD249339 50 human
540	24	2.4	1507	6	AR225245	AR225245 Sequence	613	24	2.4	2187	6	AR207293	AR207293 Sequence
541	24	2.4	1525	10	BC037042	BC037042 Mus muscu	614	24	2.4	2203	3	BD107867	BD107867 36 human
542	24	2.4	1536	10	BC011182	BC011182 Mus muscu	615	24	2.4	2209	3	AK114265	AK114265 Clona int
543	24	2.4	1547	9	BC014022	BC014022 Homo sapi	616	24	2.4	2211	9	BC007443	BC007443 Homo sapi
544	24	2.4	1549	9	BSM080772	BX648621 Homo sapi	617	24	2.4	2217	6	AX827866	AX827866 Sequence
545	24	2.4	1550	5	BC059596	BC059596 Danio rer	618	24	2.4	2217	10	RNPOLIC	X70369 R.norvegicu
546	24	2.4	1562	8	BT0095156	AJ295156 Phragmite	619	24	2.4	2234	8	AF013979	AF013979 Oryza sat
547	24	2.4	1565	8	BT009560	BT009560 Triticum	620	24	2.4	2236	9	BC003633	BC003633 Homo sapi
548	24	2.4	1573	9	BC015481	BC015481 Homo sapi	621	24	2.4	2251	10	BC030879	BC030879 Mus muscu
549	24	2.4	1579	5	BC050174	BC050174 Danio rer	622	24	2.4	2253	9	HSN803406	AL832039 Homo sapi
550	24	2.4	1582	9	BC009933	BC009933 Homo sapi	623	24	2.4	2266	9	AB070028	AB070028 Macaca fa
551	24	2.4	1585	5	BC064156	BC064156 Silurana	624	24	2.4	2268	6	AX590640	AX590640 Sequence
552	24	2.4	1588	6	AE2526	AE2526 Sequence 31	625	24	2.4	2341	3	BC036723	BC036723 Homo sapi
553	24	2.4	1588	9	AF038172	AF038172 Homo sapi	626	24	2.4	2352	3	AF193553	AF193553 Drosophi
554	24	2.4	1600	9	BC035597	BC035597 Homo sapi	627	24	2.4	2353	9	HSN801942	BC060036 Mus muscu
555	24	2.4	1616	3	AF207536	AF207536 Drosophi	628	24	2.4	2365	10	BC060036	BC064418 Homo sapi
556	24	2.4	1619	9	BC018671	BC018671 Homo sapi	629	24	2.4	2421	9	BC064418	BC064418 Homo sapi
557	24	2.4	1624	6	AR165164	AR165164 Sequence	630	24	2.4	2421	10	BC061106	BC061106 Mus muscu
558	24	2.4	1631	10	AF333243	AF333243 Rattus no	631	24	2.4	2432	8	AF080436	AF080436 Oryza sat
559	24	2.4	1631	10	AY233297	AY233297 Mus muscu	632	24	2.4	2448	9	HSN801408	AL133551 Homo sapi
560	24	2.4	1646	9	AF035287	AF035287 Homo sapi	633	24	2.4	2459	10	AF187876	AF187876 Cavia por
561	24	2.4	1660	8	AY376878	AY376878 Malus x d	634	24	2.4	2463	9	BC020957	BC020957 Homo sapi
562	24	2.4	1663	8	AF058763	AF058763 Zea mays	635	24	2.4	2480	6	AX128511	AX128511 Sequence
563	24	2.4	1689	4	FCAN916	AF009816 Felis cat	636	24	2.4	2501	9	BC000285	BC000285 Homo sapi
564	24	2.4	1702	6	AF073668	AF073668 Sequence	637	24	2.4	2508	5	AY204552	AY204552 Xenopus l
565	24	2.4	1731	8	AF408700	AF408700 Solanum t	638	24	2.4	2528	10	BC023296	BC023296 Mus muscu
566	24	2.4	1733	8	AF035252	AF035252 Glycine m	639	24	2.4	2546	9	PPY16568	Y16668 Papio papio
567	24	2.4	1734	6	AR175261	AR175261 Sequence	640	24	2.4	2554	9	BC051855	BC051855 Homo sapi
568	24	2.4	1750	9	AF175767	AF175767 Homo sapi	641	24	2.4	2627	10	BC024887	BC024887 Mus muscu
569	24	2.4	1755	8	D86591	D86591 Arabidopsis	642	24	2.4	2639	9	BC014109	BC014109 Homo sapi
570	24	2.4	1757	9	BC002336	BC002336 Homo sapi	643	24	2.4	2654	3	DDIDG17A	M18106 Dictyostell
571	24	2.4	1760	6	BD275033	BD275033 50 Human	644	24	2.4	2700	6	AX794710	AX794710 Sequence
572	24	2.4	1776	5	BC055206	BC055206 Danio rer	645	24	2.4	2724	10	BC043057	BC043057 Mus muscu
573	24	2.4	1791	3	PX489522	AJ489522 Plutella	646	24	2.4	2731	9	BC007275	BC007275 Homo sapi
574	24	2.4	1817	10	BC051174	BC051174 Mus muscu	647	24	2.4	2768	9	HSN804810	AL136842 Homo sapi
575	24	2.4	1843	9	BC021164	BC021164 Homo sapi	648	24	2.4	2775	5	PAFROAT	Z97028 Pseudopleur
576	24	2.4	1865	10	BC018252	BC018252 Mus muscu	649	24	2.4	2775	10	AB041607	AB041607 Mus muscu

650	24	2.4	2827	3	TSP005937	AJ005937	Tealia sp	723	24	2.4	69562	2	AC101403	AC101403 Mus muscu
651	24	2.4	2857	10	BC031847	BC031847	Mus muscu	724	24	2.4	70571	2	AC145071	AC145071 Mus muscu
652	24	2.4	2873	10	BC052412	BC052412	Mus muscu	725	24	2.4	72957	2	AC025304	AC025304 Homo sapi
653	24	2.4	2899	9	AB050256	AB050256	Macaca fa	726	24	2.4	73575	10	AL645766	AL645766 Mouse DNA
654	24	2.4	2924	10	AF498039	AF498039	Rattus no	727	24	2.4	74841	10	AL806529	AL806529 Mouse DNA
655	24	2.4	3012	10	AF293383	AF293383	Rattus no	728	24	2.4	76506	9	AL162588	AL162588 Human DNA
656	24	2.4	3120	10	AB078879	AB078879	Rattus no	729	24	2.4	78756	2	PFMAL6P1_13	Continuation (14 o
657	24	2.4	3213	8	BD192218	BD192218	Secreted	730	24	2.4	80019	8	ATF25E4	Continuation (14 o
658	24	2.4	3314	8	AB110951	AB110951	Delphinu	731	24	2.4	80725	9	AL137078	AL137078 Human DNA
659	24	2.4	3334	3	AY254474	AY254474	Dictyoste	732	24	2.4	83395	2	AC087137	AC087137 Mus muscu
660	24	2.4	3379	10	BC031531	BC031531	Mus muscu	733	24	2.4	83985	2	AC115684	AC115684 Dictyoste
661	24	2.4	3392	9	BC006541	BC006541	Homo sapi	734	24	2.4	84550	3	PFMAL1P2_3	Continuation (4 of
662	24	2.4	3409	10	BC036148	BC036148	Mus muscu	735	24	2.4	84554	8	AC123571	AC123571 Medicago
663	24	2.4	3452	8	AF369909	AF369909	Arabidops	736	24	2.4	84816	5	BX324216	BX324216 Zebrafish
664	24	2.4	3465	10	BC042443	BC042443	Mus muscu	737	24	2.4	85916	3	AC117080	AC117080 Dictyoste
665	24	2.4	3493	10	BC053711	BC053711	Mus muscu	738	24	2.4	88811	9	AC018401	AC018401 Homo sapi
666	24	2.4	3520	9	HSM801234	HSM801234	Homo sapi	739	24	2.4	89345	2	AC002490	AC002490 Homo sapi
667	24	2.4	3634	9	BC040239	BC040239	Homo sapi	740	24	2.4	89347	2	AP005463	AP005463 Oryza sat
668	24	2.4	3666	9	HSM805473	HSM805473	Homo sapi	741	24	2.4	90220	9	HSJ734P14	AL140548 Medicago
669	24	2.4	3916	9	HSM802253	HSM802253	Homo sapi	742	24	2.4	90587	2	AC140671	AC140671 Medicago
670	24	2.4	3919	9	HSEGL1	VO0508	Human gene	743	24	2.4	91927	9	AC004771	AC004771 Homo sapi
671	24	2.4	3967	10	BC028248	BC028248	Mus muscu	744	24	2.4	94510	9	HS390B3	Z33096 Human DNA s
672	24	2.4	4042	9	AF087142	AF087142	Homo sapi	745	24	2.4	96433	3	DMEN519	AF2225900
673	24	2.4	4044	3	AY118635	AY118635	Drosophil	746	24	2.4	101002	3	AY216936	AY216936 Plasmodi
674	24	2.4	4074	6	AX305897	AX305897	Sequence	747	24	2.4	101095	3	AY216937	AY216937 Plasmodi
675	24	2.4	4074	10	MUSGABX	M92378	Mus muscu	748	24	2.4	101158	3	AY216938	AY216938 Plasmodi
676	24	2.4	4169	10	BC059080	BC059080	Mus muscu	749	24	2.4	101167	9	HS32F7	AL009173 Human DNA
677	24	2.4	4174	8	BT004118	BT004118	Arabidops	750	24	2.4	101884	8	AC142224	AC142224 Medicago
678	24	2.4	4230	3	AF465310	AF465310	Dictyoste	751	24	2.4	103576	8	YUP8H12	AC000098 Arabidops
679	24	2.4	4254	5	CHKESTP20	D82364	Gallus gall	752	24	2.4	106260	9	AC005477	AC005477 Homo sapi
680	24	2.4	4297	9	EC038505	EC038505	Homo sapi	753	24	2.4	106267	2	AP000749	AP000749 Homo sapi
681	24	2.4	4443	10	BC049788	BC049788	Mus muscu	754	24	2.4	107650	9	AC108677	AC108677 Homo sapi
682	24	2.4	4476	9	BC063501	BC063501	Homo sapi	755	24	2.4	108028	8	AC135233	AC135233 Medicago
683	24	2.4	4662	10	BC060645	BC060645	Mus muscu	756	24	2.4	108240	2	AC146584	AC146584 Medicago
684	24	2.4	4724	9	HSM808698	HSM808698	Homo sapi	757	24	2.4	110000	9	HS523G1	AL034375 Human DNA
685	24	2.4	4778	10	BC043089	BC043089	Mus muscu	758	24	2.4	110000	2	AC091449_1	Continuation (2 of
686	24	2.4	4812	10	BC058724	BC058724	Mus muscu	759	24	2.4	110000	2	AC096457_0	AC096457 Rattus no
687	24	2.4	4842	8	AF424549	AF424549	Oryza sat	760	24	2.4	110000	2	AC096457_1	Continuation (2 of
688	24	2.4	4988	10	BC051169	BC051169	Mus muscu	761	24	2.4	110000	2	AC102983_1	Continuation (3 of
689	24	2.4	5071	10	BC052464	BC052464	Mus muscu	762	24	2.4	110000	2	AC108583_2	Continuation (3 of
690	24	2.4	5231	10	BC048170	BC048170	Mus muscu	763	24	2.4	110000	2	AC120752_2	Continuation (3 of
691	24	2.4	5361	10	BC048170	BC048170	Mus muscu	764	24	2.4	110000	2	AC123221_0	Continuation (3 of
692	24	2.4	5686	9	HSM808430	HSM808430	Mus muscu	765	24	2.4	110000	2	AL845451_0	AL845451 Mus muscu
693	24	2.4	6372	3	DDICNPA	Y23449	Dictyoselin	766	24	2.4	110000	2	BX510910_2	Continuation (3 of
694	24	2.4	6582	6	AX481755	AX481755	Sequence	767	24	2.4	110000	2	PFMAL13_09	Continuation (10 o
695	24	2.4	7860	9	HSM809154	HSM809154	Homo sapi	768	24	2.4	110000	2	PFMAL13_25	Continuation (26 o
696	24	2.4	8069	2	AC087223	AC087223	Homo sapi	769	24	2.4	110000	2	PFMAL13_26	Continuation (27 o
697	24	2.4	9751	3	AF465309	AF465309	Dictyoste	770	24	2.4	110000	2	PFMAL7P1_09	Continuation (10 o
698	24	2.4	10131	9	AB035192	AB035192	Homo sapi	771	24	2.4	110000	2	PFMAL7P1_08	Continuation (9 of
699	24	2.4	10583	5	AB040746	AB040746	Carassius	772	24	2.4	110000	2	PFMAL8P1_03	Continuation (4 of
700	24	2.4	11829	3	AE001376	AE001376	Plasmodi	773	24	2.4	110000	2	PFMAL8P1_05	Continuation (6 of
701	24	2.4	14855	10	AF187875	AF187875	Cavia por	774	24	2.4	110000	2	PFMAL8P1_07	Continuation (8 of
702	24	2.4	17839	3	AE001384	AE001384	Plasmodi	775	24	2.4	110000	2	PFMAL8P1_09	Continuation (10 o
703	24	2.4	18011	6	AX344936	AX344936	Sequence	776	24	2.4	110000	2	PFMAL13_26	Continuation (27 o
704	24	2.4	25994	4	AL722600	AL722600	Human DNA	777	24	2.4	110000	2	PFMAL7P1_08	Continuation (9 of
705	24	2.4	32256	2	AL513169	AL513169	Homo sapi	778	24	2.4	110000	2	PFMAL8P1_03	Continuation (4 of
706	24	2.4	33270	3	AC116921	AC116921	Dictyoste	779	24	2.4	110000	2	PFMAL8P1_05	Continuation (6 of
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708	24	2.4	36506	2	AC013220	AC013220	Drosophil	781	24	2.4	110000	10	AE008684_0	AE008684 Mus muscu
709	24	2.4	39459	2	AC018136	AC018136	Drosophil	782	24	2.4	110000	2	AC135465	AC135465 Medicago
710	24	2.4	44948	10	BS71769	BS71769	Mouse DNA	783	24	2.4	110000	3	AC115612	AC115612 Dictyoste
711	24	2.4	46441	9	AP003388	AP003388	Homo sapi	784	24	2.4	111882	2	AC073598	AC073598 Homo sapi
712	24	2.4	47736	3	AC004353	AC004353	Drosophil	785	24	2.4	112389	2	AC141825	AC141825 Apis mell
713	24	2.4	48500	10	AL772259	AL772259	Mouse DNA	786	24	2.4	112513	2	AC121243	AC121243 Medicago
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721	24	2.4	68456	10	BS324191	BS324191	Mouse DNA	794	24	2.4	119774	10	AL44340	AL44340 Medicago
722	24	2.4	68952	2	AC101387	AC101387	Mus muscu	795	24	2.4	120125	2	AL844545	AL844545 Mouse DNA
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C 799	24	2.4	124169	2	AC146752	AC146752 Medicago	872	24	2.4	154273	10	AC127577	AC127577 Mus muscu
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C 805	24	2.4	126122	2	AC144187	AC144187 Macaca mu	878	24	2.4	156461	2	AC027693	AC027693 Homo sapi
806	24	2.4	128503	9	AC090907	AC090907 Homo sapi	C 879	24	2.4	156630	2	AC027693	AC027693 Homo sapi
807	24	2.4	129039	10	AL808113	AL808113 Mouse DNA	880	24	2.4	157167	2	AC118616	AC118616 Mus muscu
C 808	24	2.4	129169	2	AC032038	AC032038 Homo sapi	881	24	2.4	157310	2	AC118616	AC118616 Mus muscu
C 809	24	2.4	129263	9	AL360089	AL360089 Human DNA	882	24	2.4	157350	2	AC118616	AC118616 Mus muscu
C 810	24	2.4	129285	5	AC091726	AC091726 Gallus ga	883	24	2.4	157535	2	AC118616	AC118616 Mus muscu
811	24	2.4	129412	2	AC119892	AC119892 Mus muscu	C 884	24	2.4	157583	9	AC021607	AC021607 Homo sapi
C 812	24	2.4	129490	10	AC005402	AC005402 Mus muscu	885	24	2.4	157502	2	AC145842	AC145842 Papio anu
C 813	24	2.4	129573	9	AC015564	AC015564 Homo sapi	886	24	2.4	157701	2	AC058814	AC058814 Homo sapi
C 814	24	2.4	133400	2	AC134521	AC134521 Medicago	C 887	24	2.4	157860	9	AL391241	AL391241 Human DNA
C 815	24	2.4	133971	2	AC138464	AC138464 Medicago	888	24	2.4	158186	2	BX890603	BX890603 Danio rer
816	24	2.4	134680	9	AC015726	AC015726 Homo sapi	889	24	2.4	158202	2	AC119414	AC119414 Medicago
817	24	2.4	135658	8	AC141863	AC141863 Medicago	C 890	24	2.4	158434	2	AC145373	AC145373 Mus muscu
818	24	2.4	135698	2	AL365218	AL365218 Homo sapi	891	24	2.4	158438	9	AC068757	AC068757 Homo sapi
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822	24	2.4	136445	2	AC102346	AC102346 Mus muscu	895	24	2.4	159114	2	AC132246	AC132246 Mus muscu
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C 827	24	2.4	139342	2	AC121095	AC121095 Mus muscu	900	24	2.4	160586	2	AC126319	AC126319 Mus muscu
C 828	24	2.4	140771	10	AL591611	AL591611 Mouse DNA	C 901	24	2.4	160764	9	AC107928	AC107928 Homo sapi
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836	24	2.4	144354	10	AC132102	AC132102 Mus muscu	909	24	2.4	161976	2	AC012415	AC012415 Homo sapi
C 837	24	2.4	144666	9	AL160287	AL160287 Human DNA	C 910	24	2.4	162045	10	AC125452	AC125452 Mus muscu
C 838	24	2.4	145215	2	AC102891	AC102891 Mus muscu	C 911	24	2.4	162215	9	AC004896	AC004896 Homo sapi
839	24	2.4	145391	2	AC131186	AC131186 Mus muscu	C 912	24	2.4	162242	2	AC090803	AC090803 Homo sapi
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C 846	24	2.4	147712	2	AC117939	AC117939 Caris fam	C 919	24	2.4	163926	5	BX000481	BX000481 Zebrafish
C 847	24	2.4	148230	2	AC141548	AC141548 Rattus no	C 920	24	2.4	164018	2	AC074242	AC074242 Homo sapi
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C 849	24	2.4	148930	9	AC073316	AC073316 Homo sapi	C 922	24	2.4	164470	9	AC012346	AC012346 Homo sapi
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## ALIGNMENTS

RESULT 1  
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 LOCUS Malus domestica mRNA for B-type MADS box protein (mads13 gene).  
 DEFINITION AJ251116 1102 bp mRNA linear PLN 16-NOV-2001  
 ACCESSION AJ251116  
 VERSION AJ251116.1 GI:16973293  
 KEYWORDS B-type MADS box protein; mads13 gene.  
 SOURCE Malus x domestica (apple tree)  
 ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 1  
 Vosman,B. and Smulders,M.J.M.  
 Isolation of apple B- and C-type MADS box genes from vegetative  
 tissue  
 Unpublished  
 2 (bases 1 to 1102)  
 van der Linden,C.G.  
 Direct Submission  
 Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic  
 Diversity, CPRO Wageningen University & Research Centre, PO Box 16,  
 Wageningen, 6700 AA, NETHERLANDS  
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 LGSSITLHLRLA"  
 ORIGIN  
 Query Match 81.6%; Score 801; DB 8; Length 1102;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 951; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 QY 70 AGAAGAAATGGATCTTCAAGAGGCTCAGAGCTACCGTTCTCTGTGTGACCAAGTC 129  
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 QY 190 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249  
 DB 260 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319  
 QY 250 GAGAGTCGATGAAGACACCTGTGGAAGTCAAGAGATCAACATAGCTGAGGAGA 309  
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 DB 500 AAAAATCAGAGGAGACCAACCAAGAGAGAGTTTGAAGAACTTGAGCAAAAGAGAGAAAC 559

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## gene

## CDS

490 ATGCTGATGCTATTTTTCAGGAGAGCAGCGGAGGATCCACAGTATGCTTATGAG 549  
560 ATGCTGATGCTATTTTTCAGGAGAGCAGCGGAGGATCCACAGTATGCTTATGAG 619  
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680 ACTTTCCACCTCCACACCTTACCTCCACAGGAGGAGTCTCGCTCGGCTCCTCCATT 739  
670 ACTCATCTGCAAGATCTCCGCTTGTGATCGTGTGATCTGAGATGATTAATCATCACT 729  
740 ACTCATCTGCAAGATCTCCGCTTGTGATCGTGTGATCTGAGATGATTAATCATCACT 799  
730 AAGTTATATATTAAGTCACTTAACTGCTTTTCTAAAGTGTGCTTGTGCTGACTA 789  
800 AAGTTATATATTAAGTCACTTAACTGCTTTTCTAAAGTGTGCTTGTGCTGACTA 859  
790 TCTTTAGGCAAGGATGAGCTTGGACTTACCTCTGAAAAACAGATGCATAAATGTGTGT 849  
860 TCTTTAGGCAAGGATGAGCTTGGACTTACCTCTGAAAAACAGATGCATAAATGTGTGT 919  
850 GGTGTTTAAATCAATGATAGCACTAAAAAATCCGCGCCCTTGTGCTTGTGCTTGTGT 909  
920 GGTGTTTAAATCAATGATAGCACTAAAAAATCCGCGCCCTTGTGCTTGTGCTTGTGT 979  
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980 TGTATATTAATCTTCTATCTATATATATATATATATATATATATATATATATATATAT 1033

RESULT 2  
AB081094  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AB081094  
Malus x domestica MdMADS13 mRNA for MADS-box protein, partial cds.  
AB081094  
AB081094.1 GI:22775409

Malus x domestica (apple tree)  
Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE  
1  
Matsumoto, S., Ohtsubo, T. and Soejima, J.  
Cloning and sequencing of apple MADS-box genes 'MdPI', 'MdTM6' and

Unpublished  
Ohtsubo, T. and Matsumoto, S.  
2 (bases 1 to 473)

Direct Submission  
Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,  
Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,  
Gifu 501-1193, Japan (E-mail: shmatsum@cc.gifu-u.ac.jp,  
Tel: 81-58-293-2257, Fax: 81-58-293-2207)

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
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Location/Qualifiers  
1. .473  
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/mol\_type="mRNA"  
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/tissue\_type="young floral parts"

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gene

CDS

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Best Local Similarity 99.5%; Pzed No. 2, 1e-179;  
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 470 TGGAGCAAGAGAGAAACATGTCATGCTATTTTGAACAGGAGCGCGGAGG 529  
DB 12 TGGAGCAAGAGAGAAACATGTCATGCTATTTTGAACAGGAGCGCGGAGG 71  
QY 530 ATCCACAGTATGTTATGAGGCAATGAGGAGACTACGAATCTGCATTGCTCA 589  
DB 72 ATCCACAGTATGTTATGAGGCAATGAGGAGACTACGAATCTGCATTGCTCA 131  
QY 590 ATGGGCGGAATAAATGTCACCTTTCCACCTCCACCCCTAACTCCACACGAGAA 649  
DB 132 ATGGGCGGAATAAATGTCACCTTTCCACCTCCACCCCTAACTCCACACGAGAA 191  
QY 650 GTCGCTCGGCTCCCTCATTACTCATCTGCAGACTCCGCTTGTGATCGTATCG 709  
DB 192 GTTCGCTCGGCTCCCTCATTACTCATCTGCAGACTCCGCTTGTGATCGTATCG 251  
QY 710 AGATATGATTAATCATCACTAAGTTATATATATTAAGGTCACTTAACTGCTT 769  
DB 252 AGATATGATTAATCATCACTAAGTTATATATATTAAGGTCACTTAACTGCTT 311  
QY 770 AAGTGTTCCTTGGTGACTATCTTTAGCAAGAGTAGACTTGGACTACCTCTGAA 829  
DB 312 AAGTGTTCCTTGGTGACTATCTTTAGCAAGAGTAGACTTGGACTACCTCTGAA 371  
QY 830 AGATGATTAATGATGCTGCTGTTTAACTCAATGATAGCACTAAAAAATCCGCGCC 889  
DB 372 AGATGATTAATGATGCTGCTGTTTAACTCAATGATAGCACTAAAAAATCCGCGCC 431  
QY 890 TTGTTGCTTGTGGGTTTGT 908  
DB 432 TTGTTGCTTGTGGGTTTGT 450

## RESULT 3

## AB081093

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

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## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL







Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 953 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 982  
|||||  
Db 5690 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 5719

RESULT 6  
AL935278/c  
LOCUS  
DEFINITION Mouse DNA sequence from clone RP23-84E1 on chromosome 2, complete  
sequence.  
ACCESSION AL935278  
VERSION AL935278.7 GI:27652829  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE 1 (bases 1 to 183353)  
JOURNAL Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Phillimore, B.  
Direct Submission  
Submitted (09-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT  
On Jan 11, 2003 this sequence version replaced gi:27497292.  
Sequence from the Mouse Genome Sequencing Consortium whole genome  
shotgun may have been used to confirm this sequence. Sequence data  
from the whole genome shotgun alone has only been used where it has  
a phred quality of at least 30.

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)  
-----

During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest, except on the rare  
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information  
on the WormPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-84E1 is  
from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.  
For further details see <http://www.chori.org/bacpac/home.htm>  
VECTOR: pBAC3.6.

Location/Qualifiers  
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1. 183353  
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Best Local Similarity 100.0%; Pred. No. 4.8e-05;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 953 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 982  
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Db 166463 TGCCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 166434

RESULT 7  
NTA319873  
LOCUS  
DEFINITION Nicotiana tabacum mRNA for carbamoyl phosphate synthase small  
subunit.  
ACCESSION AJ319873  
VERSION AJ319873.1 GI:21535792  
KEYWORDS carbamoyl phosphate synthase small subunit.  
SOURCE Nicotiana tabacum (common tobacco)  
ORGANISM Nicotiana tabacum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE  
AUTHORS Zrenner, R., Schroeder, M. and Giermann, N.  
TITLE Molecular analysis of de novo pyrimidine synthesis in plants  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1698)  
AUTHORS Zrenner, R.  
TITLE Direct Submission  
JOURNAL Submitted (19-JUN-2001) Zrenner R., Ruprecht-Karls-Universitaet  
Heidelberg, Botanisches Institut, INF 360, 69120 Heidelberg,  
GERMANY

Location/Qualifiers  
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ASSETLMKPDGVLFGPDPSAFAVAVKELIGKIPFGICMGHQLLQALGGKT  
FPMKFGHGGNHVRLNRGCVETSAQNEHVAVDPEISUPGVETVHNLNDGSCAGLA  
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Query Match 3.0%; Score 29; DB 8; Length 1698;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN  
QY 954 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 982  
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Db 1670 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 1698

RESULT 8  
ATHPRPHA  
LOCUS  
DEFINITION Arabidopsis thaliana protein phosphatase mRNA, complete cds.  
ACCESSION M96732  
VERSION M96732.1 GI:166820  
KEYWORDS protein phosphatase.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

REFERENCE
AUTHORS    1 (bases 1 to 1256)
            Arino,J., Perez-Callejon,E., Cunillera,N., Camps,M., Posas,F. and
            Ferrer,A.
TITLE      Protein phosphatases in higher plants: multiplicity of type 2A
JOURNAL    Plant Mol. Biol. 21 (3), 475-485 (1993)
MEDLINE    93184204
PUBMED     8382968
COMMENT    Original source text: Arabidopsis thaliana (library: lambda GT10)
            young adult in flowering stage whole plant (including root) cDNA to
            mRNA.
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Query Match      2.9%; Score 28; DB 8; Length 1256;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAAA 982
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Db 1192 CTTTGTGATAAAAAAAAAAAAAAAAAAAAAA 1219

RESULT 9
LOCUS      ATRXR1GE 1410 bp mRNA linear PLN 15-NOV-1996
DEFINITION A.thaliana mRNA for peroxidase, prxr1.
ACCESSION  X98313
VERSION     X98313.1 GI:1402903
KEYWORDS   peroxidase; prxr1 gene.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1
AUTHORS    Capelli,N., Tognolli,M., Flach,J., Overney,S., Penel,C., Greppin,H.
            and Simon,P.
TITLE      Eleven cDNA clones from Arabidopsis thaliana encoding
            isoperoxidases (Accession Nos. X98313, X98314, X98315, X98316,
            X98317, X98318, X98319, X98320, X98321, X98322, and X98323)
JOURNAL    Plant Physiol. 112, 446-446 (1996)
REFERENCE  2 (bases 1 to 1410)
AUTHORS    Simon,P.
TITLE      Direct Submission
JOURNAL    Submitted (05-JUN-1996) P. Simon, Laboratory of Plant Biochemistry
            and Physiology, University of Geneva, Place de l'Universite 3,
            CH-1211 Geneva 4, SWITZERLAND
COMMENT    Ref [1]: Plant Gene Register PCR96-066 (1996).
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Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAAA 982
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Db 1376 CTTTGTGATAAAAAAAAAAAAAAAAAAAAAA 1403

RESULT 10
LOCUS      BX897675 68291 bp DNA linear PLN 16-DEC-2003
DEFINITION Neurospora crassa DNA linkage group IV BAC clone B2E7.
ACCESSION  BX897675
VERSION     BX897675.1 GI:39979158
KEYWORDS
SOURCE      Neurospora crassa
            Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE  1
AUTHORS    Schulte,U., Aign,V., Hoheisel,J., Brandt,P., Partmann,B.,
            Holland,R., Nyakatura,G., Mewes,H.W. and Mannhaupt,G.
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 68291)
AUTHORS    German Neurospora genome project.
TITLE      Direct Submission
JOURNAL    Submitted (16-DEC-2003) MIPS, Institut fuer Bioinformatik,
            GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH,
            Ingolstaedter Landstrasse 1, D-85764 Neuherberg, FRG, E-mail:
            G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute
            of Biochemistry, Heinrich-Heine-University, D-40225 Duesseldorf,
            E-mail: ulrich-schulte@uni-duesseldorf.de
COMMENT    BAC clone 2E7 (strain OR74A) is available at the Fungal Genetic
            Stock Center, http://www.fgsc.net
            Sequencing was performed by MWG Biotech AG, Ebersberg, Germany,
            http://www.mwgna.com
            Information on performance of analysis and a more detailed
            annotation of this entry and other sequences can be viewed at:
            http://mips.gsf.de/proj/neurospora.
FEATURES   Location/Qualifiers

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contains EST gb:AA901916"
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to a frameshift"
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FREITRIDEAKRRVMVQIASLSLAETVYAVGNIGYQIESAKSARFRIRAKQEN
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/number=2
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/number=4
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/number=5
intron
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/gene="B2E7.050"
/note="similarity to hcnp protein, homo sapiens,
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SAGETAVKIWRMYQVHPDEADFIELVAVGLYTEAVHKYIEILNPRFTSKSKG
HYELSMVDLLVEHATVETGHTIDVERIIRSGIERFADQKGLWGLATYWR
GSPERADVEEGITVTMTVTRDTLVFDSYTEFEEIIISALMEMASTRAEKGEVDEVA
DFDLDIRMFELHMDRRPFLNDVLLRQNNVTEWKRVALGWDGNKEEVKVTYLD
Query Match 2.9%; Score 28; DB 8; Length 68291;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982
Db 41495 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 41468

RESULT 11
AC099530/c
LOCUS
DEFINITION Felis catus clone RP86-587N8, WORKING DRAFT SEQUENCE, 6 ordered
pieces.
AC099530
VERSION AC099530.2 GI:21070684
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Felis catus (cat)
ORGANISM Felis catus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 143793)
AUTHORS Akhtar,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
Lee-Lin,S.-O., Legaspi,R., Maduro,O.L., Maduro,V.B.,
Margulies,E.H., Magiello,C., Maskeri,B., Masrion,S.D.,
McCloskey,J.C., McDowell,J., Paquirigan,C., Pearson,R.,
Portnoy,M.E., Prasad,A., Schueler,M.G., Stantropop,S., Thomas,J.W.,
Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
REFERENCE 2 (bases 1 to 143793)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 143793)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2002) NIH Intramural Sequencing Center, 8717
Government Circle, Gaithersburg, MD 20877, USA
COMMENT On May 22, 2002 this sequence version replaced gi:16930953.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8x average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142585 bases at least Q40
Consensus quality: 143084 bases at least Q30
Consensus quality: 143214 bases at least Q20
Insert size: 131000; agarose-fp
Insert size: 143293; sum-of-contigs
Quality coverage: 11.48x in Q20 bases; agarose-fp
Quality coverage: 10.50x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 23243: contig of 23243 bp in length
* 23244 23344: gap of unknown length
* 23344 23444: contig of 33956 bp in length
* 57300 57399: gap of unknown length
* 57400 63014: contig of 11615 bp in length
* 69015 69114: gap of unknown length
* 69115 92456: contig of 23342 bp in length
* 92457 92557: gap of unknown length
* 92557 127282: contig of 34726 bp in length
* 127283 127383: gap of unknown length
* 127383 143793: contig of 16411 bp in length.
FEATURES
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127383..143793
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59677..142793
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/note="assembly_fragment"
92557..127282
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127383..143793

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Web site: <http://www.nisc.nih.gov>  
Contact: [nisc.zoo@nhgri.nih.gov](mailto:nisc.zoo@nhgri.nih.gov)  
----- Project Information  
Center project name: cox  
Center clone name: 587N08

/note="assembly\_fragment  
clone end:T7  
vector\_side::right"

## ORIGIN

Query Match 2.9%; Score 28; DB 2; Length 143793;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 955 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 982  
Db 142930 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 142803

## RESULT 12

AC141671  
LOCUS  
DEFINITION Apis mellifera clone CH224-54J9, WORKING DRAFT SEQUENCE, 16 linear HTG 19-MAR-2003  
unordered pieces.  
AC141671  
ACCESSION  
VERSION AC141671.1 GI:29123855  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.  
SOURCE Apis mellifera (honeybee)  
ORGANISM Apis mellifera

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Apoidea;  
Apidae; Apis.

## REFERENCE

1 (Bases 1 to 153829)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,  
Albrooks,S.L., Amarantunga,H.C., Are,J.R., Ayale,M., Banks,T.,  
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,  
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,  
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,  
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,  
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,  
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,  
Davila,M.L., Davis,C., Davy-Carroll,L., Dedrich,D.A.,  
Delaney,K.R., Delgado,O., Denu,A.L., Ding,Y., Dinh,H.H.,  
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,  
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,  
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,  
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,  
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,  
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,  
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Karissom,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,  
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulesged,H.,  
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,  
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,  
Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzger,M.,  
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,  
Mosier,N., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,  
Nguyen,N., Nickerson,E., Nwokwuo,S., Ogih,M., Okwuon,G.,  
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,  
Peters,L., Pickens,R., Pimus,E., Pu,L.L., Quiles,M., Ren,Y.,  
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savory,G.,  
Scherz,S., Scott,G., Shen,H., Shoohtari,N., Sisson,I.,  
Sodergren,E., Sonake,T., Sparks,A., Stanley,H., Stone,H.,  
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,  
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,  
Usmani,K., Vasquez,L., Vera,V., Villalob,D., Vinson,R., Wang,Q.,  
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,  
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,  
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.

## TITLE

## JOURNAL

REFERENCE 2 (bases 1 to 153829)

## AUTHORS

Worley,K.C.

Direct Submission

## ORIGIN

Query Match

Best Local Similarity

Matches 28; Conservative

0; Mismatches 0; Indels 0; Gaps 0;

## JOURNAL

## COMMENT

Submitted (19-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: AMHN  
Center clone name: CH224-54J9  
----- Summary Statistics  
Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 150922 bases at least Q40  
Consensus quality: 153311 bases at least Q30  
Consensus quality: 154733 bases at least Q20  
Estimated insert size: 150440; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
-----

\* NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1562: contig of 1562 bp in length  
\* 1563 1862: gap of unknown length  
\* 1663 3097: contig of 1435 bp in length  
\* 3098 3197: gap of unknown length  
\* 3198 4577: contig of 1380 bp in length  
\* 4578 4677: gap of unknown length  
\* 4679 6570: contig of 1893 bp in length  
\* 6571 6570: gap of unknown length  
\* 6671 9507: contig of 2737 bp in length  
\* 9408 9507: gap of unknown length  
\* 9508 14372: contig of 4865 bp in length  
\* 14373 14472: gap of unknown length  
\* 14473 19971: contig of 5499 bp in length  
\* 19972 26452: contig of 6381 bp in length  
\* 26453 26552: gap of unknown length  
\* 26553 34156: contig of 7604 bp in length  
\* 34157 34256: gap of unknown length  
\* 34257 45438: contig of 11182 bp in length  
\* 45439 45538: gap of unknown length  
\* 45539 58764: contig of 13126 bp in length  
\* 58765 58764: gap of unknown length  
\* 58765 70784: contig of 12020 bp in length  
\* 70785 70884: gap of unknown length  
\* 70885 84627: contig of 13743 bp in length  
\* 84628 84727: gap of unknown length  
\* 84728 98840: contig of 14113 bp in length  
\* 98841 121942: contig of 23002 bp in length  
\* 121943 122043: gap of unknown length  
\* 122043 153829: contig of 31787 bp in length.

## FEATURES

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/organism="Apis mellifera"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7460"  
/clone="CH224-54J9"

Qy 955 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 982  
Db 35497 CTTTGTGATAAAAAAAAAAAAAAAAAAAAA 35524

RESULT 13  
AC129127/c  
LOCUS Rattus norvegicus clone CH230-276B18, WORKING DRAFT SEQUENCE.  
AC129127.3 GI:25072705  
VERSION HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULTOP.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 174010)  
AUTHORS Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biwalto,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabis,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M., Hollins,B., Howells,S., Hulvik,S., Hume,J., Idlebird,D., Jackson,A., Jackson,B., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jollivet,A., Karpthy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kowar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M.P., McNeill,I.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Naif,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwokeleneh,O., Okwuonu,G., Olarinpoosagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L., L., Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steinle,M., Strong,R., Sutton,A., Svatek,A., Taborp,Z., Taylor,C., Taylor,I., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villalana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 174010)  
Worley,K.C.  
Direct Submission

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT  
Submitted (27-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 174010)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 19, 2002 this sequence version replaced gi:23816197.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
Project Information  
Center project name: GSYN  
Center clone name: CH230-276B18  
Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 143603 bases at least Q40  
Consensus quality: 145021 bases at least Q30  
Consensus quality: 145953 bases at least Q20  
Estimated insert size: 150243; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced  
\* By the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 174010: contig of 174010 bp in length.

FEATURES  
Source  
1. 174010  
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/db\_xref="taxon:10116"  
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1. 1766  
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complement(171750..172440)  
/note="clone boundary  
clone end:T7  
site:  
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ORIGIN  
Query Match 2.9%; Score 28; DB 2; Length 174010;  
Best Local Similarity 100.0%; Pred. No. 0.00065;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 955 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 982  
 Db 71677 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 71650

RESULT 14  
 AC103052/c  
 LOCUS  
 DEFINITION Rattus norvegicus clone CH230-147P15, WORKING DRAFT SEQUENCE.  
 ACCESSION AC103052  
 VERSION AC103052.5 GI:30580047  
 KEYWORDS HTG; HTGS PHASES; HTGS DRAFT; HTGS\_FULLTOP.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE  
 1 (Bases 1 to 217691)  
 Muzny D, Marle, Metzker M, Lee, Abramson S, Adams C, Alder J, Allen C, Allen H, Alebrooks S, Amin A, Anguiano D, Anyalebechi V, Aoyagi A, Aydeji W, Baca E, Baden H, Baldwin D, Bandaranaike D, Barber M, Barnstead M, Benahmed F, Biswal K, Blair J, Blankenburg K, Blyth P, Brown M, Bryant N, Buhay C, Burch P, Burrell K, Calderon E, Cardenas V, Carter K, Cavazos I, Caesar H, Center A, Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J, Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza L, Davila M, Davis C, Davy-Carroll L, De Anda C, Dederich D, Delgado O, Denison S, Deramo C, Ding Y, Dinh H, Divya K, Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Evans K, Egan A, Escotto M, Eugene C, Evans C, Falls T, Fan G, Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P, Fraser C, Gabisi A, Ganta R, Garcia A, Garner T, Garza M, Gebregorgis E, Geier K, Gill R, Grady M, Guerra W, Guevara W, Gunaratne P, Haaland W, Hamill C, Hamilton C, Hernandez J, Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J, Hernandez R, Hines S, Hladun S, Hodgson A, Hogue M, Hollins B, Howells S, Hulyk S, Hume J, Idlebird D, Jackson A, Jackson L, Jacob S, Jiang H, Johnson B, Johnson R, Jolivet A, Karpathy S, Kelly S, Khan Z, King L, Kovar C, Kowis C, Kraft C, Lebow H, Levan J, Lewis L, Li Z, Liu J, Liu J, Liu W, Liu Y, London P, Longacre S, Lopez J, Lorensuhewa L, Loulseghe H, Lozada R, Lu X, Ma J, Maheshwari M, Mahindaratne M, Mahmoud M, Malloy K, Mangum A, Mangum B, Mapua P, Martin K, Martin R, Martinez E, Mayhew S, McLeod M, McNeill T, Meenen E, Milosavljevic A, Miner G, Minja E, Montemayor J, Moore S, Morgan M, Morris K, Morris S, Mundaasa M, Murphy M, Nair L, Nankervis C, Neal D, Newton N, Nguyen N, Norris S, Nwackeleme O, Okwodu G, Olarnpunsagoon A, Pal S, Parks K, Pasternak S, Paul H, Perez A, Perez L, Pfannkuch C, Plopper F, Poindester A, Popovic D, Primus E, Pu L, Pu L, Puazo M, Quiroz J, Rachin E, Reeves K, Regier M, Reigh R, Reilly B, Reilly M, Ren Y, Reuter M, Richards S, Riggs F, Rivers C, Rodkey I, Rojas A, Rose M, Rose R, Ruiz S, Sanders W, Savery G, Scherer S, Scott G, Shatsman S, Shen H, Shetty J, Shvartsbeyn A, Sisson I, Sitter C, Smajs D, Sneed A, Sodergren E, Song X, Sorelle R, Sosa J, Steidle M, Strong N, Sutton A, Svatek A, Tabor P, Taylor C, Taylor T, Thomas N, Thomas S, Tingey A, Trejos J, Usmani K, Valas R, Vera V, Villanasa D, Waldron L, Walker B, Wang J, Wang Q, Wang S, Warren J, Warren R, Wei X, White F, Williams G, Willson R, Wleczyk R, Wooden H, Worley K, Wright D, Wright R, Wu J, Yakub S, Yen J, Yoon L, Yoon V, Yu F, Zhang J, Zhou J, Zhou X, Zhao S, Dunn D, von Niederhausern A, Weiss R, Smith D, Holt R, Smith H, O., Weinstock G, and Gibbs R.A.

Direct Submission  
 Unpublished  
 2 (Bases 1 to 217691)  
 Worley K.C.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Direct Submission  
 Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 217691)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On May 13, 2003 this sequence version replaced gi:23614691.  
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GICH  
 Center clone name: CH230-147P15  
 ----- Summary Statistics  
 Assembly program: Atlas 3.0;  
 Consensus quality: 212164 bases at least Q40  
 Consensus quality: 213776 bases at least Q30  
 Consensus quality: 215303 bases at least Q20  
 Estimated insert size: 223883; sum-of-contigs estimation  
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 217691: contig of 217691 bp in length.

FEATURES  
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 1. 217691  
 /organism="Rattus norvegicus"  
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 1. 1410  
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ORIGIN  
 Query Match 2.9%; Score 28; DB 2; Length 217691;  
 Best Local Similarity 100.0%; Pred. No. 0.00066;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 955 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 982  
 Db 13219 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 13192

RESULT 15  
 AC095577  
 LOCUS  
 262093 bp DNA linear HTG 09-MAY-2003



DEFINITION Rattus norvegicus clone CH230-8G24, WORKING DRAFT SEQUENCE.  
AC095577 GI:30467287  
AC095577.6 GI:30467287  
HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 262093)  
Murny,D,Marle., Merzker,M, Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gbregoris,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.J., Hodgson,A., Hughes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpthy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangun,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Naif,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwakenem,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Fu,L.-L., Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherter,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartbeyn,A., Sisson,I., Sitter,C.D., Smaiz,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 262093)  
Worley,K.C.  
Direct Submission  
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 262093)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On May 9, 2003 this sequence version replaced gi:24940806. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GCSX  
Center Clone name: CH230-8G24  
----- Summary Statistics  
Assembly program: Atlas;  
Consensus quality: 239870 bases at least Q40  
Consensus quality: 242191 bases at least Q30  
Consensus quality: 243343 bases at least Q20  
Estimated insert size: 257153; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* the accession number will be 262093 bp in length.

FEATURES  
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/mol\_type="genomic DNA"  
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misc\_feature  
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Best Local Similarity 100.0%; Pred. No. 0.00066;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 955 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 982  
DB 42589 CTTTGTGATATAAAAAAAAAAAAAAAAAAAAA 42616

Search completed: September 26, 2004, 01:08:38  
Job time : 4212.82 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 15:45:02 ; Search time 3100.47 Seconds  
(without alignments)  
9458.147 Million cell updates/sec

Title: US-10-069-527-3  
Perfect score: 982  
Sequence: 1-atggcgcggggaattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estlin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_htc:\*
  - 9: gb\_estli:\*
  - 10: gb\_est2:\*
  - 11: gb\_htc:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: em\_gss\_hum:\*
  - 18: em\_gss\_inv:\*
  - 19: em\_gss\_pln:\*
  - 20: em\_gss\_vrt:\*
  - 21: em\_gss\_fun:\*
  - 22: em\_gss\_lam:\*
  - 23: em\_gss\_mus:\*
  - 24: em\_gss\_pro:\*
  - 25: em\_gss\_rod:\*
  - 26: em\_gss\_phg:\*
  - 27: em\_gss\_vrl:\*
  - 28: gb\_gss1:\*
  - 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363.4	37.0	715	12	BI978526
2	354.2	36.1	624	12	BI977629
3	328	33.4	694	14	CB921382
4	307.8	31.3	502	13	BQ106725

5	307.8	31.3	503	13	BQ104750
6	306.4	31.2	710	13	BQ104750
7	299.2	30.5	497	13	BQ104187
8	295.2	30.1	639	13	BQ104187
9	293.8	29.9	605	13	BQ104187
10	293	29.8	762	14	CB971393
11	288.2	29.3	692	14	CB972246
12	285	29.0	652	12	BI924444
13	284.6	29.0	698	10	AW737915
14	282	28.7	697	10	AW737915
15	281.2	28.6	722	9	AJ559554
16	280.4	28.6	757	9	AJ568207
17	276.2	28.1	800	9	AJ568199
18	275	28.0	581	13	BQ104187
19	271.8	27.7	508	13	BQ104187
20	271.4	27.6	426	13	BQ106160
21	258	26.3	588	13	BQ106160
22	257.4	26.2	439	12	BI978252
23	255.2	26.0	727	14	CA990294
24	251.6	25.6	388	13	BQ104606
25	250.2	25.5	555	12	BI924402
26	244.8	24.9	642	14	CB087977
27	243	24.7	714	12	BI929568
28	240	24.4	573	12	BI929568
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33	234.2	23.8	618	9	AI485411
34	234.2	23.8	670	9	AI484883
35	232	23.6	623	10	AW944760
36	230.2	23.4	576	12	BI929538
37	228.8	23.2	633	14	CB078399
38	228	23.2	582	9	AU089543
39	226.6	23.1	571	14	CB076679
40	225.8	23.0	585	14	CB626851
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ALIGNMENTS

RESULT 1  
BI978526  
LOCUS  
DEFINITION  
BI978526  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.  
1 (bases 1 to 715)  
Channeliere,S., Riviere,S., Scalliet,G., Szecsi,J., Jullien,F., Dolle,C., Vergne,P., Dumas,C., Bendahmane,M., Huguency,P. and Cock,J.M.  
Analysis of gene expression in rose petals using expressed sequence tags  
FEBS Lett. 515 (1-3), 35-38 (2002)  
21940574  
11943190  
Contact: Cock JM  
RDP (UMR5667 INRA/CNRS/ENSL/UCBL)  
Ecole Normale Supérieure de Lyon  
46, Allée d'Italie, 69646 LYON Cedex 07, France  
Tel: 33472728611

BI978526 715 bp mRNA linear EST 29-OCT-2002  
ud03 Old Blush petal SMART library Rosa chinensis cDNA 5' similar to AP3 homologue (TW6), mRNA sequence.  
BI978526  
GI:24420321

```

Fax: 33472728600
Email: Mark.Cock@ens-lyon.fr
PCR Primers
FORWARD: CTGCGGAAGCGCGCCATTGTGTGGT
BACKWARD: ATACGACTCACTATAGGGGAATTGGCC.
FEATURES
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        Location/Qualifiers
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                Site_2: Sfil"
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    Matches 489; Conservative 0; Mismatches 146; Indels 8; Gaps 3;
QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC 60
DB 61 ATGGTCTGTGGAGATTGAGTCAAGCTGATCGAGAACAGACGACGACGAGGTGACC 120
QY 61 TACTCCAAAGAGAAGAAATGGATCTTCAAGAGGCTCAGAGGTCAACGTTCTCTGTGAT 120
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DB 181 GTCAGTCTCCCTCATTCATGCTGCTCCACACATTAATAATGACGAGTATACGCCCA 240
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RESULT 2
BI977629 624 bp mRNA linear EST 29-OCT-2002
LOCUS

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jD1.0 Old Blush petal SMART library Rosa chinensis cDNA 5' similar
to APETALA3 (BnAP3), mRNA sequence.
ACCESSION BI977629
VERSION BI977629.1 GI:24419435
KEYWORDS EST.
SOURCE Rosa chinensis
ORGANISM Rosa chinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1 (bases 1 to 624)
AUTHORS Channeliere,S., Riviere,S., Scalliet,G., Szecsi,J., Jullien,F.,
Delle,C., Vergne,P., Dumas,C., Bendahmane,M., Huguene,P. and
Cock,J.M.
Analysis of gene expression in rose petals using expressed sequence
tags
JOURNAL FEBS Lett. 515 (1-3), 35-38 (2002)
MEDLINE 21940574
PUBMED 11943190
COMMENT Contact: Cock JM
RDP (UMR5667 INRA/CNRS/ENSL/UCBL)
Ecole Normale Supérieure de Lyon
46, Allée d'Italie, 69616 LYON Cedex 07, France
Tel: 33472728611
Fax: 33472728600
Email: Mark.Cock@ens-lyon.fr
PCR Primers
FORWARD: CTGCGGAAGCGCGCCATTGTGTGGT
BACKWARD: ATACGACTCACTATAGGGGAATTGGCC.
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                /sex="Hermaphrodite"
                /dev_stage="Mixed (young bud, open bud, mature flower,
                senescing flower)"
                /lab_host="Escherichia coli"
                /clone_lib="Old Blush petal SMART library"
                /note="Organ: Petal; Vector: pTriplex2; Site_1: Sfil;
                Site_2: Sfil"
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    Best Local Similarity 77.5%; Pred. No. 3.4e-53;
    Matches 444; Conservative 0; Mismatches 123; Indels 6; Gaps 1;
QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC 60
DB 58 ATGGGTCTGTGGAGATTGAGATCAAGCTGATCGAGAACCCAGACGACGAGGTGACC 117
QY 61 TACTCCAAAGAGAAGAAATGGATCTTCAAGAGGCTCAGGAGCTCACCGTCTCTGTGAT 120
DB 118 TATTGGAAGCGAAGATGGGATCTTCAAGAGGCTCAGGAGCTCAGGTTCTGTGAC 177
QY 121 GCCAAGTCTCCCTCATTTATGCTCTCCAAACACTTAATAATGACGAGTATACGCCCT 180
DB 178 GCTCAGGTCTCCCTCATTCATGCTGCTCTCCACCTGACAAATCCAGAGTATATAGCCA 237
QY 181 ACCACTACGACCAAGAGTATGTATGACTATCAGAAATATGCGGATCGATCTGTGG 240
DB 238 ACCACTACGACCAAGAGTATGTATGACTATCAGAGAGATTTACAGATCAATATAG 297
QY 241 AGCACACAGGAGTCTGATGAAGACACCTTGTGAAGTTGAAGAGATCAACAATAG 300
DB 298 AGCTCACACTACGAGGCAATGAAAGAGAACTTGTGAAACTGAAAGAGGTAAACAATAG 357
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCGCATGATCTAAATGGCTGAGCTTTGACGAG 360
DB 358 CTGAGGAGGACATCAGGCAAGGCTGGGCGATGATCTTAATGGTCTGAGCTATGCTGAG 417

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QY 361 CTGGCTTCTCTGAGATGAGATGAGTCTCTCTTGGATGCGTACATCAAGGAAGTAC 420  
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 QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTAAAGAACTTGGAGCAAGA 480  
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 Db 478 CACGTGCTCAGACTCAGCAGAGACTACCAAGAGAAAGGTGAAGAACTTGGAGGAGA 537  
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 QY 481 AGAGAAACATGCTGCGATGGTATTTTGAACAGAGAGACCGCGCGAGATCCACATAT 540  
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 Db 538 AACAGTAAATTAATGCGATGGTATGGAGCTC-----CAGGTATGAGGATCCCAATAT 591  
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 QY 541 GGTATGAGGACAATGAGGAGACTTACGAATCT 573  
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 Db 592 GGGTATGCGATATGAGGGGACTATGAATCT 624  
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CB921382 694 bp mRNA linear EST 25-APR-2003  
 VMD070D08 353397 An expressed sequence tag database for abiotic  
 stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera  
 cDNA clone VMD070D08 5, mRNA sequence.

ACCESSION CB921382  
 VERSION CB921382.1 GI:30136044  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.  
 1 (bases 1 to 694)  
 Cushman, J.C.

JOURNAL An expressed sequence tag database for abiotic stressed berries of  
 COMMENT Vitis vinifera var. Chardonnay  
 Unpublished (2002)  
 Contact: Cushman JC  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer (backward)  
 Plate: 070 row: D column: 08  
 Seg primer: T3 20mer  
 High quality sequence stop: 694.

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 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"

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 Best Local Similarity 71.5%; Pred. No. 1.5e-48;  
 Matches 449; Conservative 0; Mismatches 170; Indels 9; Gaps 1;  
 7 CGCGGGAAGATTGAATCAAGCTCATCGAAACCAAGACCAAGGAGGAGTCACTCTCC 66  
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 Db 4 CGTGGAGATTGATCATAGAGATAGAGAACCCCAACAGGAGGAGTCACTCTCC 63  
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 QY 67 AAGAGAGAAATGGATCTTCAAGAGCGCTCAGAGCTCCCGTCTCTGTGATGCCAAG 126  
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Db 64 AAGCGAGAAATGGTATATTTTCAAGAAAGCCAGGAGCTCACCGTCTCTTGTGATGCTAAG 123  
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 QY 127 GTCTCCCTCATTTATGCTTCTCAACACTAATAAAATGACAGATATATACGCCCTACCACT 186  
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 Db 124 GTTCTACTCATCATGTTCTCCAATATCTGAAATATCCACGAATATACCACTCTACTATA 183  
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 QY 187 AGACCAAGAGTATGATGATGACTATCAGAAACTATGGGATCGATCTGTGGAGGACA 246  
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 Db 184 AGCAAGAAAGAGTCTTACGATCAGTATCAGAAAGCTTTAGGAGTATGATCTTTGGAGCTCT 243  
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 QY 247 CACGAGAGTCTGATGAAGACACCTTGTGGAAAGTTGAAGAGATCAACAATAAGCTGAGG 306  
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 QY 427 ATCAAACTCAGACGAGACCAACCAAGAGAGGTTAAGAACTTGGAGCAAGAGAGGA 486  
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 QY 487 AACATGCTGCATGGCTATTTTGCACGAGAGCAGCGCGGAGATCCACAGATATGTTAT 546  
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 LOCUS fcl070.e Rose Petals (Fragment Cloud) Lambda Zap Express Library  
 DEFINITION Rosa hybrid cultivar cDNA clone fcl070.e 5', mRNA sequence.  
 ACCESSION BQ106725  
 VERSION BQ106725.1 GI:20156387  
 KEYWORDS EST.  
 SOURCE Rosa hybrid cultivar  
 ORGANISM Rosa hybrid cultivar

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.  
 1 (bases 1 to 502)  
 Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M.,  
 Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J.,  
 Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and  
 Weiss, D.

TITLE Rose Scent: Genomics Approach to Discovering Novel Floral  
 Fragrance-Related Genes  
 JOURNAL Plant Cell 14 (10), 2325-2338 (2002)  
 COMMENT Contact: Naama Menda  
 Petal Genomics  
 Faculty of Agricultural, Food and Environmental Quality Sciences,  
 The Hebrew University of Jerusalem  
 P.O. Box 12, Rehovot, 76100, Israel  
 Tel: 972 8 9489 683  
 Fax: 972 8 9468 265  
 Email: shaham@agri.huji.ac.il  
 Seq primer: T3 forward  
 Location/Qualifiers  
 1..502  
 /organism="Rosa hybrid cultivar"  
 /mol\_type="mRNA"

/strain="Pragrant Cloud"		/organism="Rosa hybrid cultivar"			
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source					
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ORIGIN					
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Best Local Similarity 79.8%; Pred. No. 6.5e-45;					
Matches 363; Conservative 0; Mismatches 92; Indels 0; Gaps 0;					
QY	1	ATGGCGCGGGAGATTGAATAAATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC	60		
Db	48	ATGGGTCTGTGGAGATTGAGATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC	107		
QY	61	TACTCCAGAGAGAATAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT	120		
Db	108	TATTCGAAGCGACGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTGTGTGAC	167		
QY	121	GCCAGGTCTCCCTCATATGCTCTCCAAACACTAATAAATGACAGATATATCAGCCCT	180		
Db	168	GCTCAGGTCTCCCTCATATGCTCTCCACTGACAAAAATCCACAGTATATAGCCCA	227		
QY	181	ACCACTACGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240		
Db	228	ACCACTACGACCAAGAGATGTTTGATCTTACCGAAGAATTTAGAGATCGATCTATGG	287		
QY	241	AGGACACAGAGAGTGCATGAAGACACCTTGTGAAAGTTGAAAGAGATCAACAATAAG	300		
Db	288	AGTTCACACTACGAGGCAATGAAGAGAACTTGTGAAACTGAAGAGGTTAAACAATAAG	347		
QY	301	CTGAGGAGAGATCAGGAGAGGTTGGGCAATGATCTAAATGCGCTGAGCTTTCAGCAG	360		
Db	348	CTGAGGAGGACATCAGGCAAGGCTGGGCAATGATCTTAATGTGCTGAGCTATGCTGAG	407		
QY	361	CTGCGTTCTCTTGACGATGAGATGAGTCTTCTTTGGATGCGATACGTCGAAGGAAGTAC	420		
Db	408	CTGCAAGATCTGGAGGAACGATGATCAATCCGTCGAATCATACGTGATCGAAAGTAC	467		
QY	421	CATGTGATCAAACTCAGACGAGACCAACCAAGAA	455		
Db	468	CACGTGCTCAAGACTCAAGCAGAGACTACCAGAA	502		
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LOCUS fc1137.e Rose Petals (Pragrant Cloud) Lambda Zap Express Library					
DEFINITION Rosa hybrid cultivar cDNA clone fc1137.e 5', mRNA sequence.					
ACCESSION BQ104750					
VERSION BQ104750.1 GI:20154412					
KEYWORDS EST.					
SOURCE Rosa hybrid cultivar					
ORGANISM Rosa hybrid cultivar					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.					
1 (bases 1 to 503)					
REFERENCE					
AUTHORS Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,					
Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,					
Adam,Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and					
Weiss,D.					
TITLE Rose Scent: Genomics Approach to Discovering Novel Floral					
Fragrance-Related Genes					
JOURNAL Plant Cell 14 (10), 2325-2338 (2002)					
COMMENT Contact: Naama Menda					
Petat Genomics					
Faculty of Agricultural, Food and Environmental Quality Sciences,					
The Hebrew University of Jerusalem					
P.O. Box 12, Rehovot, 76100, Israel					

Tel: 972 8 9489 683		/organism="Rosa hybrid cultivar"			
Fax: 972 8 9468 265		/mol_type="mRNA"			
Email: shaham@agri.huji.ac.il		/strain="Pragrant Cloud"			
Seq primer: T3 forward.		/db_xref="taxon:128735"			
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Query Match 31.3%; Score 307.8; DB 13; Length 503;					
Best Local Similarity 79.8%; Pred. No. 6.5e-45;					
Matches 363; Conservative 0; Mismatches 92; Indels 0; Gaps 0;					
QY	1	ATGGCGCGGGAGATTGAATAAATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC	60		
Db	48	ATGGGTCTGTGGAGATTGAGATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC	107		
QY	61	TACTCCAGAGAGAATAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT	120		
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QY	121	GCCAGGTCTCCCTCATATGCTCTCCAAACACTAATAAATGACAGATATATCAGCCCT	180		
Db	168	GCTCAGGTCTCCCTCATATGCTCTCCACTGACAAAAATCCACAGTATATAGCCCA	227		
QY	181	ACCACTACGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240		
Db	228	ACCACTACGACCAAGAGATGTTTGATCTTACCGAAGAATTTAGAGATCGATCTATGG	287		
QY	241	AGGACACAGAGAGTGCATGAAGACACCTTGTGGAAGTTGAAAGAGATCAACAATAAG	300		
Db	288	AACTCACACTACGAGGCAATGAAGAGAACTTGTGGAACCTGAAGAGGTTAAACAATAAG	347		
QY	301	CTGAGGAGAGATCAGGAGAGGTTGGGCCATGATCTAAATGCCCTGAGCTTTCAGCAG	360		
Db	348	CTGAGGAGGACATCAGGCAAGGCTGGGCCATGATCTTAATGTGCTGAGCTATGCTGAG	407		
QY	361	CTGCGTTCTCTTGACGATGAGATGAGTCTTCTTTGGATGCGATACGTCGAAGGAAGTAC	420		
Db	408	CTGCAAGATCTGGAGGAACGATGATCAATCCGTCGAATCATACGTGATCGAAAGTAC	467		
QY	421	CATGTGATCAAACTCAGACGAGACCAACCAAGAA	455		
Db	468	CACGTGCTCAAGACTCAAGCAGAGACTACCAGAA	502		
RESULT 6					
BUB75031 710 bp mRNA linear EST 16-OCT-2002					
LOCUS V001F01 Populus flower cDNA library Populus balsamifera subsp.					
DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.					
ACCESSION BUB75031					
VERSION BUB75031.1 GI:24066555					
KEYWORDS EST.					
SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)					
ORGANISM Populus balsamifera subsp. trichocarpa					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
rosids; eurosids 1; Malpighiales; Salicaceae; Saliceae; Populus.					
1 (bases 1 to 710)					
REFERENCE					
AUTHORS Unneberg,P., Bhalarao,R.R., Jansson,S. and Sterky,F.					
TITLE The poplar tree transcriptome: Analysis of expressed sequence tags					
from multiple libraries					
JOURNAL Unpublished (2002)					

COMMENT Contact: BHALERAO RUPALI R.  
Umea Plant Science Center  
Department of Plant Physiology  
University of Umea, 901 87 Umea, Sweden  
Tel: +46 90 786 5279  
Fax: +46 90 786 6676  
Email: rupali.bhalerao@plantphys.umu.se.

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/db\_xref="taxon:3694"  
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/clone\_lib="Populus flower cDNA library"  
/note="Organ: flower"

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Best Local Similarity 70.1%; Pred. No. 1e-44;  
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGGGCGGGAAGATTGAATCAAGCTGATCGAAACCCAGACCAACAGCGAGGTGACC 60  
DB 85 ATGGGTCTGTGAAAGATTGAATCAAGAGATCGAAACCCCAACACAGGCAAGTCACC 144  
QY 61 TACTCCAGAGAAAGATGGATCTTCAAGAGGCTCAGGAGCTCACGGTCTCTGTGAT 120  
DB 145 TACTCGAAGAGAAATGGATGTTTCAAGAAACCCCAAGAACTCATGTACTTTGTGAT 204  
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
DB 205 GCTAAGGTCTCTTTATCATGTTCTCCCACTAATAAATGACGAGTATATCAGCCCT 264  
QY 181 ACCACTAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
DB 265 TCCACATCGCAAAAGAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 324  
QY 241 AGGACACACGAGGAGTGGATGAAAGACACCTTTGGGAAGTTGAAAGAGATCAACAATAG 300  
DB 325 GGCACTCAATACGAGAAATGCAAGAGCACTTGGAGAGCTGAATGATATCATATAG 384  
QY 301 CTGAGGAGAGATGACGAGAGGTTGGGCAATGATCTAAATGGCCCTGAGCTTTGACGAG 360  
DB 385 CTGAGACAAAGAAATCAGGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 444  
QY 361 CTGGCTTCTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 445 CTGGCGGCTCTTGACGACATATGATGATGATGATGATGATGATGATGATGATGATGATG 504  
QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTAAGAACTTTGGAGCAAGA 480  
DB 505 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGATTTAGAGGAGAGA 564  
QY 481 AGAGGAACATGCTGCATGCTATTTTACGAGGAGACGCGCGGAGGATCCACAGTAT 540  
DB 565 CATGGAACCT-----CTTGATGGAATATGAAGCAAACTTAGAGGATCGACAGTAT 615  
QY 541 GGTATGAGGACAAATGAGGAGACTACGAAATCTGCACTTGCATTTGTCAAATGGGGCAAT 600  
DB 616 GGTATTAGGCAAT-----GAAGCTGCTGTGCACTTGCATTTGCATTTGGGCTTCC 663  
QY 601 AACTGTACACTTTCCACCTCCACCCCTTAACCTCACCAAC 642  
DB 664 AACCTCTATGATTCGCGCTGCACTACGCGGACACCAACCAAC 705

RESULT 7  
BQ104187  
LOCUS  
DEFINITION  
Rosa hybrid cultivar cDNA clone fc2185.e 5', mRNA sequence.  
ACCESSION  
BQ104187

VERSION BQ104187.1 GI:20153849  
KEYWORDS EST.  
SOURCE Rosa hybrid cultivar  
ORGANISM Rosa hybrid cultivar  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; rosids1; Rosales; Rosaceae; Rosa.  
REFERENCE 1 (bases 1 to 497)  
AUTHORS Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M.,  
Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J.,  
Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and  
Weise, D.  
TITLE Rose Scent: Genomics Approach to Discovering Novel Floral  
Fragrance-Related Genes  
JOURNAL Plant Cell 14 (10), 2325-2338 (2002)  
COMMENT Contact: Naama Menda  
Petal Genomics  
Faculty of Agricultural, Food and Environmental Quality Sciences,  
The Hebrew University of Jerusalem  
P.O. Box 12, Rehovot, 76100, Israel  
Tel: 972 8 9489 683  
Fax: 972 8 9468 265  
Email: shaham@agri.huji.ac.il  
Seq primer: T3 forward.  
Location/Qualifiers  
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/organism="Rosa hybrid cultivar"  
/mol\_type="mRNA"  
/strain="Fragrant Cloud"  
/db\_xref="taxon:128735"  
/clone="fc2185.e"  
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/dev\_stage="Young open flower at stage four"  
/clone\_lib="Rose Petals (Fragrant Cloud) Lambda Zap  
Express Library"  
/note="Vector: pBKCMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 30.5%; Score 299.2; DB 13; Length 497;  
Best Local Similarity 79.2%; Pred. No. 2.2e-43;  
Matches 355; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1 ATGGGCGCGGGAAGATTGAATCAAGCTGATCGAAACCCAGACCAACAGGAGGTGACC 60  
DB 50 ATGGGTCTGTGGAAGATTGAGATCAAGCTGATCGAGAACCAAGACGAGGAGTACC 109  
QY 61 TACTCCAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACGGTCTCTGTGAT 120  
DB 110 TATTGAAGCGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACGGTCTGTGTGAC 169  
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
DB 170 GCTCAGGTTTCTCTCATCATGCTCAGTCTCCACTGACAAATCCACGATATATTAGCCA 229  
QY 181 ACCACTAGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
DB 230 ACCACTAGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 289  
QY 241 AGGACACACGAGGAGTGCATGAAAGACACCTTTGCGAAGTTGAAAGAGATCAACAATAG 300  
DB 290 AGCTCACACTACAGGCAATGAAAGAGACTTGTGGAACCTGAAAGAGGTTAACATAG 349  
QY 301 CTGAGGAGAGATCAGGAGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360  
DB 350 CTGAGGAGGAGATCAGGCAAGGCTGGGGCATGATCTTAATGGTCTGAGCTATCTGAG 409  
QY 361 CTGGCTTCTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 410 CTGCAAGATCTGGAGGAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 469  
QY 421 CATGTGATCAAACTCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 448  
DB 470 CACGTGCTCAAGCACTCAAGCAGAGACTA 497

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RESULT 8
BU879075          639 bp      mRNA      linear      EST 16-OCT-2002
DEFINITION
trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
BU879075
VERSION
BU879075.1 GI:24070599
KEYWORDS
EST.
SOURCE
Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 639)
REFERENCE
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
JOURNAL
Contact: BHALERAO RUPALI R.
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
FEATURES
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    /organism="Populus balsamifera subsp. trichocarpa"
    /mol_type="mRNA"
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    /db_xref="taxon:3694"
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ORIGIN
Query Match          30.1%; Score 295.2; DB 13; Length 639;
Best Local Similarity 71.0%; Pred. No. 1e-42;
Matches 409; Conservative 0; Mismatches 158; Indels 9; Gaps 1;

Yy 1 ATGCGCGCGGAGATTGAAATCAAGCTCATCGAAACCCAGACCACAGCGAGGTGACC 60
Db 71 ATGGTCTGTGAAGATTGAATCAAGAATCGAAACCCCAACACAGCGCAAGTCACC 130

Yy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTGAT 120
Db 131 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGACTCACTGTACTTTGTGAT 190

Yy 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACACTAAATAAATGCACGAGTATATCAGCCCT 180
Db 191 GCTAAGTCTCTTATCATGTTCTCCACACCTAACCAACTCAATGAGTACATTAGCCCC 250

Yy 181 ACCACTACGACCAAGAGATATGTATGATCTATCAGAAATATAGGGATTCGATCTGTGG 240
Db 251 TCCACATCGCAAGAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 310

Yy 241 AGGCACACAGGAGTCTGATGAAGACACCTCTGGAGAGTTGAAGAGATCAACATATAG 300
Db 311 GGCACTCAATACGAGAAATGCAAGAGCACTTGAAGAGCTGAATGATATCAATCATTAAG 370

Yy 301 CTGAGGAGAGATCAGGCGAGAGTGTGGCCATGATCTAAATGCCCTGAGCTTTGACGAG 360
Db 371 CTGAGACAAGAAATCAGGCGAGAGGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 430

Yy 361 CTGCGTTCTTTGACGATGAGATCGAGTCTTCTTGATGCCATAGCTCAAGAGAGATAC 420
Db 431 CTGCGCGGTCTTTGAGCAACATATGATCTGAAGCCCTTGAATGGTGTGGTGGCAGGAAGTAC 490

Yy 421 CATCTGATCAAAATCTAGACGGAGACCAACCAAGAAAGGTTAAGAACTTTGAGGCAAGA 480
Db 491 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAATTTAGAGGAGAGA 550

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Yy 481 AGAGAAACATGCTGCATGCTATTTTACCCAGGAAGCAGCGCGGAGGATCCACAGTAT 540
Db 551 CATGAAACCT-----CTTGATGAATATGAAGCAAACTAGAGGATCGACAGTAT 601

Yy 541 GGTATGAGGCAATGAGGAGACTAGCAATCTGCA 576
Db 602 GGTATGAGGCAATGAGGAGCTGCTGTTCCACTTGA 637

RESULT 9
BU877396          605 bp      mRNA      linear      EST 16-OCT-2002
LOCUS
V033E07 Populus flower cDNA library Populus balsamifera subsp.
trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION
BU877396
VERSION
BU877396.1 GI:24068920
KEYWORDS
EST.
SOURCE
Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM
Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 605)
REFERENCE
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished (2002)
JOURNAL
Contact: BHALERAO RUPALI R.
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
FEATURES
source
1..605
    /organism="Populus balsamifera subsp. trichocarpa"
    /mol_type="mRNA"
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    /db_xref="taxon:3694"
    /tissue_type="floral buds"
    /clone_lib="Populus flower cDNA library"
    /note="Organ: flower"
ORIGIN
Query Match          29.9%; Score 293.8; DB 13; Length 605;
Best Local Similarity 70.1%; Pred. No. 1.9e-42;
Matches 413; Conservative 0; Mismatches 167; Indels 9; Gaps 1;

Yy 2 TGGCGCGCGGAAAGATTGAAATCAAGCTGATCGAAAAACCCAGACCACAGCGAGGTGACCT 61
Db 16 TGGGTCTGTGAAGATTGAATCAAGAATCGAAACCCCAACACAGGCAAGTCACCT 75

Yy 62 ACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCACCGTTCTCTGTGATG 121
Db 76 ACTCGAAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTATTTGTGATG 135

Yy 122 CCAAGTCTCCCTCATTTATGCTCTCCAACTATAATAATGCACGAGTATATCAGCCCTA 181
Db 136 CTAAGTCTCTCTTATCATGTTCTCCAACTATAATAATGCACGAGTATATCAGCCCT 195

Yy 182 CCACTACGACCAAGAGTATGTATGATCTATCAGAAAACTATGGGATCGATCTGTGA 241
Db 196 CCACATCCACAAAGAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 255

Yy 242 GGACACACGAGGAGTCCGATGAAGACACCTTTGTGAAAGTTGAAAGAGATCAACAATAAGC 301
Db 256 GCATCAATACGAGAAATGCAAGAGCACTTGAGAGAGCTGAATGATATCATATAGC 315

Yy 302 TGAGGAGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAGC 361
Db 316 TGAGACAAAGAAATCAGGCGAGAGAGAGAGGAGGCGCTGAATGATCTGAGCATTCATC 375

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362 TGGCTTCTTGGAGATGAGATGAGTCTTCTTGGATGCCATACGTCAAGGAAGTACC 421
Db      TGCGGGCTTTGAGCAACATATGACTGAAGCTTTGAATGGTGTGGTGGCAGGAATACC 435
Qy      ATGTGATCAAACTCAGAGGAGAGACCACCAAGAGAGAGGTTAAGAACTTGGAGCAAGAA 481
Db      ATGTGATCAAAACACAAAACCACTACAGGAAGAGGTGAAGAAATTTAGAGAGAGAC 495
Qy      GAGGAAACATGCTGATCGCTATTTTGACCGAATAT-----GAAGCAAACTAGAGATCGACAGTATG 541
Db      ATGGAACCTTTGACCGAATAT-----GAAGCAAACTAGAGATCGACAGTATG 546
Qy      GTTATGAGGACATGAGGAGAGACTACGAATCTGCACCTTGCAATGTCAAA 590
Db      GTTATGAGGACATGAGGAGAGACTGCTGTTGACCTTGCAATGTTGGGCTTCCAA 595

RESULT 10
CB971393 762 bp mRNA linear EST 30-APR-2003
LOCUS CAB10005_Iia_Fa_B07 Cabernet Sauvignon Flower Pre-bloom - CAB1
DEFINITION Vitis vinifera cDNA clone CAB10005_Iia_Fa_B07 5', mRNA sequence.
ACCESSION CB971393
VERSION 1 GI:30254946
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
Cook, D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers
1...762
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10005_Iia_Fa_B07"
/sex="Hermaphrodite"
/dev_stages="Pre-bloom"
/lab_hosts="DHSalpha"
/clone_libs="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site 1:
Sfil; Site 2: Sfil; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptas or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGGATGATATCAGCAGAGTGGCCATTACGGCCGG-3' and
5'-ATTCTAGGCGCGGCGGACATG-dt(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

FEATURES
ORIGIN
Query Match 29.8%; Score 293; DB 14; Length 762;

Best Local Similarity 69.8%; Pred. No. 2.4e-12; Mismatches 170; Indels 9; Gaps 1;
Matches 414; Conservative 0;
Qy 1 ATGGCGCGGGGAAGATTGAAATCAAGCTGATCGTGAAGCAACAGCAACAGGAGGTGACC 60
Db 10 ATGGCTAGAGGAAGATTGAGATCAAGAGATAGAGAACTCGACGAACAGGAGGTGACC 69
Qy 61 TACTCAAGAGAGAAATGGGATCTTTCAAGAGGCTCAGGAGCTCACCGTCTCTGTGTAT 120
Db 70 TACTCAAGAGAGAAATGGTATCTTTCAAGAGGCCAGTGAGCTCACTGTTCTTTGTGAT 129
Qy 121 GCCAAGGTCTCCTCATTTATGCTCTCCACACTATAATAATGCAGAGATATATCAGCCT 180
Db 130 GCTAAGGTTTCTATCATCTGCTCTCCAGTACTTGGAAAGCTCATGAATACATCAGCCT 189
Qy 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAACCTATGGGATCGATCTGTGG 240
Db 190 TCCACTACAACGAAACAATATTTGATCAGTACCAGAACACTCTAGGAGTGGATCTATGG 249
Qy 241 AGACACACAGGAGTCTGATGAAGACACCTTGTGGAGTCTTGAAGAGATCAACAATAAG 300
Db 250 AGCTATCCTATGAGAGAAATGCAAGAAAAACCTGAAAGAACTGAAAGATGTGAACAGAAT 309
Qy 301 CTGAGGAGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCTGAGCTTTGACGAG 360
Db 310 CTCAGGAAGAGATTAGGCGAGAGATGGGTGAACATTTGAGCGATTGAGCGTTGAGGA 369
Qy 361 CTGGCTTCTTTGACATGAGATGAGTCTTCTTGGATGCCATACGTCAAGGAGATGAC 420
Db 370 CTGCGAGATCTTGAACACAGAGATGGAGAGTCTTTTGAAGATGTTCTGCTGATAGGAATAC 429
Qy 421 CATGTGATCAAACTCAGACGGAGACCCACCAAGAGAGGTTAAGAACTTTGGAGCAAGA 480
Db 430 CAGGTGATCAATAATCAGATTGAACCTTTCAAGAAAAAGGTAAAGTAATGTGGAACAAATA 489
Qy 481 AGAGGAAACATGCTGCATGGCTATTTTGACAGGAGACAGCCGCGGAGAGATCCACAGTAT 540
Db 490 CACAAAAATCTCTACATGAATTT-----GATGCAAGGAGACAGATCAATACTAT 540
Qy 541 GGTATGAGGACAAATGAGGAGACTACGAATCTGCACCTTGCAATGTCAAAATGG 593
Db 541 GGGCTAGTGACAATGGAGGGGATTACGAATCTGTTCTTTGGATTCTCAAAATGG 593

RESULT 11
CB972246 692 bp mRNA linear EST 30-APR-2003
LOCUS CAB10006_Ia_Fa_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis
DEFINITION vinifera cDNA clone CAB10006_Ia_Fa_D07 5', mRNA sequence.
ACCESSION CB972246
VERSION 1 GI:30256403
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Jones, K. and
Cook, D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers
1...692
/organism="Vitis vinifera"
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/sex="Hermaphrodite"
/dev_stages="Pre-bloom"
/lab_hosts="DHSalpha"
/clone_libs="Cabernet Sauvignon Flower Pre-bloom - CAB1"
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site 1:
Sfil; Site 2: Sfil; CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptas or caps still attached. Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dT priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGGATGATATCAGCAGAGTGGCCATTACGGCCGG-3' and
5'-ATTCTAGGCGCGGCGGACATG-dt(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

FEATURES
ORIGIN
Query Match 29.8%; Score 293; DB 14; Length 762;

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Qy 422 ATGTGATCAAACTCAGACGGAGACCAACCAAGAAAGGTTAAGAACTTGGAGCAAGAA 481
Db 421 ACGTGATCAAGAAATCAAAACAGACACCTCGCAAGAAAGAGGCGAGAACTTGAAGAGCAAA 480
Qy 482 GAGGAACATGCTGCATGGCTATTTCACAGGAGAGCAGCGCGGAGGATCCACAGTATG 541
Db 481 ATGGAACCTTGATC-----TTGACTTGGAGCAAAATGTGAAGATCCAAAGTATG 531
Qy 542 GTTATGAGGACAATGAGGAGACTACGAATCTGCATTTGCATTTGATTTCAAAATGGGCGGAATA 601
Db 532 GTGTTGTGGAATAAGAGGGGCAATACCACCTGCTGTGGCATTTGCGAATGGAGTACACA 591
Qy 602 ACTTGACACTTTCACCTCCACCA 626
Db 592 ATCTTTATGCTTTTCGGCTACAACA 616

RESULT 13
LOCUS AW737915 698 bp mRNA linear EST 18-MAY-2001
DEFINITION EST333342 tomato flower buds, anthesis, Cornell University
Lycopersicon esculentum cDNA clone cTOD4L21 5', mRNA sequence.
ACCESSION AW737915
VERSION AW737915.1 GI:7646860
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 698)
van der Hoeven,R.S., Bezzerides,J.L., Matern,A.L., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Niernan,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tanksley,S.D.
Generation of ESTs from tomato flower tissue, anthesis
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Location/Qualifiers
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/clone_lib="tomato flower buds, anthesis, Cornell
University"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
ORIGIN
Query Match 29.0%; Score 284.6; DB 10; Length 698;
Best Local Similarity 66.7%; Pred. No. 7.6e-41;
Matches 426; Conservative 0; Mismatches 204; Indels 9; Gaps 1;

Qy 2 TGGCGCGGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCAGGTGACCT 61
Db 1 TGGCCCGTGGAAATTTGAGTCAAGAGATTGAATCTGACAAACAGCAGGTCACTT 60
Qy 62 ACTCCAAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGCTTCTTGATG 121
Db 61 ACTCCAAGAGAAACGGTATTTTCAAGAAAGCTAAAGAACTTACTGTTCTTTGTGACG 120

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Qy 122 CCAAGGTCTCCCTCAATTATGCTCTCAACACTAATAAATGCACAGTATATCAAGCCCTA 181
Db 121 CTAAGATCTCTCTCATCTATCAAGTATCAAGCAGCAAGAGTATCATGAGTACACAGACCCAA 180
Qy 182 CCACCTACGACCAAGAGTATGATGATCTATCAGAAACTATGGGATCGGATCTGTGGA 241
Db 181 ACACCTACGACCAAAAGATGATGATCAGTATCAGAGTGCACTTGGAGTTGATATCTGGA 240
Qy 242 GGACACACAGAGGATCGATGAAAGACA CTTGTGGAAGTTGAAAGAGATCAACAATAAGC 301
Db 241 GCATTCACCTACGAGAAAATGCAAGAAAACCTTGAAGAGATTGAAGAGATCAATAAACAAGC 300
Qy 302 TGAGGAGAGAGATCAGGACAGAGTTGGGCCATGATCTAAATGCGCTGAGCTTTCAGGAGC 361
Db 301 TAAGAAGAGAGATAAGGACAGAGAACAGGGGAGAGACATGAGCGGACTTAATTTGCGAGGAC 360
Qy 362 TGGCTTCTCTTGACGATGAGATGCACTCTTCTTGATGCCATACGTCAAGAGAAAGTACC 421
Db 361 TATGTCACCTTGACGAGAGACATCACTGAATCTGTTGCTGAGATTCGTGAACGAAAGTACC 420
Qy 422 ATGTGATCAAACTCAGACGGAGACCAACCAAGAAAGGTTAAGAACTTGGAGCAAGAA 481
Db 421 ACGTGATCAAGAAATCAAAACAGACACCTCGCAAGAAAGAGGCGAGAACTTGAAGAGCAAA 480
Qy 482 GAGGAACATGCTGCATGGCTATTTCACAGGAAAGCAGCGCGGAGGATCCACAGTATG 541
Db 481 ATGGAACCTTGATC-----TTGACTTGGAGCAAAATGTGAAGATCCAAAGTATG 531
Qy 542 GTTATGAGGACAATGAGGAGACTACGAATCTGCATTTGCATTTGCAAAATGGGCGGAATA 601
Db 532 GTGTTGTGGAATAAGAGGGGCAATACCACCTGCTGTGGCATTTGCGAATGGAGTACACA 591
Qy 602 ACTTGACACTTTCACCTCCACCCCTCAACCTCCACC 640
Db 592 ATCTTTATGCTTTTCGGCTACAACCATTCGCCCAATC 630

RESULT 14
LOCUS AJ568191 697 bp mRNA linear EST 28-JUL-2003
DEFINITION AJ568191 Antirrhinum majus library (Stueber K) Antirrhinum majus
cDNA clone zscho13a, mRNA sequence.
ACCESSION AJ568191
VERSION AJ568191.1 GI:33294080
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Lamiales; Antirrhinaceae; Antirrhineae;
Antirrhinum.
1 (bases 1 to 697)
Stueber,K. and Schwarz-Sommer,Z.
Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer,Z.)
Unpublished (2003)
Contact: Stueber K
Molecular Plant Genetics
MPI fuer Zuechtungsforshung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 28.7%; Score 282; DB 9; Length 697;
Best Local Similarity 67.2%; Pred. No. 2.2e-40;
Matches 418; Conservative 0; Mismatches 195; Indels 9; Gaps 1;

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QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGAACCAACAGGCGAGGTGACC 60
Db 38 ATGCTCGAGGAGATCCAGATTAAGAGATAGAGAACCCAAACCAACAGGCGAGGTGACC 97
QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGTCAACCGTCTCTGTGAT 120
Db 98 TACTCCAGAGAGAAATGGTGTTCAGAGAGGACACAGGCTCTGTGTCTCTGTGAT 157
QY 121 GCCAAGTCTCCCTCATTTGCTCTCAACACATTAATAATGACGAGTATATCAGCCCT 180
Db 158 GCTAAAGTTTCCATTATCATGATCTCGTACTCAGAGCTTCACGAATACATCAGCCCA 217
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAATCTATGGGGATCGATCTGTG 240
Db 218 ACAACTCGGACAAAGCAGTTATTTCGATCATGATCAGAAAGCCGTTGGAGTTGATCTATGG 277
QY 241 AGNACACAGGAGTGCATGAAGACACCTTTGGAGTTGAAGAGATCAACAATAG 300
Db 278 AGTCAACACTATGAGAAATGCAAGAGACACTTGAAGAGCTGAATGAGGTCAACAGGAAT 337
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCATGATCTAAATGGCTGAGCTTTGACGAG 360
Db 338 CTGAGGAGGAGATCAGCAAGGATGGGTGAGGCTTGAACGATCTGGGCTACGACAA 397
QY 361 CTGGCTTCTTTCAGCATGAGTGCAGTCTTCTTGGATGCCATACGTCAAAGGAAGTAC 420
Db 398 ATTGTGAATCTTATTGAAGACATGGATACTCTCAAGCTCATTCGTGAAAGAAAGTAC 457
QY 421 CATGTGATCAAACTCAGACGGAGACCAACCAAGAGGTTAAGAACTTTGGAGCAAGA 480
Db 458 AAGTCACTAGTAACCAAGATCGACCCGACGAAAGAAAGTCAAGATTTGAAGAAATA 517
QY 481 AGAGAAACATGTGCTAGTCTATTTTGACCAAGAGACCGCGGAGGATCCACAGTAT 540
Db 518 CACAGAAACCTGGTGC-----TTGAATTTGATGCAAGGAGAGAGGATCCACACTTT 568
QY 541 GGTATGAGACATGAGGAGATCAGATCTGCATTTGCATTTGCAATTTGGGCGGAAT 600
Db 569 GGATTAGTGAATGAAGTGATTAATATCTGTCTTGGTTTCCCAAAATGAGGGCCT 628
QY 601 AACTTGTACACTTTCCACCTCC 622
Db 629 CGTATATCGCCCTACGCTCC 650

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RESULT 15
AJ559554
LOCUS AJ559554 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
DEFINITION 722 bp mRNA linear EST 12-JUN-2003
ACCESSION 018_1_10_k11, mRNA sequence.
VERSION AJ559554.1 GI:31662126
KEYWORDS EST.
ORGANISM Antirrhinum majus (snapdragon)
SOURCE Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Lamiaceae; Antirrhinaceae; Antirrhineae;
Antirrhinum.
REFERENCE 1 (bases 1 to 722)
AUTHORS Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
TITLE Antirrhinum EST collection
JOURNAL Unpublished (2003)
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 28.6%; Score 281.2; DB 9; Length 722;
Best Local Similarity 65.6%; Pred. No. 3e-40;
Matches 450; Conservative 0; Mismatches 218; Indels 18; Gaps 2;
QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGAACCAACAGGCGAGGTGACC 60
Db 24 ATGCTCGAGGAGATCCAGATTAAGAGATAGAGAACCCAAACCAACAGGCGAGGTGACC 83
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAACCGTCTCTGTGAT 120
Db 84 TACTCCAGAGAGAAATGGTGTTCAGAGAGGACACAGGCTCTGTGTCTCTGTGAT 143
QY 121 GCCAAGTCTCCCTCATTTGCTCTCAACACATTAATAATGACGAGTATATCAGCCCT 180
Db 144 GCTAAAGTTTCCATTATCATGATCTCGTACTCAGAGCTTCACGAATACATCAGCCCA 203
QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAATCTATGGGGATCGATCTGTG 240
Db 204 ACAACTCGGACAAAGCAGTTATTTCGATCATGATCAGAAAGCCGTTGGAGTTGATCTATGG 263
QY 241 AGGACACAGGAGTGCATGAAGACACCTTTGGAGTTGAAGAGATCAACAATAG 300
Db 264 AGCTCACACTATGAGAAATGCAAGAGCCTTGAAGAGGCTGAATGAGGTCAACAGGAAT 323
QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCATGATCTAAATGGCTGAGCTTTGACGAG 360
Db 324 CTGAGGAGGAGATCAGCAAGGATGGGTGAGGCTTGAACGATCTGGGCTACGACAA 383
QY 361 CTGGCTTCTTTCAGCATGAGTGCAGTCTTCTTGGATGCCATACGTCAAAGGAAGTAC 420
Db 384 ATTGTGAATCTTATTGAAGACATGGATACTCTCTCAAGCTCATTCGTGAAAGAAAGTAC 443
QY 421 CATGTGATCAAACTCAGACGGAGACCAACCAAGAGGTTAAGAACTTTGGAGCAAGA 480
Db 444 AAGTCACTAGTAACCAAGATCGACCCGACGAAAGAAAGTCAAGATTTGAAGAAATA 503
QY 481 AGAGAAACATGTGCTAGTCTATTTTGACCAAGAGACCGCGGAGGATCCACAGTAT 540
Db 504 CACAGAAACCTGGTGC-----TTGAATTTGATGCAAGGAGAGAGGATCCACACTTT 554
QY 541 GGTATGAGACATGAGGAGATCAGATCTGCATTTGCATTTGCAATTTGGGCGGAAT 600
Db 555 GGATTAGTGAATGAAGTGATTAATATCTGTCTTGGTTTCCCAAAATGAGGGCCT 614
QY 601 AACTTGTACACTTTCCACCTC-----CACACCCCTAACCTCCACACGAGGAGGAGC 651
Db 615 CGTATAATCGCCCTACGCTCCCGACTTAATCACCATCTCTCTTTCACAGCGGAGGGGCG 674
QY 652 TCGCTCGGCTCTCCATCTACTCTCT 677
Db 675 TCTGATCTCACCACCTTTTGTCTTGTCT 700

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcgagggaattga.....aaaaaaaaaaaaaaaaaaaa 982

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Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:  
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11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq2:  
14: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:  
15: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:  
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17: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:  
18: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:  
19: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	306.4	31.2	681	15	US-10-104-580-3
2	306.4	31.2	946	15	Sequence 3, Appli
3	257.8	26.3	1050	13	Sequence 2, Appli
4	252.4	25.7	1231	13	Sequence 12758, A
5	250.8	25.5	1212	13	Sequence 15025, A
6	246	25.1	1155	13	Sequence 11957, A
7	240.2	24.5	1036	13	Sequence 66649, A
8	238.4	24.3	644	17	Sequence 120794, A
9	231.8	23.6	871	13	Sequence 8631, Ap
10	228	23.2	498	12	Sequence 10670, A
11	217.4	22.1	681	16	Sequence 4479, Ap
12	194.6	19.8	2381	13	Sequence 5530, Ap
13	192	19.6	2718	13	Sequence 13190, A
14	191	19.5	407	12	Sequence 120795, A
					Sequence 3294, Ap

Sequence 14, Appli  
Sequence 13, Appli  
Sequence 16, Appli  
Sequence 3447, Ap  
Sequence 3446, Ap  
Sequence 15, Appli  
Sequence 8506, A  
Sequence 380, App  
Sequence 337, App  
Sequence 3442, Ap  
Sequence 3444, Ap  
Sequence 2121, Ap  
Sequence 14870, A  
Sequence 6326, A  
Sequence 4667, Ap  
Sequence 3293, Ap  
Sequence 3292, Ap  
Sequence 13542, A  
Sequence 8682, Ap  
Sequence 1, Appli  
Sequence 3443, Ap  
Sequence 3445, Ap  
Sequence 8899, Ap  
Sequence 10295, A  
Sequence 32218, A  
Sequence 3290, Ap  
Sequence 26809, A  
Sequence 3282, Ap  
Sequence 4580, Ap  
Sequence 7, Appli  
Sequence 12120, A

US-09-922-293-14  
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US-09-732-627A-337  
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US-09-922-293-3444  
US-10-767-795-2121  
US-10-425-114-14870  
US-10-424-599-65326  
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US-09-922-293-3292  
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US-10-021-323-8682  
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US-10-425-114-10295  
US-10-424-599-32218  
US-09-922-293-3290  
US-10-425-114-26809  
US-09-732-627A-3282  
US-10-425-114-4580  
US-10-094-458A-7  
US-10-425-114-12120

#### ALIGNMENTS

#### RESULT 1

US-10-104-580-3  
; Sequence 3, Application US/10104580  
; Publication No. US20030033628A1  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; FILE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 62486  
; CURRENT APPLICATION NUMBER: US/10/104,580  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 09/410,464  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 09/287,700  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: 60/080,851  
; PRIOR FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 681  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(681)  
US-10-104-580-3

Query Match 31.2%; Score 306.4; DB 15; Length 681;  
Best Local Similarity 70.1%; Pred. No. 1.5e-79;  
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACGACCAACAGCAGGTGACC 60

DB 1 ATGGTCTGTGGAAGATTGAATCAAGAAATCGAAACCCCAACAAACAGCAAGTACC 60

QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120

Db 61 TACTCGAGAGAGAAATGGTATTTTCAAGAGAGCCCAAGACTCACTGACTTTGTGAT 120  
Qy 121 GCAGAGTCTCCCTCATTTATGCTCTCAACACTTAATAAATGACAGAGTATATCAGCCCT 180  
Db 121 GCTAAGGTCTCTTATCATGTTCTCCAACTCAACAACTCAATGAGTACATAGCCCT 180  
Qy 181 ACCACTACGACCAAGAGTATGATGATGATCACTACAGAAACTATGGGATCGATCTGTGG 240  
Db 181 TCCATCTGCAAGAGAGATCTAGATCAATATCAGAACGCTTTAGGCAATAGATCTGTGG 240  
Qy 241 AGGACACACAGAGAGTGTGATGAAGACACCTTGTGGAAGTTGAAGAGATCAACAATAAG 300  
Db 241 GGCACCTCAATACGAGAAATGCAAGAGACCTTGAGGAAGCTGAATGATCAATCATAG 300  
Qy 301 CTGAGGAGAGATCAGGAGAGGTTGGCCATGATCTTAATGGCCCTGAGCTTGACGAG 360  
Db 301 CTGAGCAAGAAATCAGGAGAGAGGAGGAGGCTGAATGATCTGAGCATTTGATCAT 360  
Qy 361 CTGGCTTCTTTCACCATGATGATGATCTTCTTGGATGCCATAGCTCAAGGAAGTAC 420  
Db 361 CTGGCGGTCTTCAGCAACATATGATGAAGCTTGAATGGTGTGGTGGCAGGAAGTAC 420  
Qy 421 CATGTGATCAAACTCAGCGAGAGACCAAGAGAGGTTAGAACTTGGAGCAAGA 480  
Db 421 CATGTGATCAAAACACAAACGAACTTACAGGAGAGGTTGAAGAAATTTAGAGGAGAG 480  
Qy 481 AGAGGAACATGCTGATGCTATTTTGACGAGAGAGCGCGGAGGATCCACAGTAT 540  
Db 481 CATGGAAACCT-----CTTGATGGAATATGAGCAAACTAGAGGATCGACAGTAT 531  
Qy 541 GGTATGAGACAAATGAGGAGAGCTAGCAATCTGCACTTGCATGTGCAATGTCAAAATGGGCGAAT 600  
Db 532 GGTATGAGCAAT-----GAAGTGTGCTTGTGCACTTGCATGCAAAATGGGCTTCC 579  
Qy 601 AACTGTGACACTTCCACCTCCACCCCTTAACCTCCACAC 642  
Db 580 AACCTTATGATTCGCTGATCATCAGGCGCAACACACAC 621

## RESULT 2

US-10-104-580-2  
; Sequence 2, Application US/10104580  
; Publication No. US20030033628A1  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; TITLE OF INVENTION: poplar and other plant species.  
; FILE REFERENCE: 62486  
; CURRENT APPLICATION NUMBER: US/10/104,580  
; CURRENT FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: 09/410,464  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 09/287,700  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: 60/080,851  
; PRIOR FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 946  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(684)  
US-10-104-580-2

Query Match 31.2%; Score 306.4; DB 15; Length 946;  
Best Local Similarity 70.1%; Pred. No. 1.9e-79;  
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

Db 1 ATGGGTCTGTGAGAGATTGAAATCAAGAGATCGAAACCCCAACAGGCAAGTCACC 60  
Qy 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGCTCACCCTTCTCTGTGAT 120  
Db 61 TACTCGAAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 120  
Qy 121 GCCAAGTCTCCCTCATTTATGCTCTCCAACTAAATAAATGACAGAGTATATCAGCCCT 180  
Db 121 GCTAAGGTCTCTTATCATGTTCTCCAACTAACTCAATGAGTACATAGCCCC 180  
Qy 181 ACCACTACGACCAAGAGTATGATGATGATCACTACAGAAACTATGGGATCGATCTGTGG 240  
Db 181 TCCACATCGAAGAGAGATCTAGATCAATATCAGAAACGCTTTAGGCATAGATCTGTGG 240  
Qy 241 AGGACACACAGAGAGTGTGATGAAGACACCTTGTGGAAGTTGAAGAGATCAACAATAAG 300  
Db 241 GGCACCTCAATACGAGAAATGCAAGAGACCTTGAGGAAGCTGAATGATCAATCATAG 300  
Qy 301 CTGAGGAGAGATCAGGAGAGGTTGGCCATGATCTTAATGGCCCTGAGCTTGACGAG 360  
Db 301 CTGAGCAAGAAATCAGGAGAGAGGAGAGGCTGAATGATCTGAGCATTTGATCAT 360  
Qy 361 CTGGCTTCTTTCACCATGATGATGATCTTCTTGGATGCCATAGCTCAAGGAAGTAC 420  
Db 361 CTGGCGGTCTTTCAGCAACATATGATGAAGCTTGAATGGTGTGGTGGCAGGAAGTAC 420  
Qy 421 CATGTGATCAAACTCAGAGCGGAGACCAAGAGAGGTTAGAACTTGGAGCAAGA 480  
Db 421 CATGTGATCAAAACACAAACGAACTTACAGGAGAGGTTGAAGAAATTTAGAGGAGAG 480  
Qy 481 AGAGGAACATGCTGATGCTATTTTGACGAGAGAGCGCGGAGGATCCACAGTAT 540  
Db 481 CATGGAAACCT-----CTTGATGGAATATGAGCAAACTAGAGGATCGACAGTAT 531  
Qy 541 GGTATGAGACAAATGAGGAGAGCTAGCAATCTGCACTTGCATGTGCAATGTCAAAATGGGCGAAT 600  
Db 532 GGTATGAGCAAT-----GAAGTGTGCTTGTGCACTTGCATGCAAAATGGGCTTCC 579  
Qy 601 AACTGTGACACTTCCACCTCCACCCCTTAACCTCCACAC 642  
Db 580 AACCTTATGATTCGCTGATCATCAGGCGCAACACACAC 621

## RESULT 3

US-10-425-114-12758  
; Sequence 12758, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 12758  
; LENGTH: 1050  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701209467\_FLI  
US-10-425-114-12758

Query Match 26.3%; Score 257.8; DB 13; Length 1050;  
Best Local Similarity 67.4%; Pred. No. 4.8e-65;  
Matches 431; Conservative 0; Mismatches 187; Indels 21; Gaps 4;

Qy	1	ATGGCGCGGGAGAGATTGAAATCAGCTGATCGAAACACAGACCACCAAGCGAGGTGACC	60
Db	58		
Db	58	ATGGGTTCAGGCGCAAGATTGAGATTAAGTTGATTGAGAACCCACCAACAGGCAAGTCACT	117
Qy	61	TACTCCAGAGAGAAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT	120
Db	118	TACTCCAGGCGAAGGAATGGTATCTTCAAGAAAACCTCATGAACTCAGTGTCTCTGTGAT	177
Qy	121	GGCAAGGTTCCCTCATTTATGCTCTCCAACTAATTAAGATGACAGAGTATATCAGCCCT	180
Db	178		
Db	178	GGCAAGGTTTCACTTATCATGTGTTCTCTAAAACCAAGAGTCAATGATACATTAGCCCT	237
Qy	181	ACCACCTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGG---ATPCGATCTG	237
Db	238	GGCCTCACGACAAAAAGGATCATTTGATCAGTATCAGAAGACTTTGGGGGATATTGATCTG	297
Qy	238	TGGAGGACACACAGGAGTCGATGAGAGACACCTTGTGGAAGTTGAAAGAGATCAACAAT	297
Db	298	TGGCGTTCTCATGTATGAGAAAATGCTTGAAAACCTTGAGAAAGCTGATGATTAATTAACAAC	357
Qy	298	AAGCTGAGGAGAGAGATCAGGCAGAGGTT-----GGGCCATGATCTAAATGGCCCTGAGC	351
Db	358	AAGCTCAGAAGACAGATCAGGCATAGGATAGGTGAGGGTTTGACATGCGACGATGAGC	417
Qy	352	TTTGACGAGCTGGCTTCTCTTGACGATGAGATGCAGTCTTCCCTTGGATGCGCATACGTCAA	411
Db	418	TTCCAGCACTCGGCACCTCTTGAAGAGATTGGTTTCTTCCATAGGGAATAACAGAA	477
Qy	412	AGGAAGTACATGTGATCAAACTCAGACGGAGACCAACCAAGAAAGGTTAAGAACTTG	471
Db	478	CGAAAGTTCCAGCTGATCAAAACACGGACTGATACCTGCAAGGAAAAGGTTAAAGCCGTG	537
Qy	472	GAGCAAAAGAAGAGGAAAATGCTGTCATGGCTATTTTTCCACGAGGAAGCAGCGCGCAGGAT	531
Db	538	GAGCAGATGAATAGAGATCTGCTG-----TTTGAACCTTGAAAGTGTGCGATCCAT	588
Qy	532	CCACAGTATGTGTTATGAGACAAATGAGGGAGACTACGAATCTGCACCTTGCATTTGCAAT	591
Db	589	CCACAATTTTATTT---TGCAATGATGAAGGACAGGGAATCAGCAGTTGCACCTGGCCAAAC	645
Qy	592	GGGGCGGAATAAATTGTATCACTTTCCACCCTCCACACCCCT	630
Db	646	GGCGCTCCACCCCTGATGCGTTCTTGTCATCAGCACCAT	684

## RESULT 4

US-10-425-114-15025  
; Sequence 15025, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 11957  
; LENGTH: 1212  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701148021\_FLI  
US-10-425-114-11957

	Query Match	25.5%;	Score 250.8;	DB 13;	Length 1212;
	Best Local Similarity	71.3%;	Pred. No. 6.2e-63;		
	Matches 362;	Conservative 0;	Mismatches 137;	Indels 9;	Gaps 2;
Qy	1	ATCGCGCGGGGAAGATTGAAATCAAGCTGATTCGAAAAACGACCAACAGGCAAGCGAGTGACC	60		
Db	232	ATGGGTCTGGCGAAGATTGAGATAAGATTGATTGAGAACCCCAACCAAGGCAAGTCACC	291		
Qy	61	TACTCCAAGAGAAGAAATGGGATTTCTCAAGAGGCTTCAGGAGGCTACCGGTTCTCTGTGAT	120		

292	TACTCCAAAGGAAGTGGTATCTTCAAGAAAGCTCATGAAGCTCAGTGTTCCTCTGTGAT	351
121	GCCAAAGGTCCTCCTCATTTATGCTCTCCAACACTAATAAAATGCACGAGTATATCAGCCCT	180
352	GCCAAAGGTTCACTCATCATGCTTCTCTAAAAACAACAAGATGCATGAATACATTAGCCCT	411
181	ACCACTACGACCAAGAGTATGTATGATGACATATCAGAAAACTATGGG---ATCGATCTGT	237
412	GGCCTCAGCACAAAAAAGATCATTTGATCAGTATCAGAAGAACTTTGGGGATATTGATCTGT	471
238	TGGAGGACACACGAGGAGTCGATGAAGACACCTTTGTGGAAGTTGAAAGAGATCAACAAAT	297
472	TGGCATTTCTCATATGAGAAAATGCTTGAAGAACTTTGAAGAGCTGAAGAGTATTACAAAT	531
298	AAGCTGAGGAGAGAGATCAGGCAGAGGTT-----GGGCCATGATCTAAATGGCCCTGAGC	351
532	AAGCTCGGAGACAGATCAGGCATAGGATAGGTGAGGGCTTGACATGAGCAGCATGAGC	591
352	TTTGACGAGCTGGCTTCTCTTGACGATGAGATCAGTCTTCTCTTGGATGCCATACGTCAA	411
592	TTCCAGCAACTCGGCACCTCTTGAAAGAGATATGGTTTCATCCATAGGGAAAAATACGCGAA	651
412	AGGAATACCATGTGATCAAAACTCAGACGGAGACACCACGAAGAAAGGTTTAAGAACTTG	471
652	CGAAGATTTCAGTGATCAAAACTCGNACTGATACCTGTAGGAAAAGGTTTAAAGCCCTG	711
472	GAGCAAGAGAGGAAAATCTGTCATG	499
712	AAGCAGATCAATGGAATCTGCTGCTTG	739

## RESULT 6

US-10-424-599-66649  
: Sequence 66649. Application US/10424599

; Publication No. US20  
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE OF INVENTION, FIGURES AND DESCS THEREOF;  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: IIS/10/424-599

; CURRENT FILING DATE: 2003-0  
 ; CURRENT FILING DATE: 2003-0  
 ; NUMBER OF SEQ ID NOS: 285684

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; NUMBER OF SEQ
; SEQ ID NO 6664
: LENGTH: 1155

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/ LENGTH: 1153
; TYPE: DNA
: ORGANTISM: Glycine max

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; ORGANISM: GLYCINE MAX
; FEATURE:
; OTHER INFORMATION: CLONE ID. DAT MDT3047 31100C 1

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Query Match	25.1%;	Score 246;	DB 13;	Length 1155;
Best Local Similarity	70.7%;	Pred. No. 1.6e-61;		
Matches 359;	Conservative	0;	Mismatches 140;	Indels 9;
				Gaps 2;

QY 1 ATGGCCGCGGGAAGATTGAATCAAGCTGATCGAATAACAGACCCAAACGGCAGGTGACC 60

Db

61 TACTCCAA GAGAAGAAATGGGATCTTCTCAAGAGGCTCAGGAGCTCACCGCTTCTCTGTCAT 120

Qy	238	TTGAGGACACACGAGGATCGATGAAGAACAACCTTGTGGAAAGTTGAAAGAGATCAACAAT	297
Db	351	TGGCGTTCTCATATGAGAAAATCTTTGAAACATTTGAAGAAGCTGATAGATATTAACAC	410
Qy	298	AAGCTGAGGAGAGAGATCAGGCAGAGGTTGGGCCATGATCTAAAT-----GGCCTTGAGC	351
Db	411	AAGCTCAGAAGACAGATCAGGCATAGGATAGTGAGGTTTGACATGAGCACGACATGAGC	470
Qy	352	TTTGACGAGCTGGCTTCTCTTGACGATGAGATGCAGTCTTCCCTTGATGTCCTACGCTCAA	411
Db	471	TTCAGCAACTGGCCACTCTTTGAAGAGGATTTGGTTCTTCCATAGGAAATACAGAA	530
Qy	412	AGGAATACCATGTGATCAAAACTCAGACGGAGCCACACAGAAAGAGGTTTAAGAACTTG	471
Db	531	CGAAAGTTTCCACGTGATCAAAACACGGACTGATACCTGCGAGGAAAAGGTTTAAAGCCTG	590
Qy	472	GAGCAAGAAGAGGAAACATCTGCTATG	499
Db	591	GAGCAGATGAATAGAGATCTCTGCTTG	618

## RESULTS

US-10-424-599-120794

; Sequence 120794, Application US/10424599  
; Publication No. US20040031072A1

GENERAL INFORMATION: APPLICANT: La Rosa

APPLICANT: Kovalic David K  
APPLICANT: Zhou Yibua

APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; TITLE OF INVENTION: soy nutrient acid molecules and other molecules  
 ; DATE OF INVENTION: 38-21(53223)B  
 ; FILE REFERENCE: 38-21(53223)B

FILE REFERENCE: 38-21(33223/B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28

; CURRENT FILING DATE: 2003-0-  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO: 120784

```

; SEQ ID NO 1207
; LENGTH: 1036
; TYPE: DNA

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; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:

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/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
/
/ 10 124 500 13070
/

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Query Match 24.5%; Score 240.2; DB 13; Length 1036;  
Best Local Similarity 62.9%; Pred. No. 7.6e-60;  
Matches 393; Conservative 0; Mismatches 223; Indels 9; Gaps 1;

QY 1 ATGGCGCGGGGAGATTGAAATCAAGCTGATCGAAACACAGACCAACAGGCAGGTGACC 60

Db 27 ATGGCTCGAGGAAAGATCCAGATCAAGAGGATAGAGAACACCACCAACCGCAGGTCACT 86

QY 61 TACTCCAAGAGAAGAATCGGATCTTCAAGAAGGTCAGGACTCACCGTTCTCTGTGAT 120

Db 87 TATTCCTAAACGACGGAATGGCCCTTTTCAAGAAGGCCAACGAGCTCACCGTTTATGCGAT 146

QY 121 GCCAAGTCTCCCTCATTATGTCGTCTCCAACACTAATAAAATGCACGAGTATATCAGCCCT 180

361	CTGCGTCTCTTTGACGATGAGATGGAGTCTTCTCTTGGATGCCATACGCTCAAGGGAAGTAC	420
387	CTCAAGCTCTCTTGAGGAAGAATGACAAAGGCCGCAAGGTTGTCGTGAGCGTAAGTAT	446
421	CATCTGATCAAAACTCAGACGGAGACCAACGAAGAAGGTTAAGAACTTGAGGCAAGA	480
447	AAGGTGATTAACAATCAGATTGACACCCAGAGGAANAAGTTTATTAACGAGANAAGTG	506
481	AGAGGAACAATGCTGCATGGCTATTTTGCACGAGGAAGCAGCGCGCGAGATCCACAGTAT	540
507	CACAACAGACTCTCTGCA-----TCACTTGTGATGCAAAAGCAGAGAATCCACGTTTT	557
541	GGTTATGAGGACAATGAGGGAGACTACGAATCTGCACTTGCATCTCTCAAAATGGGCGCAAT	600
558	GCATTGATAGTAAATGGAGGGAGTACGAGCTGTGATCGGATCTCAAAATTAGTGCCA	617
601	AACTTGTACACTTTTCCACCTCCACC	625
618	CGCATGTTTCGATTGAGCTACAGC	642

## RESULT 8

```

US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(644)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3828-013-Q1-K6-F12
US-10-021-323-8631

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Query Match	24.3%	Score 238.4;	DB 17;	Length 644;
Best Local Similarity	66.2%;	Pred. No. 1.9e-59;		
Matches 344:	Conservative	0: Mismatches 176;	Indels 0;	Gaps 0;

Qy	1	ATGGCGCGGGAAGATTGAAATCAAGCTGATCGAAGAACCAAGACCAACAGCGAGGTGACC	60
Db	32	ATGGCTCGAGGGAAGATCCAGATCAAGCTGATAGAGAACTCGACCAACAGGCAAGTCACG	91
Qy	61	TACTCCAAGAGAAAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT	120
Db	92	TATTTCGAAGAGAGAAACGGTCTTTCAAGAAGCTAATGAACCTTACAGTTCCTTTGGCAT	151
Qy	121	GCCAAGGTCTCCCTCATTTATGCTCTCCAAACCTAATAAAATGCGACGAGTATATCAGCCCT	180
Db	152	GCTAGAGTTTCGATCATCATGTTTTCCTACTCTGCTAACTCCATGAGTTTATCAGCCCT	211
Qy	181	ACCACTACGACCAAGAGTATGTATGATGACATATCAGAAAATATGGGGGATCGATCTGGG	240
Db	212	TCCACCAACAAGAGCAAGTAAATTGATCAGTACCAGAAAACCTTGGGGATCGATATCTGG	271
Qy	241	AGGACACACGAGGAGTCGATGAAGACACCTTTGTGGAAAGTTGAAAGAGATCAACAATAAG	300
Db	272	AACACCCCACTATGAGAAAATGCAAGACAGTTGAAGCAGCTGAAAGAGCTTAAACAGGAAC	331

Qy	301	CTGAGGAGAGAGATACGCACAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACAG	360
Db	332	CTGGCGAAAGAGATTAGGAGAAGGATGGCGACTGTTTGAATGATTTTGAGCATCGAAGAT	391
Qy	361	CTGGCTTCTCTTGACGATGAGATGCAGCTTCCTTGGATGCCATACGTCAAAGGAAGTAC	420
Db	392	CTTGGTGCCTTTGGAAACAGAANAATGGAGAGCTCTGTCACTCTTATTTCTGTGATAGAAGTAT	451
Qy	421	CATGTGATCAAAACTCAGACGGGAGACCAACGAAGAAGGTTTAAAGACTTGAGGCAAGA	480
Db	452	CGTGTCTCTCCACCAGATCGATCTTCCAGGAAAAGGTCGGAATGTGGAGAGATA	511
Qy	481	AGAGGAACAATGCTGCATGGCTATTTTGACCCAGGAAGCAG	520
Db	512	CACAAAATCTCTTACATGAACCTGGAATCCCTGAAAGAAG	551

RESULT 9

```

RES001. 3
US-10-425-114-10670
/ Sequence 10670, Application US/10425114
/ Publication NO. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules
/ TITLE OF INVENTION: Plants and Uses Thereo
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 10670
/ LENGTH: 871
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700958586_FLI
US-10-425-114-10670

```

Query Match	23.6%	Score 231.8;	DB 13;	Length 871;
Best Local Similarity	62.4%	Pred. No. 2.1e-57;		
Matches 384:	Conservative	0: Mismatches 222;	Indels 9;	Gaps 1;

QY	11	GGAGAATTGAAATCAAGCTGATCGAAAAACAGAGAGGTGACCTTACTCTCAAGA	70
Db	1	GAAAGATCCAGATCAAGAGGATAGAGAACACCAACCGCCAGGTCACTTATTCTTAAC	60
QY	71	GAAAGAAATGGGATCTTCAAGAAAGCTCAGGAGCTCACGGTTCTCTGTGATGCCAAGGTCT	130
Db	61	GACGGAATGGGCTTTTCAAGAAAGGCCAAGAGCTCACCGTTCTATGCGATGCCAAGTTT	120
QY	131	CCCTCAATTATGCTCTCCAACTAATAAAATGCAGAGTATATCAGCCCTCACCTACGA	190
Db	121	CTATTATATGTTCTCCAGCACTGGGAACCTCCAGGATCATCAGCCCTCCACCTCAA	180
QY	191	CCAGAGATGATGATGACTATACAGAAAACATAAGGGATCGATCTGTGGAGGACACAGC	250
Db	181	CAGAAGCAGTTCTCGATCAGTACCAGATGACTCTAGGAGTCGATCTCTGGAACTCTCAT	240
QY	251	AGGAGTCGATCAAGACACCTTGTGGAAGTTCAAGAGATCAACAATAGCTGAGGAGAG	310
Db	241	ACGAGAATATCAAGAGAACTTTGAAGAACTCAAAAGATGTGAATAGGAATCTTCGTAA	300
QY	311	AGATCAGGCAGAGGTGGGCCCATGATCTTAAATGGCGCTGAGCTTTGACGAGCTGGGTTCT	370
Db	301	AGATTGACAGAGGATGGAGATTCTCTGAACGATCTGGGCATGGAAGATCTCAAGCTCC	360
QY	371	TTGACGATGAGATGCAGTCTCTCTTGGATGCCATACGTCAAAGGAAGTACCAATGTGATCA	430
Db	361	TTGAGGAAGAAATGGACAAGGCCGCAAGGTTGTTCGTGAACGTAAGTATAAGGTGATAA	420



QY 431 AAATCTCAGCGGAGACACCAAGAGAGGTTAAGACTTGGACCAAGAGAGGAAACA 490  
DB 421 CAATCAGATTGACACCAAGAGGAAAGTTTAAACAGAGAAAGAGTGCACAAAGAC 480  
QY 491 TGCTGCATGGCTATTTCACAGAGAGAGCGCGGAGGATCCACAGTATGGTTATGAGG 550  
DB 481 TCCTGC-----GTGACTTGGATGAAGAGAGAGATCCACGCTTTTGCATTGATAG 531  
QY 551 ACAATGAGGAGATAGATCTCCATCTGCATTTGCAATGCGGGGCAATTAATCTGTACA 610  
DB 532 ATAATGAGGGGAGTACGAGTCTGTGATCGGATTTCTCAAAATTTAGGTCCACGATGTTG 591  
QY 611 CTTTCCACCTCCAC 625  
DB 592 CATTGAGCCTACAGC 606

RESULT 10  
US-09-732-627A-4479  
; Sequence 4479, Application US/09732627A  
; Publication No. US2004012338A1  
; GENERAL INFORMATION:  
; APPLICANT: Fincher, Karen L.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(51770)B  
; CURRENT APPLICATION NUMBER: US/09732,627A  
; CURRENT FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 4930  
; SEQ ID NO 4479  
; LENGTH: 498  
; TYPE: DNA  
; ORGANISM: Gossypium hirsutum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)...(498)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: LIB3493-034-P1-M1-H12  
US-09-732-627A-4479

Query Match 23.2%; Score 228; DB 12; Length 498;  
Best Local Similarity 67.8%; Pred. No. 1.9e-56;  
Matches 318; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCAAGAGGCTCACCGTTCTCTGTAT 120  
DB 25 ATGCGCTCGAGGAGATCCAGATCAAGCTGATAGAGAACTCGACCAACAGGCAAGTCAAG 84  
QY 61 TACTCCAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTAT 120  
DB 85 TATTGGAAGAGAGAAACGGTCTTTTCAAGAGCTTAAGAACTTACAGTTCTTTGCGAT 144  
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
DB 145 GCTAGAGTTTCGATCATGATGTTTCCACTTACTGTTAACTCCATGATGTTATCAGCCCT 204  
QY 181 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
DB 205 TCACCAACAAGCAAGCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATG 264  
QY 241 AGGACACACGAGGAGTGCATGAAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAAG 300  
DB 265 AACACCCATCTAGAAATGCAAGAGCAGTGAAGCAGCTGAAGAGGTTAACAGGAC 324  
QY 301 CTGAGGAGAGATCAGGAGAGGTTGGCCATGATCTTAATGCGCCCTGAGCTTTGACGAG 360  
DB 325 CTCGCAAGAGATTTAGGAGAGGATGGGCGACTGTTTGAATGATTTGAGCATTCGAAGAT 384  
QY 361 CTGGCTTCTTCCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 385 CTTTGGTCTTTGAAACAAGAAATGGAGGCTCTGTCTCTTATTCTGTGATGAAAGATAT 444

QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTTAAAGT 469  
DB 445 CGTGTCTCTCCACCAGATCGATACCTTNCAGGAAAAAAGTGAGGAAT 493

RESULT 11  
US-10-260-238-5530  
; Sequence 5530, Application US/10260238  
; Publication No. US2004001602SA1  
; GENERAL INFORMATION:  
; APPLICANT: Budworth, Paul R.  
; APPLICANT: Moughamer, Todd G.  
; APPLICANT: Briggs, Steven P.  
; APPLICANT: Cooper, Bret  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Goff, Stephen A.  
; APPLICANT: Katagiri, Fumiyaki  
; APPLICANT: Kreps, Joel  
; APPLICANT: Provart, Nicholas  
; APPLICANT: Rieke, Darrell  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
; FILE REFERENCE: 6011-NP  
; CURRENT APPLICATION NUMBER: US/10/260,238  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,448  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,277  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/370,620  
; PRIOR FILING DATE: 2002-04-04  
; NUMBER OF SEQ ID NOS: 6077  
; SEQ ID NO 5530  
; LENGTH: 681  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-260-238-5530

Query Match 22.1%; Score 217.4; DB 16; Length 681;  
Best Local Similarity 64.7%; Pred. No. 3.2e-53;  
Matches 323; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATGAAATCAAGCTGATCGAAACCAAGAGGCTCACCGTTCTCTGTAT 120  
DB 1 ATGCGCGCGGAGATGAAATCAAGCTGATCGAAACCAAGAGGCTCACCGTTCTCTGTAT 120  
QY 61 TACTCCAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTAT 120  
DB 61 TACTCCAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTAT 120  
QY 121 GCGAAGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
DB 121 GCGAAGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
QY 181 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
DB 181 GGAACCCAGATCAAGACCACTTTGACCGGTACCAAGAGGCTCAGGAGCTCACCGTTATGG 240  
QY 241 AGGACACACGAGGAGTGCATGAAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAAG 300  
DB 241 ATCGAGCAGTATGAGATATGACGCGCAGCTGAGCCATCTCAAGGACATCAATCGTGT 300  
QY 301 CTGAGGAGAGATCAGGAGAGGTTGGGCCATGATCTTAATGCGCTGAGCTTTGACGAG 360  
DB 301 CTGCGCACAGATTTAGGCAAGAGATGGGCGAGATCTGGACAGTCTGGACTTCGACGAG 360  
QY 361 CTGGCTTCTTCTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 361 CTGCGCGCTCTCGAGCAAAACGTCGACGCGCTCTCAAGAGGTTTCGCCATAGAAAGTAC 420  
QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTTAAAGT 480  
DB 421 CATGTGATCAGCGCAGACTGATACCTTCAAGAAAAAGGTGAAGCACTCGCAGGCG 480



Qy 481 AGAGGAAACATGCTGCATG 499  
Db 481 TACAAGAACCTGCAGCAGG 499

## RESULT 12

US-10-425-114-13190  
; Sequence 13190, Application US/10425114  
; Publication No. US20040034889A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 13190  
; LENGTH: 2237  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: jC-gmfl02220148909\_FLI  
US-10-425-114-13190

Query Match 19.8%; Score 194.6; DB 13; Length 2237;  
Best Local Similarity 66.7%; Pred. No. 3.8e-46;  
Matches 278; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
Qy 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60  
Db 109 ATGGCTAGAGAAAGATCCAGATCAAGAGGATAGAGAAACCAACCAACCGCCAGGTCACT 168  
Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCACCGTTCTCTGTGAT 120  
Db 169 TACTCTAAACAGCGGAATGGCCCTTTCAAGAGGCCAACAGGCTTACCCTTCTCTGGAT 228  
Qy 121 GCCAAGTCTCCCTCATTATGCTCTCCACACACTAATAAAATGCAAGTAGTATATCAGCCCT 180  
Db 229 GCCAAGTTCTATTATTAATGTTCTCCAGCACTGGAAAACTCCACCAAGTACATCAGCCCT 288  
Qy 181 ACCACTAGGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
Db 289 TCCACCTCAACAAAGCAGATCTTCCGATCAATACCAGATGACTCTGGGAGTTGATCTCTGG 348  
Qy 241 AGGACACAGGAGGATCGATGAAGACACCTTTGGGAAGTTGAAGAGATCAACAAATAAG 300  
Db 349 AACTCTCATACGAGATATGCAAGAGAACTTTGAAGAACTGAAGAGGTGAATAGGAAT 408  
Qy 301 CTGAGGAGAGATCAGGACAGGTTGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360  
Db 409 CTTCGTAAGGAGATTAGGACAGAAATGGAGATTTCTGAACGAGCTGGGCATGGAAGAT 468  
Qy 361 CTGGCTTCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417  
Db 469 CTCAGCTCTTGAAGAGAAATGGACAGGCCCAAGGTTGTGTGTGAGCGTAAG 525

## RESULT 13

US-10-424-599-120795  
; Sequence 120795, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 120795  
; LENGTH: 2718  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_80084C.1  
US-10-424-599-120795

Query Match 19.6%; Score 192; DB 13; Length 2718;  
Best Local Similarity 65.8%; Pred. No. 2.6e-45;  
Matches 279; Conservative 0; Mismatches 145; Indels 0; Gaps 0;  
Qy 1 ATGGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60  
Db 126 ATGGCTCGAGGAAGATCCAGATCAAGAGGATAGAGAACACCACCAACCGCCAGGTCACT 185  
Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCACCGTTCTCTGTGAT 120  
Db 186 TATTCTAAACGACGGAATGGCCCTTTTCAAGAGGCCAACGAGCTCACCGTTCTATGCGAT 245  
Qy 121 GCCAAGTCTCCCTCATTATGCTCTCCACACACTAATAAAATGCAAGTAGTATATCAGCCCT 180  
Db 246 GCCAAGTTCTATTATTAATGTTCTCCAGCACTGGAAAACTCCACAGTACATCAGCCCT 305  
Qy 181 ACCACTAGCACCAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
Db 306 TCCACCTCAACAAAGCAGTTCTTCGATCAGTACCAGATGACTCTAGGAGTGCATCTCTGG 365  
Qy 241 AGGACACAGGAGGATCGATGAAGACACCTTTGTGGAAGTTGAAGAGATCAACAAATAAG 300  
Db 366 AACTCTCATACGAGATATGCAAGAGAACTTTGAAGAACTCAAGATGTGAATAGGAAT 425  
Qy 301 CTGAGGAGAGATCAGGACAGAGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360  
Db 426 CTTCGTAAGGAGATTAGGACAGAGGATGGAGATTCTCTGAAGATCTGGGCATGGAAGAT 485  
Qy 361 CTGGCTTCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
Db 486 CTCAGCTCTTGGAGAGAAATGGACAGGCCCAAGGTTGTTCGTGAGCGTAGGCTC 545  
Qy 421 CATG 424  
Db 546 GAGG 549

## RESULT 14

US-09-922-293-3294  
; Sequence 3294, Application US/09922293  
; Publication No. US2004012339A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 16517.254  
; CURRENT APPLICATION NUMBER: US/09/922,293  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: US 60/069,472  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: US 60/071,479  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/074,201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,282

[illegible]

; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-922-293-3294

Query Match 19.5%; Score 191; DB 12; Length 407;  
Best Local Similarity 68.7%; Pred. No. 1,4e-45;  
Matches 263; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAAGATTGAATCAAGCTGTTCGAAACCCAGAACCAACAGGCAGGTGACC 60  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
25 ATGGCTCAGAGGAAGATCCAGATCAAGAGGATAGAGAACCACCAACCGCCAGGTCACT 84  
QY 61 TACTCCAAGAGAGAAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
85 TATCTTAACAGCGAATGGCCCTTTTCAAGAAAGGCCAAGAGCTCACCGTTCTATGGAT 144  
QY 121 GCCAAGGTTCCCTCATTTATGCTCTCCCAACACTATAAATGCAAGTAGTATACAGCCCT 180  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
145 GCCAAGGTTCTATTATTATTATGTTCTCCAGCACTGGAACTCCACGAGTACATCAGCCCC 204  
QY 181 ACCACTACCAACAAGATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
205 TCACCTCAACAAAGACAGTCTTCCGATCAGTACCAGATGACTCTAGGAGTCGATCTGTGG 264  
QY 241 AGCACACAGGAGGTCCGATGAAACACACCTTTGGAGTTTGAAAGAGATCAACAATAAG 300  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
265 AACTCTCATTACGAGATATGCAAGAGAACTTGAAGAACTCAAGATGTGATAGGAAT 324  
QY 301 CTCAGAGAGAGATCAGGACGAGGTGGGCCATGATCTAAATGCCCTGAGCTTTGACGAG 360  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
325 CTTTCGTAAGGAGATTAGGCAGAGGATGGGAGATTGTCTGAACGATCTTGACATGGAAGAT 384  
QY 361 CTGGCTTCTCTTGACATCAGAT 383  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
385 CTCAAAGCTCTTGAGGAAGAAT 407

RESULT 15  
US-09-922-293-14  
; Sequence 14, Application US/09922293  
; Publication No. US2004012339A1  
; GENERAL INFORMATION:  
; APPLICANT: Conner, Timothy W.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: Liu, Jingdong  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 16517.254  
; CURRENT APPLICATION NUMBER: US/09/922,293  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/067,000  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: US 60/069,472  
; PRIOR FILING DATE: 1997-12-09  
; PRIOR APPLICATION NUMBER: US 60/071,479  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: US 60/074,201  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,282  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,280  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,281  
; PRIOR FILING DATE: 1998-02-10  
; PRIOR APPLICATION NUMBER: US 60/074,566  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,567  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,565  
; PRIOR FILING DATE: 1998-02-12  
; PRIOR APPLICATION NUMBER: US 60/075,462  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/074,789  
; PRIOR FILING DATE: 1998-06-30

; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,459  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,461  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,464  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,460  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/075,463  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: US 60/077,231  
; PRIOR FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 60/077,229  
; PRIOR FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 60/077,230  
; PRIOR FILING DATE: 1998-03-09  
; PRIOR APPLICATION NUMBER: US 60/078,368  
; PRIOR FILING DATE: 1998-03-18  
; PRIOR APPLICATION NUMBER: US 60/080,844  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/083,067  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: US 60/083,386  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 60/083,387  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 60/083,388  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 60/083,389  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: US 60/085,224  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,223  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,222  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,533  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 60/086,186  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,187  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,185  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,184  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,183  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/086,188  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: US 60/089,524  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: US 60/089,810  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,814  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,808  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,812  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,807  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,806  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,813  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,811  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/089,793  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: US 60/091,405  
; PRIOR FILING DATE: 1998-06-30

;; PRIOR APPLICATION NUMBER: US 60/091,247  
;; PRIOR FILING DATE: 1998-06-30  
;; PRIOR APPLICATION NUMBER: US 60/099,667  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/099,668  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/099,670  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/099,697  
;; PRIOR FILING DATE: 1998-09-09  
;; PRIOR APPLICATION NUMBER: US 60/100,674  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: US 60/100,673  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: US 60/100,672  
;; PRIOR FILING DATE: 1998-09-16  
;; PRIOR APPLICATION NUMBER: US 60/100,963  
;; PRIOR FILING DATE: 1998-09-17  
;; PRIOR APPLICATION NUMBER: US 60/101,131  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: US 60/101,132  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: US 60/101,130  
;; PRIOR FILING DATE: 1998-09-21  
;; PRIOR APPLICATION NUMBER: US 60/101,508  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,344  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,347  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,343  
;; PRIOR FILING DATE: 1998-09-22  
;; PRIOR APPLICATION NUMBER: US 60/101,707  
;; PRIOR FILING DATE: 1998-09-25  
;; PRIOR APPLICATION NUMBER: US 60/104,126  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,128  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,127  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/104,124  
;; PRIOR FILING DATE: 1998-10-13  
;; PRIOR APPLICATION NUMBER: US 60/109,018  
;; PRIOR FILING DATE: 1998-11-18  
;; PRIOR APPLICATION NUMBER: US 60/108,996  
;; PRIOR FILING DATE: 1998-11-18  
;; PRIOR APPLICATION NUMBER: US 09/199,129  
;; PRIOR FILING DATE: 1998-11-24  
;; PRIOR APPLICATION NUMBER: US 09/210,297  
;; PRIOR FILING DATE: 1998-12-08  
;; PRIOR APPLICATION NUMBER: US 60/111,981  
;; PRIOR FILING DATE: 1998-12-11  
;; PRIOR APPLICATION NUMBER: US 60/113,224  
;; PRIOR FILING DATE: 1998-12-22  
;; PRIOR APPLICATION NUMBER: US 09/229,413  
;; PRIOR FILING DATE: 1999-01-12  
;; NUMBER OF SEQ ID NOS: 3853  
;; SEQ ID NO 14  
;; LENGTH: 425  
;; TYPE: DNA  
;; ORGANISM: Arabidopsis thaliana  
US-09-922-293-14

Query Match 19.0%; Score 186.4; DB 12; Length 425;  
Best Local Similarity 65.2%; Pred. No. 3.4e-44;  
Matches 274; Conservative 0; Mismatches 146; Indels 0; Gaps 0;  
QY 3 GGC GCG GCG GGA AGT TGA AAT C AAG CT GAT C G A A A A C C A G A C C A A G G A G G T G A C C T A 62  
Db 1 GGC GAG AGG GGA AGT TCC AGT C AAG AGG A T A G A G A A C C A G A C A A A C A G A C A A G T G A C G T A 60  
QY 63 CTC C A A G A G A A A A T G G G A T C T T C A A G A A G G C T C A G G A G C T C A C C G T T C T C T G T G A T G C 122

Db 61 TTCAAAGAGAGAAATGGTTTATTCAAGAAAGCAGATGAGCTCAGGTTTTGTGTGATGC 120  
QY 123 CAAGGTCTCCCTCATTTATGCTCTCCAAACACTAATAAATGCACGAGTATATCAGCCCTAC 182  
Db 121 TAGGGTTTCGATTATCATGTTCTCTAGCTCCAAACAGCTTCATGAGTATATCAGCCCTAA 180  
QY 183 CACTACGACCAAGAGTATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGGAG 242  
Db 181 CACCACAACGAGGAGATCGTAGATCTGTACCAAACTATTTCTGATGTCGATGTTTGGGC 240  
QY 243 GACACACGAGGAGTCGATGAAGACACCTTGTGAAGTTGAAGAGATCAACAATAGCT 302  
Db 241 CACTCAATATGAGCGAATGCAAGAAACCAAGAGAAACTGTTGGAGACAAATAGAAATCT 300  
QY 303 GAGGAGAGAGATCAGGCGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAGCT 362  
Db 301 CCGGACTCAGATCAAGCAGAGGCTAGGTGAGTGTGGACAGCTTGACATTCAGGAGCT 360  
QY 363 GCTTCTCTTACGATGAGATGCGAGTCTTCTTGGATGCCATAGCTCAAGGAAGTACCA 422  
Db 361 GCGTCGTCTTGAGGATGAATGGAACACTTTCAAACTCGTTCCGAGCGCAAGTTCAA 420

Search completed: September 25, 2004, 22:22:19  
Job time : 541.304 secs

Result No.	Query		Score	Match	Length	DB	ID	Description
1	306.4	31.2	681	4	US-09-410-464-3	Sequence 3, Appli		
2	306.4	31.2	946	4	US-09-410-464-2	Sequence 2, Appli		
3	131.4	13.4	4285	4	US-09-410-464-1	Sequence 1, Appli		
4	100.6	10.2	1180	2	US-08-867-087B-16	Sequence 16, Appli		
5	96.8	9.9	1059	2	US-08-867-087B-14	Sequence 14, Appli		
6	94.4	9.6	1345	1	US-08-592-214A-7	Sequence 7, Appli		
7	94.4	9.6	1345	3	US-08-659-188-7	Sequence 7, Appli		
8	94.4	9.6	1345	3	US-08-655-227-7	Sequence 7, Appli		
9	94.4	9.6	1345	3	US-08-655-241-7	Sequence 7, Appli		
10	94.4	9.6	1345	3	US-09-149-976-7	Sequence 7, Appli		
11	94.4	9.6	1345	4	US-09-398-326-7	Sequence 7, Appli		
12	94	9.6	1043	2	US-08-867-087B-12	Sequence 12, Appli		
13	93.6	9.5	945	2	US-08-485-981-9	Sequence 9, Appli		
14	93.6	9.5	945	2	US-08-867-087B-10	Sequence 10, Appli		
15	93.2	9.5	779	1	US-08-592-214A-9	Sequence 9, Appli		
16	93.2	9.5	779	3	US-08-659-188-9	Sequence 9, Appli		
17	93.2	9.5	779	3	US-08-655-227-9	Sequence 9, Appli		
18	93.2	9.5	779	3	US-08-655-241-9	Sequence 9, Appli		
19	93.2	9.5	779	3	US-09-149-976-9	Sequence 9, Appli		
20	93.2	9.5	779	4	US-09-398-326-9	Sequence 9, Appli		
21	93.2	9.5	5855	1	US-08-592-214A-20	Sequence 20, Appli		
22	93.2	9.5	5855	3	US-09-149-976-20	Sequence 20, Appli		
23	91	9.3	1027	2	US-08-867-087B-54	Sequence 54, Appli		
24	89.2	9.1	795	3	US-08-904-284-2	Sequence 2, Appli		
25	87.8	8.9	1141	2	US-08-323-449B-1	Sequence 1, Appli		
26	87.8	8.9	1141	2	US-08-485-981-1	Sequence 1, Appli		
27	87.8	8.9	1141	2	US-08-867-087B-1	Sequence 1, Appli		

QY 301 CTGAGGAGAGATCAGGAGAGGTTGGCCCATGATCTAAATGSCCTGAGCTTTGACGAG 360  
DB |||||  
QY 301 CTGAGACNAGAAATCAGGCAGAGAGAGAGGGCTGATGATCTGAGCATTTGATCAT 360  
DB |||||  
QY 361 CTGCTCTCTTTGACGATGAGATGCACTCTTCTTTGATGCCATACGTCNAAAGAAAGTAC 420  
DB |||||  
QY 361 CTGCGCGCTCTTGAGCAACATATGACTGAAGCCTTTGAATGGTGGCTGGCAGAAAGTAC 420  
DB |||||  
QY 421 CATGTGATCAAAATCTGAGCGAGACCAAGAGAGAGGTTAAGACTTTGGAGCAAGA 480  
DB |||||  
QY 421 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480  
DB |||||  
QY 481 AGAGAAACATGCTGCTGCTATTTTTCAGCAGGAAGCAGCGCGGAGGATCCACAGTAT 540  
DB |||||  
QY 481 CATGGAACCTT-----CTTGATGGAATATGAACCAAACTAGAGGATCGACAGTAT 531  
QY 541 GGTATGAGGACATGAGGAGACTACGAATCTGCACCTTGCATTTGATTCNAAATGGGGCAAT 600  
DB |||||  
QY 532 GGTATTAGTGGACAAT-----GAAGCTGCTGTTGCATTTGCAATGGGGCTTCC 579  
DB |||||  
QY 601 AACTTGTACACTTTCCACCTCCACCACCTTAACCTCCACCAC 642  
DB |||||  
QY 580 AACCTCTATGATTCGCGCTGCATCAGCGGCACACACCAC 621  
DB |||||

RESULT 2  
US-09-410-464-2  
; Sequence 2, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; EARLIER FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 946  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(684)  
US-09-410-464-2

Query Match 31.2%; Score 306.4; DB 4; Length 946;  
Best Local Similarity 70.1%; Pred. No. 3.2e-76;  
Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;  
QY 1 ATGGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60  
DB 1 ATGGGTCTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAGGCGAAGTCAACC 60  
QY 61 TACTCCAAAGAGAAATGGGATCTTCAAGAGGCTCAGAGTCAACCGTTCTCTGTGAT 120  
DB 61 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 120  
QY 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACTAAATAAATGACAGGATATACAGCCCT 180  
DB 121 GCTAAGTCTCTTATCATGTTCTTCCACACTAACTCAATGATGATACATAGCCCC 180  
QY 181 ACCACTACGACCAAGAGATGTATGATGACTATCAGAAAACTATGGGGATTCGATCTGTG 240  
DB 181 TCCACATCGACAAAGAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240  
QY 241 AGGACACACGAGGATGATGAAGACACCTTGTGGAGTTGAAGAGATCAACAATAG 300  
DB |||||

DB 241 GGCACTCAATACGAGAAAATCAAGAGCACTTGAGGAAGCTGAATGATCAATCATAAG 300  
QY 301 CTGAGAGAGAGATCAGGAGAGGTTGGCCCATGATCTAAATGSCCTGAGCTTTGACGAG 360  
DB |||||  
QY 301 CTGAGACNAGAAATCAGGCAGAGAGAGAGGGCTGATGATCTGAGCATTTGATCAT 360  
DB |||||  
QY 361 CTGCTCTCTTTGACGATGAGATGCACTCTTCTTTGATGCCATACGTCNAAAGAAAGTAC 420  
DB |||||  
QY 361 CTGCGCGCTCTTGAGCAACATATGACTGAAGCCTTTGAATGGTGGCTGGCAGAAAGTAC 420  
DB |||||  
QY 421 CATGTGATCAAAATCTGAGCGAGACCAAGAGAGAGGTTAAGACTTTGGAGCAAGA 480  
DB |||||  
QY 421 CATGTGATCAAAACACAAACGAAACCTACAGGAAGAGGTGAAGAAATTTAGAGGAGAGA 480  
DB |||||  
QY 481 AGAGAAACATGCTGCTGCTATTTTTCAGCAGGAAGCAGCGCGGAGGATCCACAGTAT 540  
DB |||||  
QY 481 CATGGAACCTT-----CTTGATGGAATATGAACCAAACTAGAGGATCGACAGTAT 531  
QY 541 GGTATGAGGACATGAGGAGACTACGAATCTGCACCTTGCATTTGATTCNAAATGGGGCAAT 600  
DB |||||  
QY 532 GGTATTAGTGGACAAT-----GAAGCTGCTGTTGCATTTGCAATGGGGCTTCC 579  
DB |||||  
QY 601 AACTTGTACACTTTCCACCTCCACCACCTTAACCTCCACCAC 642  
DB |||||  
QY 580 AACCTCTATGATTCGCGCTGCATCAGCGGCACACACCAC 621  
DB |||||

RESULT 3  
US-09-410-464-1  
; Sequence 1, Application US/09410464  
; Patent No. 6395892  
; GENERAL INFORMATION:  
; APPLICANT: Strauss et al.  
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
; FILE REFERENCE: 53375  
; CURRENT APPLICATION NUMBER: US/09/410,464  
; EARLIER FILING DATE: 1999-10-01  
; EARLIER APPLICATION NUMBER: 09/287,700  
; EARLIER FILING DATE: 1999-04-06  
; EARLIER APPLICATION NUMBER: 60/080,851  
; EARLIER FILING DATE: 1998-04-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4285  
; TYPE: DNA  
; ORGANISM: Populus balsamifera subsp. trichocarpa  
US-09-410-464-1

Query Match 13.4%; Score 131.4; DB 4; Length 4285;  
Best Local Similarity 76.1%; Pred. No. 8.8e-27;  
Matches 162; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 1 ATGGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACAGGCGAGGTGACC 60  
DB 2001 ATGGGTCTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAGGCGAAGTCAACC 2060  
QY 61 TACTCCAAAGAGAAATGGGATCTTCAAGAGGCTCAGAGTCAACCGTTCTCTGTGAT 120  
DB 2061 TACTCGAAGAGAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTTGTGAT 2120  
QY 121 GCCAAGGTCTCCCTCATTATGCTCTCAACACTAAATAAATGACAGGATATACAGCCCT 180  
DB 2121 GCTAAGTCTCTTATCATGTTCTTCCACACTAACTCAATGATGATACATAGCCCC 2180  
QY 181 ACCACTACGACCAAGAGATGTATGATGACTAT 213  
DB 2181 TCCACATCGTACGTATATCTCGTATCATGTTTCT 2213  
DB |||||

RESULT 4  
US-08-867-087B-16

Sequence 16, Application US/08867087B  
 Patent No. 5990386  
 GENERAL INFORMATION:  
 APPLICANT: An, Gynheung  
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT  
 TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
 ADDRESSEE: Winston, LLP  
 STREET: One World Trade Center  
 STREET: 121 S.W. Salmon Street  
 STREET: Suite 1600  
 CITY: Portland  
 STATE: Oregon  
 COUNTRY: United States of America  
 ZIP: 97204  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disk, 3-1/2 inch  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/867,087B  
 FILING DATE: June 2, 1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/323,449  
 FILING DATE: October 14, 1994  
 APPLICATION NUMBER: U.S. 08/485,981  
 FILING DATE: June 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Alan E.  
 REGISTRATION NUMBER: 35,123  
 REFERENCE/DOCKET NUMBER: 4630-47071  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (503) 226-7391  
 TELEFAX: (503) 228-9446  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1180 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double stranded  
 TOPOLOGY: linear  
 US-08-867-087B-16

Query Match 10.2%; Score 100.6; DB 2; Length 1180;  
 Best Local Similarity 68.5%; Pred. No. 2e-18;  
 Matches 139; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy	1	ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC	60
Db	110	ATGGGAGAGGAGGTGGAGCTGAAGAGATCGAGACAGATCAACAGCGAGGTGACG	169
Qy	61	TACTCCAGAGAGAAATGGGATCTTCAAGAGCTCAGAGCTCAGCGTCTCTGTGAT	120
Db	170	TTCCGAAGCGGAGGAATGGCTGCTCAAGAAGCGTACGAGCTCTCCGTCTCTGGAC	229
Qy	121	GCCAGGTCTCCCTCATTTATCTCTCAACACTATAAATGACAGATATATCAGCCCT	180
Db	230	GCCAGGTCTCCCTCATTTATCTCTCAACCGGGCAAGCTCTACGAGTTCTGCGGGC	289
Qy	181	ACCACTACGACCAAGATATGTA	203
Db	290	CAAGCATGACCAAGACTTTGGA	312

RESULT 5  
 US-08-867-087B-14  
 Sequence 14, Application US/08867087B  
 Patent No. 5990386  
 GENERAL INFORMATION:  
 APPLICANT: An, Gynheung

TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT  
 TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
 ADDRESSEE: Winston, LLP  
 STREET: One World Trade Center  
 STREET: 121 S.W. Salmon Street  
 STREET: Suite 1600  
 CITY: Portland  
 STATE: Oregon  
 COUNTRY: United States of America  
 ZIP: 97204  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disk, 3-1/2 inch  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: MS DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/867,087B  
 FILING DATE: June 2, 1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/323,449  
 FILING DATE: October 14, 1994  
 APPLICATION NUMBER: U.S. 08/485,981  
 FILING DATE: June 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dow, Alan E.  
 REGISTRATION NUMBER: 35,123  
 REFERENCE/DOCKET NUMBER: 4630-47071  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (503) 226-7391  
 TELEFAX: (503) 228-9446  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1059 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double stranded  
 TOPOLOGY: linear  
 US-08-867-087B-14

Query Match 9.9%; Score 96.8; DB 2; Length 1059;  
 Best Local Similarity 68.4%; Pred. No. 2.2e-17;  
 Matches 134; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy	1	ATGCGCGCGGGAAGATTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC	60
Db	98	ATGGGAGAGGCGGGTGGAGCTGAAGAGATCGAGACAGATCAACCGGAGGTGACG	157
Qy	61	TACTCCAGAGAGAAATGGGATCTTCAAGAAGGCTCAGAGCTCAGCGTCTCTGTGAT	120
Db	158	TTCCGACAGAGAGGAGATGGCTGCTCAAGAAGCGGTACGAGCTCTCCGTCTCTGGAC	217
Qy	121	GCCAGGTCTCCCTCATTTATGCTCTCCAACTATAAATGACAGATATATCAGCCCT	180
Db	218	GCCAGGTCTCCCTCATTTATGCTCTCCAAACCGGCAAGCTCTACGAGTTCTGCGAGC	277
Qy	181	ACCACTACGACCAAGA	196
Db	278	CAGAGCATGACTAAA	293

RESULT 6  
 US-08-592-214A-7  
 Sequence 7, Application US/08592214A  
 Patent No. 5811536  
 GENERAL INFORMATION:  
 APPLICANT: Yanofsky, Martin F.  
 TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
 TITLE OF INVENTION: Genes and Methods of Using Same  
 NUMBER OF SEQUENCES: 33  
 CORRESPONDENCE ADDRESS:



ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 149..968  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1345  
OTHER INFORMATION: /note= "product = 2ea mays AP1."  
US-08-592-214A-7

Query Match 9.6%; Score 94.4; DB 1; Length 1345;  
Best Local Similarity 67.0%; Pred. No. 1.2e-16;  
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAATAACAGACCAACAGCGGAGGTGACC 60  
DB 149 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAATAACAGACCAACAGCGGAGGTGACC 208  
QY 61 TACTCCAGAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGTCCACCGTTCTCTGTGAT 120  
DB 209 TTCTCCAGAGCGCGGAGCGGCTGCTCAAGAGGCGGACAGAGATCTCCGTCCTCTCGGAT 268  
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAAATAAATGACGAGTATATCAGCCCT 180  
DB 269 GCCGAGTCCGCGTCATCGTCTTCTCCCAAGGCGAGCTTACGAGTACGCCACCGAC 328  
QY 181 ACCACTAGCAGCAAGAGTAT 200  
DB 329 TCCCGCATGGACAAATCT 348

RESULT 7  
US-08-592-188-7  
Sequence 7, Application US/08659188  
Patent No. 6002069  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early  
TITLE OF INVENTION: Reproductive Development and Methods of Making Same  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/659,188  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1946  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 149..968  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..1345  
OTHER INFORMATION: /note= "product = Zea mays AP1."  
US-08-659-188-7

Query Match 9.6%; Score 94.4; DB 3; Length 1345;  
Best Local Similarity 67.0%; Pred. No. 1.2e-16;  
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 1 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAATAACAGACCAACAGCGGAGGTGACC 60  
DB 149 ATGCGCGCGGGAAGATTGAAATCAAGCTGATCGAATAACAGACCAACAGCGGAGGTGACC 208  
QY 61 TACTCCAGAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGTCCACCGTTCTCTGTGAT 120  
DB 209 TTCTCCAGAGCGCGGAGCGGCTGCTCAAGAGGCGGACAGAGATCTCCGTCCTCTCGGAT 268  
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAAATAAATGACGAGTATATCAGCCCT 180  
DB 269 GCCGAGTCCGCGTCATCGTCTTCTCCCAAGGCGAGCTTACGAGTACGCCACCGAC 328  
QY 181 ACCACTAGCAGCAAGAGTAT 200  
DB 329 TCCCGCATGGACAAATCT 348

RESULT 8  
US-08-655-227-7  
Sequence 7, Application US/08655227  
Patent No. 6025483  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
TITLE OF INVENTION: Maize and Cauliflower APETALAL Gene  
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays AP1."
;
US-08-655-227-7

Query Match          9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 149 ATGGCGCGCGGAGAGTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 208
QY 61 TACTTCCAAAGAGAGAAATGGGATCTTCAAGAAGGCTCAGAGGTCACCGTTCTCTGTGAT 120
Db 209 TTCTTCCAAAGCGCGGACGGCTGCTCAAGAGGCGGACAGATCTCCGTCCTCTGCGAT 268
QY 121 GCCAAGGTCCTCCATATGCTTCCCAACTATATAAATGACGAGTATATACGCCCT 180
Db 269 GCCGAGTCCGCGTCATCGTCTTCCCGCAAGGCAAGCTCTACGAGTACGCCACCGAC 328
QY 181 ACCACTACGACCAAGAGTAT 200
Db 329 TCCCGCATGGACAAAATTCT 348

RESULT 9
US-08-655-241-7
; Sequence 7, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays AP1."
;
US-08-655-241-7

Query Match          9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 60
Db 149 ATGGCGCGCGGAGAGTGAATCAAGCTGATCGAAACACAGACCAACAGCGAGGTGACC 208
QY 61 TACTTCCAAAGAGAGAAATGGGATCTTCAAGAAGGCTCAGAGGTCACCGTTCTCTGTGAT 120
Db 209 TTCTTCCAAAGCGCGGACGGCTGCTCAAGAGGCGGACAGATCTCCGTCCTCTGCGAT 268
QY 121 GCCAAGGTCCTCCATATGCTTCCCAACTATATAAATGACGAGTATATACGCCCT 180
Db 269 GCCGAGTCCGCGTCATCGTCTTCCCGCAAGGCAAGCTCTACGAGTACGCCACCGAC 328
QY 181 ACCACTACGACCAAGAGTAT 200
Db 329 TCCCGCATGGACAAAATTCT 348

RESULT 10
US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays API"
US-09-149-976-7

Query Match          9.6%; Score 94.4; DB 3; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACAGACCAACAGGAGGTGACC 60
DB 149 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACAGACCAACAGGAGGTGACC 208
QY 61 TACTTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCACCGTTCTCTGTGAT 120
DB 209 TTCTTCCAAAGCGCGGAGCGGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGGAT 268
QY 121 GCCAAGTCTCCCTCATATGCTTCTCCAACTAATAAATGACAGGATATATCAGCCCT 180
DB 269 GCCAGGTCGCCGTCATGCTTCTCCAACTAATAAATGACAGGATATATCAGCCCT 328
QY 181 ACCACTACGACCAAGAGTAT 200
DB 329 TCCCGCATGGACAAATCT 348

RESULT 11
US-09-398-326-7
Sequence 7, Application US/09398326
Patent No. 6355963
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays API."
US-09-398-326-7

Query Match          9.6%; Score 94.4; DB 4; Length 1345;
Best Local Similarity 67.0%; Pred. No. 1.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACAGACCAACAGGAGGTGACC 60
DB 149 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACAGACCAACAGGAGGTGACC 208
QY 61 TACTTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGAGGCTCACCGTTCTCTGTGAT 120
DB 209 TTCTTCCAAAGCGCGGAGCGGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGGAT 268
QY 121 GCCAAGTCTCCCTCATATGCTTCTCCAACTAATAAATGACAGGATATATCAGCCCT 180
DB 269 GCCAGGTCGCCGTCATGCTTCTCCAACTAATAAATGACAGGATATATCAGCCCT 328
QY 181 ACCACTACGACCAAGAGTAT 200
DB 329 TCCCGCATGGACAAATCT 348

RESULT 12
US-08-867-087B-12
Sequence 12, Application US/08867087B
Patent No. 5990386
GENERAL INFORMATION:
APPLICANT: An, Gynheung
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell Leigh &
ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,087B
FILING DATE: June 2, 1997

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1043 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-867-087B-12

Query Match          9.6%; Score 94; DB 2; Length 1043;
Best Local Similarity 68.4%; Pred. No. 1.3e-16;
Matches 130; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAGAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCGAGGTGACC 60
DB 34 ATGGGAGGGGAGAGATTGAGCTGAGCGGATCGAGAACAGATCAACAGGCGAGGTGACC 93
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGAGCTCAGCGTTCTCTGTGAT 120
DB 94 TTCTCCAGGCGCCGAAAGCGGCTCTCAAGAGGCTTACAGAGGCTGTCGGTTCTCTGGAC 153
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACAGAGTATATCAGCCCT 180
DB 154 GCCGAGGTGGGCTCATCTCTTCCAGCGCGGCGAGCTTACAGAGTTGGCGAGCGCC 213
QY 181 ACCACTACGA 190
DB 214 GGCATAACAA 223

RESULT 13
US-08-485-981-9
; Sequence 9, Application US/08485981
; Patent No. 5861542
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND
; TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,981
; FILING DATE: June 7, 1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,449
; FILING DATE: October 14, 1994

```

```

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-42933
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
US-08-485-981-9

Query Match          9.5%; Score 93.6; DB 2; Length 945;
Best Local Similarity 67.3%; Pred. No. 1.6e-16;
Matches 132; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGGCGCGGGAGAGATTGAATCAAGCTGATCGAAACACAGACCAACAGGCGAGGTGACC 60
DB 16 ATGGGAGGGGAGGTTAGGCTTAAAGAGATAGAGAACAGATCAACAGGCGAGGTGACC 75
QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAAAGGCTCAGAGCTCACCCTTCTCTGTGAT 120
DB 76 TTGGCTAAGAGAGAAATGGACTTTTGAAAAAGCTTATGAGCTTCTGTTCTTGTGAT 135
QY 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACAGAGTATATCAGCCCT 180
DB 136 GTGAGGTTGGCTCATCATCTTCTCCAAATAGGGGAAAACTGTACGAGTTCTGCAGTAGC 195
QY 181 ACCACTACGACCAAGA 196
DB 196 TCTAGCATGCTCAAGA 211

RESULT 14
US-08-867-087B-10
; Sequence 10, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123

```

REFERENCE/DOCKET NUMBER: 4630-47071  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 945 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-867-087B-10

Query Match 9.5%; Score 93.6; DB 2; Length 945;  
Best Local Similarity 67.3%; Pred. No. 1.6e-16;  
Matches 133; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGATTGAATCAAGCTGATCGAAACCAAGACCAACAGCGAGGTGACC 60  
Db 16 ATGGGAAGGGGTAGGGTTGAGCTTAAGAGAAATAGAGAACAAAGATCAACAGGCAAGTGACC 75  
QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120  
Db 76 TTGCTTAGAGAGAAATGAGCTTTTGAAGAAAGCTTAAGAGCTTCTGTCTTTGTGAT 135  
QY 121 GCCAAGGTCCTCCCTCATATGCTCTCCAACTAATAAATGACAGATATATACGCCCT 180  
Db 136 GCTGAGGTTGCTCTCATCATCTTCTCCATAGGGGAAACCTGTACGAGTTCTGCAGTAGC 195  
QY 181 ACCACTAGCACCAGA 196  
Db 196 TCTAGCATGCTCAAGA 211

RESULT 15  
US-08-592-214A-9  
Sequence 9, Application US/08592214A  
Patent No. 5811536  
GENERAL INFORMATION:  
APPLICANT: Yanoofsky, Martin F.  
TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
TITLE OF INVENTION: Genes and Methods of Using Same  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,214A  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1927  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 779 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 10..775  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 778..779 /note= "N = one or more  
OTHER INFORMATION: nucleotides."  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: /note= "product = Arabidopsis  
thaliana CAL"  
US-08-592-214A-9

Query Match 9.5%; Score 93.2; DB 1; Length 779;  
Best Local Similarity 71.8%; Pred. No. 1.9e-16;  
Matches 122; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGAGATTGAATCAAGCTGATCGAAACCAAGACCAACAGCGAGGTGACC 60  
Db 10 ATGGGAAGGGGTAGGGTTGAAATTGAAGAGGATAGAGAACCAAGATCAATAGACAAGTGACA 69  
QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120  
Db 70 TTCTCGAAGAGAAAGAACTGGTCTTTTGAAGAAAGCTCAGGAGATCTCTGTCTTTGTGAT 129  
QY 121 GCCAAGGTCCTCCCTCATATGCTCTCCAACTAATAAATGACAGGTA 170  
Db 130 GCCGAGGTTTCCCTTATTGTCTTCTCCATAAGGGCAAATTGTTTCGAGTA 179

Search completed: September 25, 2004, 22:05:12  
Job time : 86.4605 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 13:15:32 ; Search time 455.966 Seconds  
(without alignments)  
9149.204 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcggggaagtga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001as.\*
- 5: Geneseq2001bs.\*
- 6: Geneseq2002s.\*
- 7: Geneseq2003as.\*
- 8: Geneseq2003bs.\*
- 9: Geneseq2003cs.\*
- 10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	306.4	31.2	946	8	ACA62518
6	303.2	30.9	924	3	Aaz57943
7	247.2	25.2	989	3	AAC55879
8	237	24.1	926	6	AAD42259
9	236.4	24.1	882	2	AAQ51189
10	227.4	23.2	954	3	AAQ51525
11	227.4	23.2	959	3	AAQ40831
12	225.8	23.0	1170	3	AAC51790
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27	129	13.1	780	6	Abk82086	Abk82086 Novel flo
28	129	13.1	783	6	Abk82087	Abk82087 Novel flo
29	129	13.1	1065	6	Abk82127	Abk82127 DNA encod
30	129	13.1	1065	6	Abk82124	Abk82124 DNA encod
31	128.2	13.1	592	6	Abk82090	Abk82090 Novel flo
32	128.2	13.1	4192	3	Aaz57942	Aaz57942 Poplar fl
33	126.2	12.9	1004	3	AAQ46623	AAQ46623 Zea mays
34	121	12.3	10139	6	ABQ81397	ABQ81397 Truncated
35	116.6	11.9	1089	6	AAD42258	Corr AP3
36	110.6	11.3	896	9	ADD55880	Thalecres
37	110.6	11.3	947	3	AAC39436	Aac39436 Arabidops
38	106	10.8	446	3	AAC48151	Aac48151 Zea mays
39	106	10.8	495	3	AAC48125	Aac48125 Zea mays
40	105.4	10.7	780	2	AAQ55089	Aac55089 fbpl cDNA
41	103.4	10.5	909	3	AAC35208	Aac35208 Arabidops
42	101	10.3	560	3	AAC34803	Aac34803 Arabidops
43	100.6	10.2	1181	2	AAV71741	AAV71741 Rice OsMA
44	100.6	10.2	1181	3	AAI44855	AAI44855 Plant flo
45	100.2	10.2	706	3	AAC55965	Aac55965 Eucalyptu

#### ALIGNMENTS

RESULT 1  
AAS00104  
ID AAS00104 standard; cDNA; 982 BP.  
XX  
AC AAS00104;  
XX  
DT 11-SEP-2003 (revised)  
DT 17-MAY-2001 (first entry)  
XX  
DE Granny Smith apple cDNA encoding MdAP3.  
XX  
XX Granny Smith apple; MdAP3; seedless fruit; horticulture;  
KW accelerated breeding programme; cross pollination; transgenic plant;  
KW biennial bearing tendency; codling moth; ss.  
XX  
OS Malus x domestica; var. Granny Smith.  
XX  
FH Key Location/Qualifiers  
CDS 1..699  
FT /\*tag= a  
FT /product= "MdAP3"  
XX  
XX WO200117334-A1.  
XX  
PD 15-MAR-2001.  
XX  
PF 07-SEP-2000; 2000WO-NZ000176.  
XX  
XX 07-SEP-1999; 99NZ-00337688.  
XX  
XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.  
XX  
XX Yao J, Morris BA;  
XX WPI; 2001-235145/24.  
XX P-RSDB; AAU00187.  
XX  
XX New genetically modified fruiting plants that does not functionally  
XX express MdPI or MdAP3 peptides, useful for producing seedless fruits,  
XX specifically apple and its related species.  
XX  
XX Claim 17; Fig 6; 41pp; English.  
XX  
XX The sequence encodes Granny Smith apple MdAP3. The invention concerns a  
XX fruiting plant that has been genetically modified so that it does not  
XX functionally express the MdPI or MdAP3 peptide, producing seedless

CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3  
 CC may be used to transform fruiting plants, specifically apple and pear.  
 CC The polynucleotides may be used in modulating, reducing or eliminating  
 CC seed-bearing capacity in fruiting plants, used in horticulture, and in  
 CC breeding programmes to monitor the progress in breeding a stable seedless  
 CC fruiting plant. The polynucleotides may also be used in programmes for  
 CC identifying nucleic acid variants from fruiting plants. They can be used  
 CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),  
 CC for use in an accelerated breeding programme to produce seedless fruit.  
 CC They may also be used in designing probes and primers for MdPI or MdAP3,  
 CC or their variants. The seedless fruiting plant is more convenient than  
 CC seeded fruit since these can be cropped without pollination, reducing  
 CC dependence on bees, pollinator varieties and warm weather at flowering.  
 CC The absence of pollen is also advantageous to alleviate environmental  
 CC concerns regarding the transfer of transgenes to non-transgenics by cross  
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing  
 CC tendencies that have been attributed to the inhibition of flower bud  
 CC formation by developing seeds and are less susceptible to codling moth  
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 982 BP; 308 A; 203 C; 226 G; 245 T; 0 U; 0 Other;

Query Match 100.0%; Score 982; DB 4; Length 982;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-252;  
 Matches 982; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGGAGATTGAATCAACCTCATCGAATCCAGAACCCAGACGAGGAGTACC 60  
 DB 1 ATGGCGCGCGGAGATTGAATCAACCTCATCGAATCCAGAACCCAGACGAGGAGTACC 60  
 QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 120  
 DB 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 120  
 QY 121 GCCAAGGTCTCCCTCATATGCTCTCCACACATTAATAATGACAGATATACGCCCT 180  
 DB 121 GCCAAGGTCTCCCTCATATGCTCTCCACACATTAATAATGACAGATATACGCCCT 180  
 QY 181 ACCACTACGACCAAGAGATATGATGATGACTATCAGAAATCTATGGGATCGATCTGTGG 240  
 DB 181 ACCACTACGACCAAGAGATATGATGATGACTATCAGAAATCTATGGGATCGATCTGTGG 240  
 QY 241 AGGACACACAGAGAGTGCATGAAGACACCTTTGTGAAGTTGAAGAGATCAACATAAG 300  
 DB 241 AGGACACACAGAGAGTGCATGAAGACACCTTTGTGAAGTTGAAGAGATCAACATAAG 300  
 QY 301 CTGAGGAGAGAGATCAGGACAGAGTTGGGCTCATGATCTAAATGGCTGAGCTTGAACGAG 360  
 DB 301 CTGAGGAGAGAGATCAGGACAGAGTTGGGCTCATGATCTAAATGGCTGAGCTTGAACGAG 360  
 QY 361 CTGCTTCTCTTGACGATGAGATGCGAGTCTCTTGATGCCATACGTCAAGAGAGTAC 420  
 DB 361 CTGCTTCTCTTGACGATGAGATGCGAGTCTCTTGATGCCATACGTCAAGAGAGTAC 420  
 QY 421 CATGTGATCAAACTCAGCGGAGACACCAAGAGAGGTTAAGAACTTGGAGCAAGA 480  
 DB 421 CATGTGATCAAACTCAGCGGAGACACCAAGAGAGGTTAAGAACTTGGAGCAAGA 480  
 QY 481 AGAGGAAACATGTGCTGCTATTTTGAACGAGAGACCGCGGAGGATCCACAGTAT 540  
 DB 481 AGAGGAAACATGTGCTGCTATTTTGAACGAGAGACCGCGGAGGATCCACAGTAT 540  
 QY 541 GGTATGAGACAAATGAGGAGATCAGGATCTGCACTTGCATTGTCATATGGGCGAAT 600  
 DB 541 GGTATGAGACAAATGAGGAGATCAGGATCTGCACTTGCATTGTCATATGGGCGAAT 600  
 QY 601 AACTTGTACACTTTCACCTCCACCCCTTAACCTCCACGAGGAGAGCTCGCTCGGC 660  
 DB 601 AACTTGTACACTTTCACCTCCACCCCTTAACCTCCACGAGGAGAGCTCGCTCGGC 660  
 QY 661 TCCTCATTAATCTCATGACAGATCTCCGCTTGTGATCTGATCTGATGATGATGATTA 720

DB 661 TCCTCATTAATCTCATGACAGATCTCCGCTTGTGATCTGATGATGATGATTA 720  
 QY 721 ATCATCATCAAGTATATATTAAGGTCACTTATAAAGTCTTTTCTCTTAAAGTGTGCT 780  
 DB 721 ATCATCATCAAGTATATATTAAGGTCACTTATAAAGTCTTTTCTCTTAAAGTGTGCT 780  
 QY 781 TGGTGACTATCTTTAGGCAAGGATTAGACTTGGACTACCTCTGAAAACAGATGATATA 840  
 DB 781 TGGTGACTATCTTTAGGCAAGGATTAGACTTGGACTACCTCTGAAAACAGATGATATA 840  
 QY 841 TATGTGTGTGTGTTTAAATCAATCATAGCACTAAAAAATCCGCGCTTTGCTTGT 900  
 DB 841 TATGTGTGTGTGTTTAAATCAATCATAGCACTAAAAAATCCGCGCTTTGCTTGT 900  
 QY 901 GGGTTTGTGTATTAATTAATTAATCTTCTATCTATATATATCATGCGAGATTCCTTTG 960  
 DB 901 GGGTTTGTGTATTAATTAATTAATCTTCTATCTATATATATCATGCGAGATTCCTTTG 960  
 QY 961 ATAAAAAATAAAAAATAAAAA 982  
 DB 961 ATAAAAAATAAAAAATAAAAA 982

RESULT 2  
 AAF85393  
 ID AAF85393 standard; cDNA; 681 BP.  
 XX  
 AC AAF85393;  
 XX  
 DT 23-JUL-2001 (first entry)  
 XX  
 DE Nucleotide sequence of the floral homeotic protein PTD.  
 XX  
 KW Floral homeotic gene; PTD; PTLF; PTAG-1; PTAG-2; floral tissue; LEAFY;  
 KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;  
 KW fertility; sterility; ss.  
 XX  
 OS Populus balsamifera.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..681  
 FT /\*tag= a  
 FT /product= "PTD"  
 XX  
 CA2319853-A1.  
 XX  
 PD 01-APR-2001.  
 XX  
 PF 02-OCT-2000; 2000CA-02319853.  
 XX  
 PR 01-OCT-1999; 99US-00410464.  
 XX  
 PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX  
 PI Rottman WH, Strauss SH, Brunner AM, Sheppard LA;  
 XX  
 DR WPI; 2001-336098/36.  
 DR P-PSDB; AAB68435.  
 XX

Novel isolated polynucleotide derived from Populus species, useful for  
 producing transgenic plants having modified fertility characteristic,  
 particularly sterility.

Claim 25; Page 42-43; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD.  
 It is derived from Populus balsamifera subsp. trichocarpa. The  
 specific location also describes PTLF, PTAG-1 and PTAG-2 proteins. The floral  
 homeotic proteins are expressed in floral tissues. PTLF is a homologue of  
 LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature  
 inflorescences on which floral primordia are developing. PTD is a  
 homologue of DEFICIENS (DEF), and is strongly expressed in stamen  
 primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are





QY 481 AGAGGAAACATGCTGCATGCTATTTTGACAGGAAGCAGCCGCGAGGATCCACAGTAT 540  
 DB |||||  
 QY 481 CATGGAACCT- - - - -CTTGATGGAATATGAGCAAAACTAGAGGATCGACAGTAT 531  
 DB |||||  
 QY 541 GGTATGAGGACATGAGGAGACTAGCAATCTGCATCTGCAATGTCCTGCAATGGGGGAAT 600  
 DB |||||  
 QY 532 GGTATGAGGACAT- - - - -GAAGCTGCTGTTGCACTTGCCTGCAATGGGGTTC 579  
 DB |||||  
 QY 601 AACTTGTACACTTTCACCTCCACCCCTAACTCCACCAC 642  
 DB |||||  
 QY 580 AACCTTATGATTCCTCGCTGCATCAGGCGCAACCCACCAC 621  
 DB |||||

## RESULT 4

ABK88485  
 ID ABK88485 standard; cDNA; 946 BP.

AC ABK88485;

DT 29-AUG-2003 (revised)  
 DT 07-OCT-2002 (first entry)

XX Poplar protein transduction domain, PTD, cDNA.

XX Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;  
 KW protein transduction domain; floral homeotic gene;  
 KW floral-specific expression; cytotoxin; fertility; sterility; PTLF;  
 KW PTAG-1; PTAG-2.

XX Populus balsamifera; subsp. trichocarpa.

XX Key Location/Qualifiers  
 FT CDS 1..684  
 FT /\*tag= a  
 FT /product= "PTD"

PN US6395892-B1.

XX 28-MAY-2002.

XX 01-OCT-1999; 99US-00410464.

XX 06-APR-1998; 98US-0080851P.

XX 06-APR-1999; 99US-00287700.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Strauss SH, Rottmann W, Brunner A, Sheppard L;

XX WPI; 2002-572853/61.

XX P-PSDB; ABG30865.

PT New protein transduction domain promoter nucleic acid molecule useful for  
 PT producing transgenic plants having modified fertility characteristics,  
 PT particularly sterility.

XX Example 1; Col 35-38; 46pp; English.

XX The invention relates to an isolated nucleic acid molecule especially a  
 CC protein transduction domain (PTD) promoter; (i) that hybridises under  
 CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium  
 CC dodecyl sulphate) at 65 plusoc to nucleotides or (ii) comprising 35  
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene  
 CC and is the homologue of DEFICIENS. Also includes are a recombinant  
 CC nucleic acid comprising the PTD promoter, a cell transformed with the  
 CC recombinant nucleic acid and a transgenic plant comprising the  
 CC transformed cell. The PTD promoter is useful to obtain floral-specific  
 CC expression of genes such as cytotoxins, that are employed in genetic  
 CC ablation strategies to produce trees having modified fertility  
 CC characteristics, including sterility. Genetic constructs comprising  
 CC antisense versions or dominant negative mutants of PTD are useful in  
 CC producing genetically engineered Poplars and other trees, and for sense

CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1 and  
 CC PTAG-2 (none are defined). The present sequence is the PTD cDNA. (Updated  
 CC on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 31.2%; Score 306.4; DB 6; Length 946;

Best Local Similarity 70.1%; Pred. No. 1.4e-71;

Matches 450; Conservative 0; Mismatches 171; Indels 21; Gaps 2;

QY 1 ATGGCGCGGGAAGATTGAAATCAAGCTGATCGAAACCAACAGACACAGCGAGTAC 60

DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAGATCGAAACCCCAACAAAGTCAAGTCA 60

QY 61 TACTCCAAAGAGAAGAAATGGGATCTTCAAGAAAGCTCAGGAGCTCAGCGTTCTCTGTGAT 120

DB 61 TACTCGAAGAGAGAAATGGTATTTTCAGAAAGCCCAAGAACTACTGTACTTTGTGAT 120

QY 121 GCCAAGTCTCCCTCATATATGCTCTCCAACTATAATAATGCACAGATATATCAGCCCT 180

DB 121 GCTAAGTCTCTCTTATCATGTTCTCCAACTATACTCAATGAGTACATTTAGCCCC 180

QY 181 ACCCTACGACCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 240

DB 181 TCCCATCGAAGAGAGATCTAGATCATATATCAGAACGCTTTAGGATAGATCTGTGG 240

QY 241 AGGACACACGAGGAGTCTGATGAAAGACACCTTTGTGAGTTGAAAGAGATCAACAATAAG 300

DB 241 GGCATCAATACGAGAAATCAAGAGACCTTTGAGGAAGCTGATGATATCAATCAATAAG 300

QY 301 CTGAGGAGAGATCAGGACAGGTTGGGCCATGATCTAAATGSCCTGAGCTTTGACGAG 360

DB 301 CTGAGACAAAGAAATCAGGACAGGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360

QY 361 CTGGCTTCTCTTGACGATGAGATGATGATGATGATGATGATGATGATGATGATGATG 420

DB 361 CTGGCGGCTCTTGAGCAACATATGATGAAAGCTTTGAATGTTGCTGCTGGCAGGAGTAC 420

QY 421 CATGTGATCAAACTCAGACGGAGACCAACAGAGAGTTTAAAGGTTTAAAGCTTTGGAGCAAGA 480

DB 421 CATGTGATCAAAACACAAACCAACCTACAGGAGAAAGGTGAAGAAATTTAGAGGAGAGA 480

QY 481 AGAGGAAACATGCTGCTGCTATTTTACAGGAGACAGCGCGAGGATCCACAGTAT 540

DB 481 CATGGAACCT- - - - -CTTGATGGAATATGAGCAAACTAGAGAGATCGACATAT 531

QY 541 GGTATGAGGACATGAGGAGAGACTACGAATCTGCACTTGCATTTGTCATTTGTCATTTG 600

DB 532 GGTATTAGTGGACAAT- - - - -GAAGCTGCTGTTGCACTTGCATTTGCAATTTGGGCTTCC 579

QY 601 AACTTGTACACTTTCACCTCCACCCCTTAACCTCCACCAC 642

DB 580 AACCTTATGATTCCTCGCTGCATCAGGCGCAACCCACCAC 621

## RESULT 5

ACA62518

ID ACA62518 standard; cDNA; 946 BP.

XX ACA62518;

XX 18-AUG-2003 (first entry)

XX Poplar homeotic gene PTD, cDNA.

XX Poplar; ss; gene; PTD; deficient; homeotic gene; floral development;  
 KW sterile tree; pulp; paper; plant.

XX Populus balsamifera subsp. trichocarpa.

XX Key Location/Qualifiers

FT CDS 1..684

FT /\*tag= a

FT	/product= "PTD"
FT	/note= "This CDS is specifically claimed in claim 1"
XX	
PN	US2003033628-A1.
XX	
PD	13-FEB-2003.
XX	
PF	21-MAR-2002; 2002US-00104580.
XX	
PR	06-APR-1998; 98US-0080851P.
PR	06-APR-1999; 99US-00287700.
PR	01-OCT-1999; 99US-00410454..
XX	
XX	(UYOR-) UNIV OREGON HEALTH SCI.
XX	
PI	Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX	
PI	WPI; 2003-456273/44.
DR	P-PSDB; ABU61893.
XX	
PT	New floral homeotic nucleic acid molecules, useful for the manipulation
PT	of flowering in poplar and other plant species, and for producing
PT	transgenic plants having modified fertility characteristics, particularly
PT	sterility.
XX	
PS	Claim 1; Page 20-21; 48pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule comprising at
CC	least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
CC	4 homeotic genes from poplar, PTUF (UEAFY and FLORICA homologue), PTD
CC	(DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).
CC	Also included are a recombinant nucleic acid molecule comprising a
CC	promoter sequence operably linked to the nucleic acid molecule, a cell
CC	transformed with the nucleic acid molecule, a transgenic plant comprising
CC	the recombinant nucleic acid molecule, and the purified proteins encoded
CC	by the nucleic acids, The nucleic acid molecules are useful for the
CC	manipulation of flowering in poplar and other plant species, for
CC	producing transgenic plants having modified fertility characteristics
CC	(particularly sterility) and in the pulp and paper industries. The
CC	present sequence is the poplar PTD cDNA
XX	
XX	
SQ	Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;
Query Match	31.2%; Score 306.4; DB 8; Length 946;
Best Local Similarity	70.1%; Pred. No. 1.4e-71;
Matches 450; Conservative	0; Mismatches 171; Indels 21; Gaps 2
Qy	1 ATGGCGCGCGGAAGATTGAATCAAGCTGATCGAAACAGACACCAAGCGAGGTGACC 60
Db	1 ATGGGTGTGGAAAGATTGAATCAAGAAGATCGAAACCCCAACACGAGCAATGCC 60
Qy	61 TACTCCAGAGAAGAAATGGGATCTTCAAGAAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120
Db	61 TACTCGAAGAAGAAATGGTATTTTCAAGAAAGCCCAAGAACTCACTGTACTTGTGAT 120
Qy	121 GCCAGGTCTCCTCATTTATGCTCTCGAAGCTAATAAATGACAGATATACAGCCCT 180
Db	121 GCTAAGGTCTCTCTTATCATGTTCTCCAACTAACAATCTCAATGAGTACATTAGCCCC 180
Qy	181 ACCACTTACCAACAGAGTATGTATGATCACTATCAGAAAACTATGGGGATCGATCTGTGG 240
Db	181 TCCACATCGACAAGAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240
Qy	241 AGGACACAGAGAGTTCGATGAAGACACCTTGTGGAAAGTTGAAAGAGATCAACAATAAG 300
Db	241 GGCACCTCAATACGAGAAAATGCAAGAGACACTTGGGAAGCTGAATGATATCAATCATAAAG 300
Qy	301 CTGAGGAGAGAGATCAGGCAGAGGTTGGGCCATGATCTAAATGGCCTGAGCTTTGACGAG 360
Db	301 CTGAGACAGAATTCAGGACGAGGAGAGAGGGCTTGATGATCTGACATTTGATCAT 360
Qy	361 CTGGCTTCTTTGACGATGAGATGCAGTCTTCTTGGATGCCATACGTCAAAGGAATGAC 420

CC antisense versions of PTG, dominant negative mutants, and constructs  
 CC useful for sense suppression. Promoter sequences may be used to obtain  
 CC floral specific expression of genes such as cytotoxins that may be used  
 CC in genetic ablation strategies to produce trees having modified fertility  
 CC characteristics, including sterility. Sterile trees allow increased wood  
 CC yield and a reduction in the production of allergens such as pollen  
 XX  
 SQ Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Query Match 30.9%; Score 303.2; DB 3; Length 924;  
 Best Local Similarity 69.8%; Pred. No. 9.7e-71;  
 Matches 448; Conservative 0; Mismatches 173; Indels 21; Gaps 2;

Qy 1 ATGCGCGCGGAGATGAAATCAAGCTGATCGAAACCCAGACCAACGCGAGGTGACC 60  
 Db |||||  
 Qy 1 ATGCGTCTGGAAGATTGAAATCAAGAGATCGAAACCCCAACACGCGCAAGTCACC 60  
 Db |||||  
 Qy 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGTCAACGCTTCTCTGTAT 120  
 Db |||||  
 Qy 61 TACTCGAGAGAGAAATGGATCTTCAAGAGGCTCAGGAGTCAACGCTTCTCTGTAT 120  
 Db |||||  
 Qy 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
 Db |||||  
 Qy 121 GCTAAGGTCTCTTATCATTTGCTCCCAACACACTAACAATCAATGAGTACATTAGCC 180  
 Db |||||  
 Qy 181 ACCACTAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 Db |||||  
 Qy 181 TCCACATCGAAGAGAGATCTAGATCAATATCAGAACGCTTTAGGCAATAGTCTGTG 240  
 Db |||||  
 Qy 241 AGGACACACAGAGAGTCTGATGAAAGACACCTTTGGAAGTTGAAAGAGATCAACAATAAG 300  
 Db |||||  
 Qy 241 GGCACTCAATACGAGAAATGCAAGACCTTGAGGAGCTGATGATATCATCATATAG 300  
 Db |||||  
 Qy 301 CTGAGGAGAGATCAGGAGAGTGGGCCATGATCTAAATGGCCGTGAGCTTTGACGAG 360  
 Db |||||  
 Qy 301 CTGAGACAAGAAATCAGGAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT 360  
 Db |||||  
 Qy 361 CTGGCTTCTTGTACGATGAGATGAGTCTTCTTGTGATGCCATACGTCAGGAGAGTAC 420  
 Db |||||  
 Qy 361 CTGGCGGTCTTGTGACACATATGATGAGGCTTGAATGCTGTGCGGAGAGATGATAC 420  
 Db |||||  
 Qy 421 CATGTATCAAACTCAGACGAGACACCAAGAGAGGTTAAGAACTTTGAGGAGCAAGA 480  
 Db |||||  
 Qy 421 CATGTATCAAAACACAAACGAAACCTACAGGAGAGGTTAAGAAATTTAGAGGAGAGA 480  
 Db |||||  
 Qy 481 AGAGGAACATGCTGATGCTATTTTGACGAGAGGAGGCGGCGGAGGATCCACAGTAT 540  
 Db |||||  
 Qy 481 CATGGAACCTT-----CTTGATGGAATATGAGGCAAACTAGAGGATGACAGTAT 531  
 Db |||||  
 Qy 541 GGTATGAGGACATGAGGAGACTACGAACTTGCACCTTGCATTTGCAATGGCGGCAAT 600  
 Db |||||  
 Qy 532 GGTATGAGGACAT-----GAGGCTGCTGTGCACTTGCATTTGCAATGGCGGCTTCC 579  
 Db |||||  
 Qy 601 AACTGTGACACTTCCACCTCCAGCCCTTAACCTCCACCAC 642  
 Db |||||  
 Qy 580 AACCTCTATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621  
 Db |||||

RESULT 7

AAC55879

ID AAC55879 standard; DNA; 999 BP.

AC AAC55879;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Eucalyptus grandis.  
 OS  
 XX WO200053724-A2.  
 PN  
 XX 14-SEP-2000.  
 PD  
 XX 09-MAR-2000; 2000WO-US006112.  
 PF  
 XX 11-MAR-1999; 99US-00266513.  
 PR  
 XX 18-AUG-1999; 99US-0149485P.  
 XX  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA  
 XX Wood M, McGrath A, Shenk MA, Glenn M;  
 PI  
 XX WPI; 2000-579369/54.  
 DR  
 XX  
 XX New isolated polynucleotide encoding a plant transcription factor for  
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
 PT having modified gene expression or modified activity of a polypeptide.  
 XX  
 XX Claim 1; Page 46-47; 747pp; English.  
 XX  
 CC The present invention relates to novel plant transcription factors from  
 CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding  
 CC sequence for one such transcription factor. The transcription factor may  
 CC be used to produce a plant having modified gene expression such as a  
 CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or  
 CC mahogany species or to modify the activity of a polypeptide in a plant.  
 CC The transcription factors of the present invention are members from the  
 CC following families of regulatory proteins: bZIP, bZIP family of G-box  
 CC binding factors, basic helix-loop-helix zipper,  
 CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2  
 CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and  
 CC MYB  
 XX  
 SQ Sequence 989 BP; 292 A; 233 C; 262 G; 202 T; 0 U; 0 Other;

Query Match 25.2%; Score 247.2; DB 3; Length 989;  
 Best Local Similarity 64.5%; Pred. No. 9.8e-56;  
 Matches 388; Conservative 0; Mismatches 208; Indels 6; Gaps 1;

Qy 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAACCCAGACCAACGAGGTGACC 60  
 Db |||||  
 Qy 7 ATGCGGAGGGGAGATCCAGATCAAGCTGATGAGAACACGACGACCGGAGGTGACC 66  
 Db |||||  
 Qy 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGTCAACGCTTCTCTGTAT 120  
 Db |||||  
 Qy 67 TACTCGAAGCAGCGACGGGCTCTTCAAGAGGCGAACGAGCTCACCGTCTTAGGGGAC 126  
 Db |||||  
 Qy 121 GCCAAGGTCTCCCTCATTTATGCTCTCCAACTAATAAATGACGAGTATATCAGCCCT 180  
 Db |||||  
 Qy 127 CCCAAGGTCTCCATCATCATGATCTCCAGCACCGGCAAGCTCCACGAGTACATCAGCCCC 186  
 Db |||||  
 Qy 181 ACCACTAGCAGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 Db |||||  
 Qy 187 TCCACCTCAACGAAAGATGTACATCAGTATCAGCAGGCGCTCGAGGTGTATCTCTGG 246  
 Db |||||  
 Qy 241 AGGACACACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
 Db |||||  
 Qy 247 AGCTCTCATATGAGAGATGCAAGAGAACTGAGGAGCTGAGGAGGTGGAACAAGAG 306  
 Db |||||  
 Qy 301 CTGAGGAGAGATCAGGCGAGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTTGACGAG 360  
 Db |||||  
 Qy 307 CTTGAGCTGGAGGTTCAGGAGGAGGTTTCGGGAGAGGACTGAATGATGATGATGATG 366  
 Db |||||  
 Qy 361 CTGGCTTCTTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 Db |||||  
 Qy 367 TTGTGCGGTCTTGAGCAAGATATGGAACACGCGCTTAGCTGATCCCTGTAACGAGTAC 426  
 Db |||||  
 Qy 421 CATGTGATCAAACTCAGACGAGGAGGACCAACCAAGAGAGGTTAAGAACTTTGAGGAC 480  
 Db |||||

25-JAN-2001 (first entry)

Eucalyptus grandis transcription factor DNA sequence #10.

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;  
 XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
 XX basic helix-loop-helix zipper; homeotic; homeodomain; MADS;  
 XX homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;  
 XX type 2 Cys2His2; CCAAT box element; MYB; ss.

Db 427 AAGACGCTCGCAATCAATCGACACCGCCAGGAGAGAAAGAAAGATGCTGAGGAATA 486  
 Qy 481 AGAGGAACATGCTGATGGCT-----ATTTCACCAAGAGCAGCCGCGGAGATCCA 534  
 Db 487 AACAAAAGTCTCTGCAAGACTGACCAATCTGATCAAGCATCTGAGGGAGGACGACCG 546  
 Qy 535 CAGTATGTTATGAGGACAATGAGGAGACTTACGAATCTGCACCTTGCATTGTCAAATGGG 594  
 Db 547 CACTTCGAATGGTCGACACCGCAGGAGATTACGAGGCTGTGATCGGGTATACAGAGCC 606  
 Qy 595 GC 596  
 Db 607 GC 608

RESULT 8

AAD42259 standard; cDNA; 926 BP.

AC AAD42259;

04-NOV-2002 (first entry)

Soybean AP3 homologue cDNA from clone sfln.pk001.116.

Floral developmental protein; flowering locus T; APETALA3; transgenic;  
 FW; AP3; transgenic plant; fertility; flower development; gene mapping;  
 sterility; plant growth; inflorescence architecture; plant morphology;  
 tissue culture; cell division; soybean; gene; ss.

Glycine max.

Key Location/Qualifiers  
 CDS 11..694  
 /tag= a  
 /product= "Soybean AP3 homologue protein"

WO200244390-A2.

06-JUN-2002.

21-NOV-2001; 2001WO-US043750.

28-NOV-2000; 2000US-0253415P.

(DUPO ) DU PONT DE NEMOURS & CO E I.

Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

WPI; 2002-547703/58.

P-PSDB; AAE25757.

New floral developmental polypeptide having flowering locus T or Ap3  
 homolog activity, useful for immunological screening of cDNA expression  
 libraries.

Claim 6; Page 80; 88pp; English.

The present invention relates to novel floral developmental proteins,  
 more specifically flowering locus T (FT) or APETALA3 (AP3) homologue  
 proteins and polynucleotides encoding such proteins. Floral developmental  
 polynucleotides are useful for transforming cells or for producing plants  
 by transforming the plant cells with the polynucleotides and regenerating  
 the plants from the transformed plant cells. Sequences of the invention  
 are useful for immunological screening of cDNA expression libraries. They  
 are also useful for creating transgenic plants. Polynucleotides of the  
 invention are used as probes for genetically and physically mapping the  
 genes that they are a part of and as markers for traits linked to those  
 genes. AP3 homologues may be useful for engineering plant sterility or  
 fertility, flower development and morphology. FT or TFL1 homologues are  
 useful for engineering flowering time, plant growth rate, inflorescence  
 architecture, tissue culture morphology and rate of cell division to

CC enhance transformation. The present sequence is soybean AP3 homologue  
 CC cDNA  
 XX  
 SQ Sequence 926 BP; 304 A; 195 C; 194 G; 233 T; 0 U; 0 Other;  
 Query Match 24.1%; Score 237; DB 6; Length 926;  
 Best Local Similarity 62.6%; Pred. No. 5.1e-53;  
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 Db 11 ATGGCTAGAGGAAGATCCAGATCAAGAGATAGAGAACACCAACCGCCAGGTCACT 70  
 Qy 61 TACTCAAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACGCTTCTCTGTGAT 120  
 Db 71 TACTCTAAACGACGAGATGGCCCTTTTCAAGAGGCAACAGAGCTTACCGTTCTCTGCGAT 130  
 Qy 121 GCCAAGGTCTCCCTCATTATGCTCTCCACACTAATAAATGCACAGTATATACGCCCT 180  
 Db 131 GCCAAGGTCTTCTATTATGTTCTCCAGCACTGGAAACCTCCACAGTACATACGCCCC 190  
 Qy 181 ACCACTACGACCAAGAGATGTATGATGACTATCAGAAAACTATGGGGATCGATCTGTGG 240  
 Db 191 TCCACCTCAACAAAGCAGTTCTTCGATCAATACAGATGACTCTGGAGTTGATCTCTGG 250  
 Qy 241 AGGACACAGGAGTGGATGAAAGACACCTTGTGGAGTTGAAAGAGATCAACATATAG 300  
 Db 251 AACTCTCATTACGAGATATGCAAGAGAACTTTGAAGAACTGAAAGAGGTGAATAGGAAT 310  
 Qy 301 CTGAGGAGAGATCAGGCGAGAGTTGGGCCATGATCTAAATGGCTGAGCTTTTACACGAG 360  
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 Db 431 AAGGTGATCAAAATCAGATTGACACCCAGAGAAAAAGTTTAAATACAGAGAAAGATG 490  
 Qy 481 AGAGGAAACATGCTGATGGCTATTTTTCACAGGAGAGCGCGGAGGATCCACAGTAT 540  
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 Qy 541 GGTATGAGGACAATGAGGAGACTACGAATCTGCACTTGCATTGCTCAATGGGCGGAT 600  
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 Qy 601 AACTTGATACACTTTCACCTCCACC 625  
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RESULT 9

AAQ51189

ID AAQ51189 standard; DNA; 882 BP.

AC AAQ51189;

XX 25-MAR-2003 (revised)

DT 19-JUN-1994 (first entry)

XX Homeotic gene green petal.

XX Plant; organ morphogenesis; control; petunia; petals; ss.

XX Petunia.

XX Key Location/Qualifiers  
 CDS 17..713  
 /tag= a

PN W09321322-A1.  
 PD 28-OCT-1993.  
 XX 13-APR-1993; 93WO-US003508.  
 XX 13-APR-1992; 92US-00867580.  
 PR 06-JUL-1992; 92US-00909589.  
 XX (UVRQ ) UNIV ROCKEFELLER.  
 XX Halfter U, Van Der Krol AR, Kush A, Chua N;  
 DR WPI; 1993-351732/44.  
 DR P-PSDB; AAR43385.  
 XX  
 PT Plant organ morphogenesis control and determ. - by regulating the  
 PT expression of homeotic genes which determine the identity of the organ.  
 XX  
 PS Claim 13; Fig 2; 74pp; English.  
 XX  
 CC The homeotic gene green petal from petunia has been cloned and  
 CC characterised previously. The gene was used in a new method for  
 CC controlling the morphogenesis of plant organs comprising regulating the  
 CC expression of the gene using ectopic expression. Such a method can be  
 CC used to determine and control plant organ morphogenesis, such as  
 CC modifying petals without altering the reproductive portions of the  
 CC flower. See also A0951190-1. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 882 BP; 306 A; 155 C; 182 G; 239 T; 0 U; 0 Other;

Query Match 24.18; Score 236.4; DB 2; Length 882;  
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 Db 78 TATTCTAAGAGAGAAATGGACTTTTCAAGAGGCTTAATGAATCACTGTTCTTTGTGAT 137  
 Qy 121 GCCAAGTCTCCCTCATTTATGCTCTCAACACATAATAAATGACGAGTATATCAGCCCT 180  
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 Qy 181 ACNCTACGACCAAGAGATGTATGATGACTATCAGAAACTATGGGATCGATCTGTGG 240  
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 Qy 301 CTGAGGAGAGAGATCAGGACAGAGTTGGGCCATGATCTTAATGGCTGAGCTTTGACGAG 360  
 Db 318 CTCGAAAGAGAGATCAGGACAGAGATGGGAGAAAGCTTAACCGATCTGAATATGAGCAG 377  
 Qy 361 CTGGCTTCTCTGACGATGAGATGCACTTCTCTGATGCCATAGCTCAAGAGGAGTAC 420  
 Db 378 TTGAGAGAGCTCATGGAATATGCAATTTCTCAAGCTTTATCTGGAAGAAAGTAT 437  
 Qy 421 CATGTGATCAAACTCAGACGAGACCAACAGAGAGGTTAAGAACTTGGAGCAAGA 480  
 Db 438 AAGGTGATTGGCAATCAGATTGAGACATTCAGAGAGAGTCAAGAAATGGAAGAAAT 497  
 Qy 481 AGAGGAAACATGCTGATGCTATTTTGACCAGAGAGCGCGGAGGATCCACAGTAT 540  
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Db 546 GGGCTAGTTGAACAAGAGGTGACTACAAATCTGTGTTTCCAAATGGAGGCAT 605  
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 AC AAC51525;  
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 DT 18-OCT-2000 (first entry)  
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 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 69842.  
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 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic pathway;  
 KW promoter; termination sequence; ss.  
 XX  
 OS Arabidopsis thaliana.  
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 PN EP1033405-A2.  
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 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-00301439.  
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Query Match 23.2%; Score 227.4; DB 3; Length 954;

Best Local Similarity 61.0%; Pred. No. 1.9e-50;

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Matches 391; Conservative 0; Mismatches 241; Indels 9; Gaps 1;
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QY 61 TACTCCAGAGAGAAATGGGATCTTCAAGAGGCTCAGGAGCTCACCGTTCTCTGTGAT 120
DB 93 TATTCAAGAGAGAAATGGTTTATTCAAGAAAGCACATGAGCTCACGGTTTGTGTGAT 152
QY 121 GCCAAGTCTCCCTCATTTATGCTCTCCAACACTATAATAATCCAGAGTATATCAGCCT 180
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QY 181 ACCACTTACCAACAGAGATATGATGATGACTATCAGAAACTATGGGATCGATCTGTGG 240
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QY 241 AGGACACAGGAGTGCGATGAAAGACCTTGTGGAGTGTGAAGAGATCAACATATAG 300
DB 273 GCCACTCAATATGAGCGAATGCAAGAAACCAAGAGGAACTGTTGGAGCAATAGAAAT 332
QY 301 CTGAGGAGAGATCAGGCAGAGGTTGGGCCATGATCTAAATGGCTTGAGCTTTGACGAG 360
DB 333 CTCGGACTCAGATCAAGCAGAGGCTAGTGAGTGTGTAACAACTTGACATTCAGAG 392
QY 361 CTGGCTTCTTTGACGATGAGATGAGTCTTCTTTGGATGCGCATACGTCAAGAGGATAC 420
DB 393 CTGGCTGCTTTGAGGATGAAATGGAACACTTTTCAAACTGTTTGGGAGCGCAAGTTC 452
QY 421 CATGTGATCAAACTCAGACGAGACCAACCAAGAGAGGTTAAGACTTGGAGCAAGA 480
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DB 513 CAAAGNATCTCATACA-----TGAGCTGGAACCTAAGAGCTGAAGATCTCTACATAT 563
QY 541 GGTATGAGGACAATGAGGAGACTACGAACTGCACTTGCTGCTTCAATGGGCGGAT 600
DB 564 GGAATAGTAGACAATGGAGGAGATACGACTAGTCTTTGGATACCAATCGAGGGTCA 623
QY 601 AACTTGTACATTTCCACCTCCACCACTCAACCTCCACCA 641
DB 624 CGTGCTTAGCTCTTCGTTTCCACCAAGCAACATCACTACTA 664
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XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
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XX  
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QY 421 CATGTGATCAAAACTCAGACGGAGACCAACCAAGAGAGAGTTAAGAACTTGAGGCAAGA 480
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DB 784 GGACTAGTAGACATGAGGAGAGATTACGACTCAGTCTTTGGATACCAAAATCGAAGGGTCA 843
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DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29191.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 09-MAR-1999; 99US-0123548P.
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RESULT 15  
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 DT 25-JAN-2001 (first entry)  
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 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
 KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;  
 KW type 2 Cys2His2; CCAAT box element; MYB; ss.  
 XX  
 OS Eucalyptus grandis.  
 XX  
 PN WO200053724-A2.  
 XX  
 PD 14-SEP-2000.  
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 PF 09-MAR-2000; 2000WO-US006112.  
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 PR 18-AUG-1999; 99US-0149485P.  
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 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 XX  
 XX Wood M, McGrath A, Shenk MA, Glenn M;  
 XX WPI; 2000-579369/54.  
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 XX New isolated polynucleotide encoding a plant transcription factor for  
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
 PT having modified gene expression or modified activity of a polypeptide.  
 XX  
 XX Claim 1; Page 515; 747pp; English.

CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and  
 CC MYB  
 XX  
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Job time : 457.966 secs



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OM nucleic - nucleic search, using sw model

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Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcggggaagtga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
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30: em\_hgt\_hum.\*  
31: em\_hgt\_inv.\*  
32: em\_hgt\_other.\*  
33: em\_hgt\_mus.\*  
34: em\_hgt\_pln.\*  
35: em\_hgt\_rdi.\*  
36: em\_hgt\_mam.\*  
37: em\_hgt\_vrt.\*  
38: em\_sy.\*  
39: em\_hgt\_hum.\*  
40: em\_hgt\_mus.\*  
41: em\_hgtg\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	953.4	97.1	1102	8	MDO251116	AJ251116 Malus dom
2	633.8	64.5	1043	8	AB081093	AB081093 Malus x d
3	452.8	46.1	473	8	AB081094	AB081094 Malus x d
4	391.4	39.9	1014	8	AB055966	AB055966 Rosa rugo
5	306.4	31.2	681	6	AR372459	AR372459 Sequence
6	306.4	31.2	946	6	AR372458	AR372458 Sequence
7	297.4	30.3	906	8	GHY9724	AJ009724 Gerbera h
8	282.8	28.8	998	8	AMDEPI	X52023 A.majus def
9	276.8	28.2	994	8	AF230704	AF230704 Petunia x
10	276.6	28.2	895	8	LEIDR6	X60759 L.esculentu
11	275.2	28.0	939	8	AF230703	AF230703 Hydrangea
12	273.4	27.8	945	8	AY098734	AY098734 Lycopersi
13	254.6	25.9	924	8	STPD4	X67508 S.tuberosum
14	248.6	25.3	1005	8	AB071378	AB071378 Lilium re
15	244	24.8	1039	8	AF503913	AF503913 Lilium lo
16	239.6	24.4	965	8	ALFMBP	L41727 Medicago sa
17	237	24.1	926	6	AX478039	AX478039 Sequence
18	236.4	24.1	881	8	PHGP	X69946 P.hybrida m
19	235.2	24.0	952	8	AB094964	AB094964 Asparagus
20	234.2	23.8	1113	8	NTMADSBX	X96428 N.tabacum m
21	228	23.2	1002	8	AB094965	AB094965 Tulipa ge
22	227.4	23.2	730	8	AY142590	AY142590 Arabidops
23	227.4	23.2	959	8	AY087369	AY087369 Arabidops
24	227.4	23.2	960	8	AY070397	AY070397 Arabidops
25	226.2	23.0	763	8	AY162881	AY162881 Platanus
26	225.8	23.0	1010	8	ATHAPETELA	M86357 A.thaliana
27	225.8	23.0	1084	8	AB003323	AB003323 Oryza sat
28	225.8	23.0	1210	8	AK069317	AK069317 Oryza sat
29	225.2	22.9	791	8	AB090869	AB090869 Silene co
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31	222.2	22.6	959	8	AB007506	AB007506 Trifolium
32	221.4	22.5	830	8	AY397762	AY397762 Chloranth
33	220.6	22.5	1129	8	AB099875	AB099875 Rosa rugo
34	220.2	22.4	920	8	BOU67455	U67455 Brassica ol
35	219.6	22.4	887	8	DCA271149	AJ271149 Daucus ca
36	219.6	22.4	941	8	AF124814	AF124814 Brassica
37	218.6	22.3	675	8	AY131391	AY131391 Brassica
38	218.4	22.2	844	8	AY173070	AY173070 Helianthu
39	218.2	22.2	852	8	AB050649	AB050649 Magnolia
40	217.4	22.1	1004	8	AF181479	AF181479 Zea mays
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43	216.8	22.1	1016	8	AB094966	AB094966 Tulipa ge
44	216.6	22.1	762	8	AY162882	AY162882 Platanus
45	215.6	22.0	793	8	AB090867	AB090867 Silene di

# ALIGNMENTS

RESULT 1  
MDO251116  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

MDO251116  
Malus domestica mRNA for B-type MADS box protein (mads13 gene).  
AJ251116  
AJ251116.1 GI:16973293  
B-type MADS box protein; mads13 gene.  
Malus x domestica (apple tree)  
Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
1  
Vosman,B. and Smulders,M.J.M.  
Isolation of apple B- and C-type MADS box genes from vegetative

Pred. No. is the number of results predicted by chance to have a

tissue  
 Unpublished  
 REFERENCE  
 2 (bases 1 to 1102)  
 van der Linden, C.G.  
 Direct Submission  
 Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic  
 Diversity, CPRO Wageningen University & Research Centre, PO Box 16,  
 Wageningen, 6700 AA, NETHERLANDS  
 JOURNAL  
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 Best Local Similarity 99.4%; Pred. No. 8.2e-247;  
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 QY 1 ATGCGCGCGGAGATTGAAATCAAGCTGATCGAAAAACAGACCAAGCGAGGTGACC 60  
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 QY 61 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 120  
 DB 131 TACTCCAGAGAGAAATGGATCTTCAAGAGGCTCAGAGCTCACCGTCTCTGTGAT 190  
 QY 121 GCCAAGTCTCCCTCAATATGCTCTCCACACATAATAAAATGCACGAGTATATCAGCCCT 180  
 DB 191 GCCAAGTCTCCCTCAATATGCTCTCCACACATAATAAAATGCACGAGTATATCAGCCCT 250  
 QY 181 ACCACTACGACCAAGAGTATGTATGATGACTATCAGAAAATCTAGGGATCGATCTGTGG 240  
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 QY 301 CTGAGGAGAGATCAGGACAGAGGTTGGGCCATGATCTAAATGGCCCTGAGCTTGCAGAG 360  
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 QY 361 CTGGCTCTCTTGACATGAGTGCAGTCTTCTTGATGCGCATGCTCAAGAGGAAGTAC 420  
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 AB081093  
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 DEFINITION  
 Malus x domestica MdTM6 mRNA for MADS-box protein, complete cds.  
 ACCESSION  
 AB081093  
 VERSION  
 AB081093.1 GI:22775407  
 KEYWORDS  
 Malus x domestica (apple tree)  
 ORGANISM  
 Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 REFERENCE  
 1  
 Matsumoto, S., Ohtsubo, T. and Soejima, J.  
 Cloning and sequencing of apple MADS-box genes 'MdPI', 'MdTM6' and  
 'MdMADS13'  
 JOURNAL  
 Unpublished  
 REFERENCE  
 2 (bases 1 to 1043)  
 Ohtsubo, T. and Matsumoto, S.  
 Direct Submission  
 TITLE  
 Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,  
 Department of Biology, Faculty of Education, 1-1, Yanagido, Gifu,  
 Gifu 501-1193, Japan (E-mail:shmatsumo@gifu-u.ac.jp,  
 Tel:81-58-293-2257, Fax:81-58-293-2207)  
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Best Local Similarity	85.3%; Pred. No. 2.8e-160;
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RESULT 6  
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LOCUS AR372458 946 bp DNA linear PAT 12-SEP-2003  
DEFINITION Sequence 2 from patent US 6395892.  
ACCESSION AR372458  
VERSION AR372458.1 GI:34609785  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 946)  
AUTHORS Strauss,S.H., Rottmann,W., Brunner,A. and Sheppard,L.  
TITLE Floral homeotic genes for manipulation of flowering in poplar and other plant species  
JOURNAL Patent: US 6395892-A 2 28-MAY-2002;  
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RESULT 7  
GHY9724  
LOCUS GHY9724 906 bp mRNA linear PLN 02-APR-2003  
DEFINITION Gerbera hybrida cv. 'Terra Regina' mRNA for MADS-box protein, GDEF1.  
ACCESSION AJ009724  
VERSION AJ009724.1 GI:4218168  
KEYWORDS gdef1 gene; MADS-box protein.  
SOURCE Gerbera hybrida cv. 'Terra Regina'  
ORGANISM Gerbera hybrida cv. 'Terra Regina',  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Mutisiae; Gerbera.  
REFERENCE 1  
AUTHORS Yu,D., Kotilainen,M., Pollanen,E., Mehto,M., Elomaa,P.,  
Helariutta,Y., Albert,V.A. and Teeri,T.H.  
TITLE Organ identity genes and modified patterns of flower development in Gerbera hybrida (Asteraceae)  
JOURNAL Plant J. 17 (1), 51-62 (1999)  
MEDLINE 99168221  
PUBMED 10069067  
REFERENCE 2 (bases 1 to 906)  
AUTHORS Teeri,T.H.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUL-1998) Teeri T.H., Institute of Biotechnology,  
University of Helsinki, P.O. Box 56, FIN-00014 Univ. Helsinki,  
FINLAND

FEATURES  
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Query Match 30.3%; Score 297.4; DB 8; Length 906;  
Best Local Similarity 68.4%; Pred. No. 3.4e-69;  
Matches 444; Conservative 0; Mismatches 196; Indels 9; Gaps 2;  
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## RESULT 8

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LOCUS A.majus deficiencies mRNA. 998 bp mRNA linear PLN 26-NOV-1992  
DEFINITION X52023  
ACCESSION X52023.1 GI:16019  
VERSION X52023.1  
KEYWORDS deficiencies gene; homeotic flower gene.  
SOURCE Antirrhinum majus (snapdragon)  
ORGANISM Antirrhinum majus  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae;  
Antirrhinum.  
1 (bases 1 to 998)  
Sommer, H., Beltran, J. P., Huijser, P., Pape, H., Lonig, W. E.,  
Saedler, H. and Schwarz-Sommer, Z.  
TITLE Deficiens, a homeotic gene involved in the control of flower  
morphogenesis in Antirrhinum majus: the protein shows homology to

transcription factors  
EMBO J. 9 (3), 605-613 (1990)  
90181955  
1968830

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## ORIGIN

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Best Local Similarity 65.7%; Pred. No. 3.1e-65;  
Matches 451; Conservative 0; Mismatches 217; Indels 18; Gaps 2;  
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DB 85 ATGGCTCAGGGAAGATCCAGATTAAAGAGATAGAAACCAACAAACAGCAGGTCAAC 144  
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QY 652 TCGTCGGCTCTCCATTACTCATCT 677
Db 736 TCTGATCTCACCACCTTTTGTCTTGT 761

RESULT 9
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LOCUS Petunia x hybrida MADS box transcription factor TM6 mRNA, partial
DEFINITION cds.
ACCESSION AF230704
VERSION AF230704.1 GI:8163949
KEYWORDS
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.
REFERENCE 1 (bases 1 to 994)
AUTHORS Kramer, E.M. and Irish, V.F.
TITLE Evolution of the petal and stamen developmental programs: Evidence
from comparative studies of the lower eudicots and basal
angiosperms
JOURNAL Int. J. Plant Sci. (2000) In press
REFERENCE 2 (bases 1 to 994)
AUTHORS Kramer, E.M. and Irish, V.F.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) MDCB, Yale University, PO Box 208104, New
Haven, CT 06511-8104, USA
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Matches 436; Conservative 0; Mismatches 207; Indels 15; Gaps 2;

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Db 121 GCTAAGATCTGTCTCATCTGCTCTCCAGTACTAGGAAATTCATGAGTATACAGTCCC 180
QY 181 ACCACTACGACCAAGAGTATGATGACTATCAGAAAACATATGGGATCGATCTGTGG 240
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## RESULT 10

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LOCUS L. esculentum TDR6 mRNA. 895 bp mRNA linear PLN 20-MAR-1992
ACCESSION X60759 GI:19385
VERSION X60759.1
KEYWORDS MADS box; TDR6 gene.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Lycopersicon.
REFERENCE 1 (bases 1 to 895)
AUTHORS Pnueli, L., Abu-Abeid, M., Zamir, D., Nacken, W., Schwarz-Sommer, Z. and
Lifschitz, E.
TITLE The MADS box gene family in tomato: temporal expression during
floral development, conserved secondary structures and homology
with homeotic genes from Antirrhinum and Arabidopsis
JOURNAL Plant J. 1 (2), 255-266 (1991)
MEDLINE 93251098
PUBMED 1688249
REFERENCE 2 (bases 1 to 895)
AUTHORS Pnueli, L.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1991) L. Pnueli, Dept of Biology, Technion-Israel
Inst of Technology, Haifa 32000, ISRAEL
COMMENT See also X60756-X60760.
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DEFINITION Lycopersicon esculentum TDR6 transcription factor mRNA, partial cds.  
ACCESSION AY098734  
VERSION AY098734.2 GI:24967131  
KEYWORDS  
SOURCE Lycopersicon esculentum (tomato)  
ORGANISM Lycopersicon esculentum  
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AUTHORS Busi, M.V., Bustamante, C., D'Angelo, C., Hidalgo-Cuevas, M., Boggio, S.B., Valle, E.M. and Zabaleta, E.  
TITLE MADS-box genes expressed during tomato seed and fruit development  
JOURNAL Plant Mol. Biol. 52 (4), 801-815 (2003)  
MEDLINE 22856390  
PUBMED 13677468  
REFERENCE 2 (bases 1 to 945)  
AUTHORS Busi, M.V., D'Angelo, M.C. and Zabaleta, E.J.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-2002) Plant Molecular Biology, IIB-INTECH, Camino de Circunvalacion de la Laguna Km6, Chascomus, BA 7130, Argentina  
REFERENCE 3 (bases 1 to 945)  
AUTHORS Busi, M.V., D'Angelo, M.C. and Zabaleta, E.J.  
TITLE Direct Submission  
JOURNAL Submitted (14-NOV-2002) Plant Molecular Biology, IIB-INTECH, Camino de Circunvalacion de la Laguna Km6, Chascomus, BA 7130, Argentina  
REMARK Sequence update by submitter  
COMMENT On Nov 14, 2002 this sequence version replaced gi:23428889.  
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VERSION def4 gene; deficiens; MADS-box protein; transcriptional activator.  
KEYWORDS Solanum tuberosum (potato)  
SOURCE Solanum tuberosum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.  
REFERENCE 1 (bases 1 to 924)  
AUTHORS Garcia-Maroto, F., Salamini, F. and Rohde, W.  
TITLE Molecular cloning and expression patterns of three alleles of the Deficiens-homologous gene St-deficiens from Solanum tuberosum  
JOURNAL Plant J. 4 (5), 771-780 (1993)  
MEDLINE 94100991  
PUBMED 7903890  
REFERENCE 2 (bases 1 to 924)  
AUTHORS Maroto, Salamini and Rohde.  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 924)  
AUTHORS Garcia-Maroto, F.  
TITLE Direct Submission  
JOURNAL Submitted (24-AUG-1992) F. Garcia-Maroto, MPI f  
Zuechtungsforchung, Carl-von-Linne-Weg 10, 5000 koeln 30, FRG  
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Db 155 GCTAAAGTTTCAATTTGTTATGTTCTTACTAGTGAAGAACTTCAAGTTTAAAGTCCC 214
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Db 626 CATATATTAGCTTAGGCTTCAACCAACAATCATCA 666

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RESULT 14
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DEFINITION Liliun regale LEDEF mRNA for MADS-box transcription factor,
complete cds.
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VERSION AB071378.1
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SOURCE Liliun regale
ORGANISM Liliun regale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Lilium.
REFERENCE
1
AUTHORS Winter,K.U., Weiser,C., Kaufmann,K., Bohne,A., Kirchner,C.,
Kanno,A., Saedler,H. and Theissen,G.
TITLE Evolution of class B floral homeotic proteins: obligate
heterodimerization originated from homodimerization
JOURNAL Mol. Biol. Evol. 19 (5), 587-596 (2002)
MEDLINE 21959322
PUBMED 11961093
REFERENCE
2 (bases 1 to 1005)
AUTHORS Kanno,A., Bohne,A., Saedler,H. and Theissen,G.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2001) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail:kanno@ige.tohoku.ac.jp,
Tel:81-22-217-5725(ex-5725), Fax:81-22-217-5725)
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GenCore version 5.1.6  
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blcsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	358	32.5	946	4	US-09-410-464-2
3	346	31.4	1345	1	US-08-592-214A-7
4	346	31.4	1345	3	US-08-659-188-7
5	346	31.4	1345	3	US-08-655-227-7
6	346	31.4	1345	3	US-08-655-241-7
7	346	31.4	1345	3	US-09-149-976-7
8	346	31.4	1345	4	US-09-398-326-7
9	334	30.3	798	4	US-09-611-659A-3
10	334	30.3	1010	4	US-09-611-659A-2
11	330	29.9	1062	3	US-09-067-800-1
12	330	29.9	1062	3	US-09-105-652-1

13	330	29.9	1062	3	US-09-349-677-1	Sequence 1, Appli
14	330	29.9	1062	4	US-09-708-584-1	Sequence 1, Appli
15	321.5	29.1	945	2	US-08-485-981-9	Sequence 9, Appli
16	321.5	29.1	945	2	US-08-867-087B-10	Sequence 10, Appli
17	321	29.1	779	1	US-08-592-214A-9	Sequence 9, Appli
18	321	29.1	779	3	US-08-659-188-9	Sequence 9, Appli
19	321	29.1	779	3	US-08-655-227-9	Sequence 9, Appli
20	321	29.1	779	3	US-08-655-241-9	Sequence 9, Appli
21	321	29.1	779	3	US-08-149-976-9	Sequence 9, Appli
22	321	29.1	779	4	US-09-398-326-9	Sequence 9, Appli
23	320.5	29.1	896	3	US-09-067-800-5	Sequence 5, Appli
24	320.5	29.1	896	3	US-09-349-677-5	Sequence 5, Appli
25	319.5	29.0	959	3	US-09-067-800-7	Sequence 7, Appli
26	319.5	29.0	959	3	US-09-349-677-7	Sequence 7, Appli
27	319	28.9	768	1	US-08-592-214A-5	Sequence 5, Appli
28	319	28.9	768	3	US-08-659-188-5	Sequence 5, Appli
29	319	28.9	768	3	US-08-655-227-5	Sequence 5, Appli
30	319	28.9	768	3	US-08-655-241-5	Sequence 5, Appli
31	319	28.9	768	3	US-09-149-976-5	Sequence 5, Appli
32	319	28.9	768	4	US-09-398-326-5	Sequence 5, Appli
33	319	28.9	1457	1	US-08-460-512-1	Sequence 1, Appli
34	318	28.8	794	1	US-08-592-214A-3	Sequence 3, Appli
35	318	28.8	794	3	US-08-659-188-3	Sequence 3, Appli
36	318	28.8	794	3	US-08-655-227-3	Sequence 3, Appli
37	318	28.8	794	3	US-08-655-241-3	Sequence 3, Appli
38	318	28.8	794	3	US-09-149-976-3	Sequence 3, Appli
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41	318	28.8	1057	3	US-08-659-188-1	Sequence 1, Appli
42	318	28.8	1057	3	US-08-655-227-1	Sequence 1, Appli
43	318	28.8	1057	3	US-08-655-241-1	Sequence 1, Appli
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#### ALIGNMENTS

RESULT 1

US-09-410-464-3

; Sequence 3, Application US/09410464

; Patent No. 6395892

; GENERAL INFORMATION:

; APPLICANT: Strauss et al.

; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in poplar and other plant species.

; FILE REFERENCE: 53375

; CURRENT APPLICATION NUMBER: US/09/410,464

; CURRENT FILING DATE: 1999-10-01

; EARLIER APPLICATION NUMBER: 09/287,700

; EARLIER FILING DATE: 1999-04-06

; EARLIER APPLICATION NUMBER: 60/080,851

; EARLIER FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 681

; TYPE: DNA

; ORGANISM: Populus balsamifera subsp. trichocarpa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(681)

US-09-410-464-3

Alignment Scores:

Pred. No.:

Score: 1.13e-33

Percent Similarity: 358.00

Best Local Similarity: 57.94%

Query Match: 32.46%

DB: 4

Length: 681

Matches: 83

Conservative: 41

Mismatches: 82

Indels: 9

Gaps: 2

US-10-069-527-2 (1-215) x US-09-410-464-3 (1-681)

QY 1 MetGlyArgGlyLysValGluLeuLysArgGlyLeuLysSerSerAsnArgGlnValThr 20  
 Db 1 ATGGGTCTGGAAGATTGAATCAAGAGATCGAAACCCCAACAAACAGGCAAGTCACC 60  
 QY 21 TyrSerLysArgGlnGlyLeuLysValGluLeuLysAlaLysGluLeuThrValLeuCysAsp 40  
 Db 61 TACTCGAAGAGAAATGGTATTTCAAGAAAGCCCAAGAACTCACTGTTGTGTAT 120  
 QY 41 AlaLysValSerLeuLeuLysSerSerGlyLysMetValGluLysCysSerPro 60  
 Db 121 GCTAAGGTCTCTTATCATGTTCTCCACACTACAAACTCAATGAGTACATTAGCCCC 180  
 QY 61 SerThrThrLeuThrGluLeuLysArgGlyLysHisGlyGlnSerGlyLysLeuTrp 80  
 Db 181 TCCACATCGCAAGAAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240  
 QY 81 AspAlaLysHisGluLeuSerSerAsnGluValAspArgValLysLysAsnAspSer 100  
 Db 241 GGCACTCAATACAGAAATGCAAGAGCACTTGAGGAAGCTGAATCATATCATTAAG 300  
 QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120  
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 QY 121 LeuMetAlaLeuGluLysGlnLysGlnGlnLysGlnGlnLysGlnGlnVal 176  
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 QY 157 AsnLysArgLeuThrTyrGluLeuGlnLysGlnGlnLysGlnGlnLysGlnGln 196  
 Db 481 CATGGAACCTCTTGATGGAA-----TATGAAGCAAACTAGAGGATCGACAG 528  
 QY 177 ArgAsnMetGluAsnGlyTyrHisGlnArgGlnLysGlnGlnLysGlnGln 210  
 Db 529 TATGGTTTATGGCAATGAAGCTGCTGTGCACTTGCAATGGGCTTCCACCTCTAT 588

## RESULT 2

US-09-410-464-2  
 ; Sequence 2, Application US/09410464  
 ; Patent No. 6395892  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Straus et al.  
 ; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in  
 ; FILE REFERENCE: 53375  
 ; CURRENT APPLICATION NUMBER: US/09/410,464  
 ; CURRENT FILING DATE: 1999-10-01  
 ; EARLIER APPLICATION NUMBER: 09/287,700  
 ; EARLIER FILING DATE: 1999-04-06  
 ; EARLIER APPLICATION NUMBER: 60/080,851  
 ; EARLIER FILING DATE: 1998-04-06  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 946  
 ; TYPE: DNA  
 ; ORGANISM: Populus balsamifera subsp. trichocarpa  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(684)  
 ; US-09-410-464-2

Alignment Scores: 1.82e-33 Length: 946  
 Pred. No.: 358.00 Matches: 83  
 Score:

Percent Similarity: 57.94% Conservative: 41  
 Best Local Similarity: 38.79% Mismatches: 82  
 Query Match: 32.46% Indels: 9  
 DB: Gaps: 2

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 QY 21 TyrSerLysArgGlnGlyLeuLysValGluLeuLysAlaLysGluLeuThrValLeuCysAsp 40  
 Db 61 TACTCGAAGAGAAATGGTATTTCAAGAAAGCCCAAGAACTCACTGTTGTGTAT 120  
 QY 41 AlaLysValSerLeuLeuLysSerSerGlyLysMetValGluLysCysSerPro 60  
 Db 121 GCTAAGGTCTCTTATCATGTTCTCCACACTACAAACTCAATGAGTACATTAGCCCC 180  
 QY 61 SerThrThrLeuThrGluLeuLysArgGlyLysHisGlyGlnSerGlyLysLeuTrp 80  
 Db 181 TCCACATCGCAAGAAAGATCTACGATCAATATCAGAACGCTTTAGGCATAGATCTGTGG 240  
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 QY 121 LeuMetAlaLeuGluLysGlnLysGlnGlnLysGlnGlnLysGlnGlnVal 176  
 Db 361 CTGCGCGGCTTTGAGCAACATATGATGAAAGCTTGAATGGTGGCGGAGGAAGTAC 420  
 QY 141 LysPheVal-----AspMetMetArgAsnGlyLysAlaLeuGluAspGlu 156  
 Db 421 CATGTGATCAAAACACAAACGAACTACAGGAAGAGTGAAGAAATTTAGAGGAGAGA 480  
 QY 157 AsnLysArgLeuThrTyrGluLeuGlnLysGlnGlnLysGlnGlnLysGlnGlnVal 176  
 Db 481 CATGGAACCTCTTGATGGAA-----TATGAAGCAAACTAGAGGATCGACAG 528  
 QY 177 ArgAsnMetGluAsnGlyTyrHisGlnArgGlnLysGlnGlnLysGlnGln 196  
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 QY 197 GlnIleProPheAlaPheArgValGlnProAsn 210  
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## RESULT 3

US-08-592-214A-7  
 ; Sequence 7, Application US/08592214A  
 ; Patent No. 5815336  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yanofsky, Martin F.  
 ; TITLE OF INVENTION: Cauliflower Floral Meristem Identify  
 ; TITLE OF INVENTION: Genes and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: United States  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/592,214A  
 FILING DATE: 26-JAN-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-UD 1927  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1345 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 149..968  
 NAME/KEY: misc feature  
 LOCATION: 1..1345  
 OTHER INFORMATION: /note= "product = Zea mays AP1"  
 US-08-592-214A-7  
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 Score: 346.00 Matches: 83  
 Percent Similarity: 59.29% Conservative: 51  
 Best Local Similarity: 36.73% Mismatches: 58  
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 QY 21 TyrSerLysArgArgAsnGlyLlelleLysLysAlaLysGluLeuThrValLeuCysAsp 40  
 Db 209 TTCTCCACGCGCGGAACCGCTCTCAAGAGGCGCGAGATCTCCGTCCTCTCGCAT 268  
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 QY 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78  
 Db 329 TCC--CGGATGGACAAAATCTTGAACGCTATGACGATATCTCTATGCTGCTGAAAAGGCT 385  
 QY 79 LeuTyrAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95  
 Db 386 CITATTTCAGCTGAATCTGAAGTGAAGGAATTTGGTCCACGATACAGGAAGTGAAG 445  
 QY 96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSer 115  
 Db 446 GCCAAAATTGAGACCATACAAAAATGCCACAGCACCTGATGGGAGAGGATCTAGAGTCT 505  
 QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135  
 Db 506 TTGAATCCCAAGAGAGTCCAGCACTAGACGAGAGCTGGATGCTCTACTGAAGCAGATC 565  
 QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetAspAsnGlyLys 151  
 Db 566 AGATCAAGGAAGAGGCACCTTATGGCCGAGTCTATTCTGTAGCTACAGAGAAGGAGG 625  
 QY 152 AlaLeuGluAspGluAsnLysArgIleThrThrGluLeu----- 164  
 Db 626 TCAGTCCAGGAGAACCAAGGCTCTGCAGAGGAACCTTGGCGAGAGCAGACAGGCGGCTC 685  
 QY 165 -----GlnLysGlnGlnGluMetLysIle-----Lys 173

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QY 21 TyrSerLysArgAsnGlyLeuLeuLysLysAlaLysGluLeuThrValLeuCysAsp 40
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QY 41 AlaLysValSerLeuLeuLeuLysSerSerSerGlyLysMetValLeuTyrCysSerPro 60
Db 269 GCGAGGTGCGCTGCTGCTCTCTCCCAAGGCGAGCTCTACAGTACGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuLysLysTyr-----HisGlyGlnSerGlyLysLys 78
Db 329 TCC---CGCATGCACAAAATCTTGAACGCTATGACGATATCTCTATGCTGAAAAGGCT 385
QY 79 LeuTyrAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
Db 386 CTTATTTCAGCTGAATCTGAAAGTGAGGAAATTTGGTCCACCAATACAGAAACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuGluHisLysLysGlyLysLeuThrSer 115
Db 446 GCCAAAATTGAGACCAATACAAAATGCCACACACCTGATGGAGAGGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135
Db 506 TTGAATCCCAAGAGCTCCAGCAACTAGACGAGCTGATAGCTCACTGAAGCACATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
Db 566 AGATCAAGGAGGACCACTTATGGCCGAGTCTATTCTGAGCTACAGAAAGAGGAGG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 164
Db 626 TCCTGAGGAGGAGAACAGAGGCTCTGCAGAAAGAACTTCCGAGAGGAGAGGCGCTC 685
QY 165 -----GlnLysGlnGlnMetLysIle-----Lys 173
Db 686 GCGAGCGCGGACGAGCAACAGCAGCAGCTGCTGGGAGGAGGAGGAGGAGGAGGAGG 745
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## RESULT 5

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US-08-655-227-7
Sequence 7, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin P.
TITLE OF INVENTION: Maize and Cauliflower APETALAL Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays API."
US-08-655-227-7
Alignment Scores:
Pred. No.: 8,21e-32 Length: 1345
Score: 346.00 Matches: 83
Percent Similarity: 59.29% Conservative: 51
Best Local Similarity: 36.73% Mismatches: 58
Query Match: 31.37% Indels: 34
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QY 21 TyrSerLysArgAsnGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 40
Db 209 TTCTCCAAAGCGCGAAGCGCTGCTCAAGAAAGCGCAGAGATCTCGCTCTCTCGCAT 268
QY 41 AlaLysValSerLeuLeuLeuLysSerSerSerSerSerSerSerSerSerSerSerSer 60
Db 269 GCGAGGTGCGCTGCTGCTCTCTCCCAAGGCGAGCTCTACAGTACGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuLysLysTyr-----HisGlyGlnSerGlyLysLys 78
Db 329 TCC---CGCATGCACAAAATCTTGAACGCTATGACGATATCTCTATGCTGAAAAGGCT 385
QY 79 LeuTyrAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
Db 386 CTTATTTCAGCTGAATCTGAAAGTGAGGAAATTTGGTCCACCAATACAGAAACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuGluHisLysLysGlyLysLeuThrSer 115
Db 446 GCCAAAATTGAGACCAATACAAAATGCCACACACCTGATGGAGAGGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIle 135
Db 506 TTGAATCCCAAGAGCTCCAGCAACTAGACGAGCTGATAGCTCACTGAAGCACATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
Db 566 AGATCAAGGAGGACCACTTATGGCCGAGTCTATTCTGAGCTACAGAAAGAGGAGG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 164
Db 626 TCCTGAGGAGGAGAACAGAGGCTCTGCAGAAAGAACTTCCGAGAGGAGAGGCGCTC 685
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QY 174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsn 193
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QY 194 AsnGlnGlnGlnPro 199
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RESULT 6
US-08-655-241-7
; Sequence 7, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1345
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays APL."
US-08-655-241-7

Alignment Scores:
Pred. No.: 8,21e-32 Length: 1345
Score: 346.00 Matches: 83
Percent Similarity: 59.29% Conservative: 51
Best Local Similarity: 36.73% Mismatches: 58
Query Match: 31.37% Indels: 34
DB: 3 Gaps: 7

US-10-069-527-2 (1-215) x US-08-655-241-7 (1-1345)
QY 1 MetGlyArgGlyValGluLeuLysArgGluAsnSerSerAsnArgGlnValThr 20
Db 149 ATGGGCGCGCGAAGTACGTGAAGCGGATAGAACAAAGTAAACCGCGAGTGACC 208
QY 21 TyrSerLysArgAsnGlyLeuLysAlaLysGluLeuThrValLeuCysAsp 40
Db 209 TTCTCAAGCGCGGACGCTGCTCAAGAGGGCGCAGAGATCTCCGCTCTGCGAT 268
QY 41 AlaLysValSerLeuLeuLeuTyrSerSerGlyLysMetValGluTyrCysSerPro 60
Db 41 AlaLysValSerLeuLeuLeuTyrSerSerGlyLysMetValGluTyrCysSerPro 60
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Db 269 GCCAGGTGCGCGTATCGTCTTCTCCCAAGGCAAGCTCTACGAGTAGCCACCGAC 328
QY 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78
Db 329 TCC---CGCATGGACAAAATCTTTGAACGCTATGACGCGATATCTCTATGCTGAAGAGCT 365
QY 79 LeuTrpAspAlaLysHisGlu-----AsnLeuSerAsnGluValAspArgValLys 95
Db 386 CTATTTCAGCTGAATCTGAAGTGAGGAAATTTGGTCCACGAATACAGGAAACTGAAG 445
QY 96 LysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSer 115
Db 446 CCAAAAATTGAGACCATACAAAAATGCCACAAGCAGCTGATGGAGAGGATCTAGAGTCT 505
QY 116 LeuAsnHisValGluLeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIle 135
Db 506 TTGAATCCCAAGAGCTCCAGCAACTAGACGAGCAGCTGGATAGCTCACTGAACCATC 565
QY 136 ArgAspLysGlnSer-----LysPheValAspMetMetArgAspAsnGlyLys 151
Db 566 AGATCAAGAGAGAGCCACCTTATGCGCGAGTCTATTCTGAGCTACAGAAGAAGAGAGG 625
QY 152 AlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeu-----Lys 173
Db 626 TCACTGAGGAGGAGAACAGGCTCTGCAGAGGAATTTGCGGAGAGCAGAGCGCGTC 685
QY 165 -----GlnLysGlnGlnMetLysIle-----Lys 173
Db 686 GCGAGCGCGCAGCAGCAGCAACAGCAGCAGCGTGGCGGACCAGCAGACACATGCCACG 745
QY 174 GluAsnValArgAsnMetGluAsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsn 193
Db 746 GCCAGACAACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 787
QY 194 AsnGlnGlnGlnPro 199
Db 788 GATCAGCAGGACTGCG 805

RESULT 7
US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/149,976
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
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QY	205	GlnProileGlnProasnLeuGlnluArglle 215	1062
Db	707	ACTCTCCAGAGATGGCTTTTGTGGAGAGATT 739	
RESULT 12			
US-09-105-652-1			
; Sequence 1, Application US/09105652			
; Patent No. 6229068			
; GENERAL INFORMATION:			
; APPLICANT: Yanofsky, Martin F.			
; APPLICANT: Martienssen, Robert			
; APPLICANT: Ferrandiz, Cristina			
; APPLICANT: GU, Qing			
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant			
; FILE REFERENCE: P-UD 3040			
; CURRENT APPLICATION NUMBER: US/09/105,652			
; CURRENT FILING DATE: 1998-06-26			
; EARLIER APPLICATION NUMBER: 60/051,030			
; EARLIER FILING DATE: 1997-06-27			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 1062			
; TYPE: DNA			
; ORGANISM: Arabidopsis sp.			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (101)..(826)			
; FEATURE:			
; NAME/KEY: polyA signal			
; LOCATION: (1061)			
US-09-105-652-1			
Alignment Scores:			
Pred. No.: 4,74e-30 Length: 1062			
Score: 330.00 Matches: 83			
Percent Similarity: 55.84% Conservative: 46			
Best Local Similarity: 35.93% Mismatches: 68			
Query Match: 29.92% Indels: 34			
DB: 3 Gaps: 7			
US-10-069-527-2 (1-215) x US-09-105-652-1 (1-1062)			
QY	1	MetGlyArgGlyValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20	
Db	101	ATCGGAGAGGTTAGGTTTCAGCTGAGAGAGATAGAGACAAGATCAATAGGCAAGTTACT 160	
QY	21	TyrSerIlyArgArgAsnGlyllelleLysLysAlaLysGluIleThrValLeuCysasp 40	
Db	161	TTCTCAAGAGAGAGGTCGTGTTTGTCTCAAGAAAGCTCATGAGATCTCTGTTCTCGCAT 220	
QY	41	AlaLysValSerLeuIlelleTySerSerSerGlyLysMetValGluTyCysSerPro 60	
Db	221	GCTGAGGTTGCTCTCATGCTTCTCTTTCAGAGGCAACTCTTCGATAT---TCCACC 277	
QY	61	SerThrThrLeuThrGluIleLeuAspLysTyr-----HisGlyGlnSerGlyLysLys 78	
Db	278	GACTCTTGATGAGAGAGATACCTTGAACGCTATGATCGCTATTATATTACAGACAAACAA 337	
QY	79	Leu-----TroAspAlaLysHisGluAsnLeuSer 88	
Db	338	CTTGTTGGCCGACAGCTTTCACAAAGTAAATGGGTTCTAGAACATCTTAAGCTCAAG 397	
QY	89	AsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeu 108	
Db	398	GCAAGAGTTGAGGTACTTGTGAGAGAGACAAA-----AGGAATTTT 436	
QY	109	LysGlyGluAspIleThrSerLeuAsnHisValGluLeuMetAlaLeuGluAlaLeu 128	
Db	437	ATGGGGGAAGATCTTGATTCTGTTGAGCTTGAAGAGAGCTCCAAAGCTTGGAGATCAGCTC 496	
QY	129	GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValasp 144	



OTHER INFORMATION: Amino Acid Sequences of the AGL8 cDNA clone.  
US-09-349-677-1

Alignment Scores: 4.74e-30 Length: 1062  
Pred. No.: 330.00 Matches: 83  
Percent Similarity: 55.84% Conservative: 46  
Best Local Similarity: 35.93% Mismatches: 68  
Query Match: 29.92% Indels: 34  
DB: 7 Gaps: 7

US-10-069-527-2 (1-215) x US-09-349-677-1 (1-1062)

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Qy 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 101 ATGGGAAGAGGTAGGCTTCAGCTGAAGAGGATAGAGACCAAGATCAATAGGCAAGTTACT 160
Qy 21 TyrSerLysArgAsnGlnGlyLeuLysLysLysLysLysLysLysLysLysLysLys 40
Db 161 TTCTCAAGAGAGGTTCAGCTTCAGCTGAAGAGGATAGAGACCAAGATCAATAGGCAAGTTACT 220
Qy 41 AlaLysValSerLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 60
Db 221 GCTGAGGTTCCTTCATCGCTTCCTTCCTCAAGAGGCAAACTCTTCGAATAT---TCCACC 277
Qy 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLys 78
Db 278 GACTCTTGATGAGAGGATCTTGAACGCTATGATCGCTATTTATTTATTTACAGCAAAACAA 337
Qy 79 Leu-----TTPAspAlaLysHisGluAsnLeuSer 88
Db 338 CTGTGTCGCGACGCTTTTCAAAAGTGAAATGGTTCCTAGAACATGCTAGCTCAAG 397
Qy 89 AsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeu 108
Db 398 GCAAGAGTTGAGGTACTTGGAGAGACAAA-----AGGAATTTT 436
Qy 109 LysGlyGlnGluMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 128
Db 437 ATGGGGGAAGATTCATTCGTTGAGCTTCAAGAGCTCCAAAGCTTCGAGCATCAGCTC 496
Qy 129 GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValAsp 144
Db 497 GATGAGCTATCAAGAGCATTAGTCAAGAAAGAACCAAGCTATGTTTCCGAATCTATCT 556
Qy 145 MetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrThrGluLeu 164
Db 557 GCGCTCCAGAGAGGATTAAGCTTCGAGCTTCAAGAGCTCCAAAGCTTCGAGCATCAGCTC 607
Qy 165 GlnLysGlnGlnMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 184
Db 608 -----AAAAAGATTAGGAG-----AGGAGAGAGAAACGGGTTCAGCAA 646
Qy 185 GlnArgGlnLeuGlyAsnThrAsnAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 204
Db 647 GAAGGCAATATAGTCCAAATGCTCCAACTCTTTCAGTTCTTCTGCTCAATACTACTGCTA 706
Qy 205 GlnProIleGlnProAsnLeuGlnGluArgIle 215
Db 707 ACCTCTCCAGAGATGGCTTTTGGAGAGATT 739

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RESULT 14

US-09-708-584-1  
Sequence 1, Application US/09708584  
Patent No. 6541683  
GENERAL INFORMATION:  
APPLICANT: Yanofsky, Martin F.  
APPLICANT: Martienssen, Robert  
APPLICANT: Ferrandiz, Cristina  
APPLICANT: Gu, Qing  
TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant  
FILE REFERENCE: P-UD 3040  
CURRENT APPLICATION NUMBER: US/09/708,584

; CURRENT FILING DATE: 2000-11-07  
 ; PRIOR APPLICATION NUMBER: 09/105,652  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/051,030  
 ; PRIOR FILING DATE: 1997-06-27  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1062  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis sp.  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (101)..(826)  
 ; NAME/KEY: polyA signal  
 ; LOCATION: (1061)  
 ; US-09-708-584-1  
 Alignment Scores: 4.74e-30 Length: 1062  
 Pred. No.: 330.00 Matches: 83  
 Percent Similarity: 55.84% Conservative: 46  
 Best Local Similarity: 35.93% Mismatches: 68  
 Query Match: 29.92% Indels: 34  
 DB: 7 Gaps: 7

US-10-069-527-2 (1-215) x US-09-708-584-1 (1-1062)

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Qy 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 101 ATGGGAAGAGGTAGGCTTCAGCTGAAGAGGATAGAGACCAAGATCAATAGGCAAGTTACT 160
Qy 21 TyrSerLysArgAsnGlnGlyLeuLysLysLysLysLysLysLysLysLysLysLys 40
Db 161 TTCTCAAGAGAGGTTCAGCTTCAGCTTCCTTCCTCAAGAGGCAAACTCTTCGAATAT---TCCACC 277
Qy 41 AlaLysValSerLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 60
Db 221 GCTGAGGTTCCTTCATCGCTTCCTTCCTCAAGAGGCAAACTCTTCGAATAT---TCCACC 277
Qy 61 SerThrThrLeuThrGluLeuLeuAspLysTyr-----HisGlyGlnSerGlyLys 78
Db 278 GACTCTTGATGAGAGGATCTTGAACGCTATGATCGCTATTTATTTATTTACAGCAAAACAA 337
Qy 79 Leu-----TTPAspAlaLysHisGluAsnLeuSer 88
Db 338 CTGTGTCGCGACGCTTTTCAAAAGTGAAATGGTTCCTAGAACATGCTAGCTCAAG 397
Qy 89 AsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeu 108
Db 398 GCAAGAGTTGAGGTACTTGGAGAGACAAA-----AGGAATTTT 436
Qy 109 LysGlyGlnGluMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 128
Db 437 ATGGGGGAAGATTCATTCGTTGAGCTTCAAGAGCTCCAAAGCTTCGAGCATCAGCTC 496
Qy 129 GluAsnGlyLeuThrSerIleArgAspLysGlnSer-----LysPheValAsp 144
Db 497 GATGAGCTATCAAGAGCATTAGTCAAGAAAGAACCAAGCTATGTTTCCGAATCTATCT 556
Qy 145 MetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrThrGluLeu 164
Db 557 GCGCTCCAGAGAGGATTAAGCTTCGAGCTTCAAGAGCTCCAAAGCTTCGAGCATCAGCTC 607
Qy 165 GlnLysGlnGlnMetLysLysLysLysLysLysLysLysLysLysLysLysLysLys 184
Db 608 -----AAAAAGATTAGGAG-----AGGAGAGAGAAACGGGTTCAGCAA 646
Qy 185 GlnArgGlnLeuGlyAsnThrAsnAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 204
Db 647 GAAGGCAATATAGTCCAAATGCTCCAACTCTTTCAGTTCTTCTGCTCAATACTACTGCTA 706
Qy 205 GlnProIleGlnProAsnLeuGlnGluArgIle 215

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Db 707 ACCTCTCCAGAGATGGCTTTGTGGAGAGATT 739  
RESULT 15  
US-08-485-981-9  
; Sequence 9, Application US/08485981  
; Patent No. 5861542  
; GENERAL INFORMATION:  
; APPLICANT: An, Gynheung  
; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND  
; TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
; ADDRESSEE: Whinston  
; STREET: One World Trade Center  
; STREET: 121 S.W. Salmon Street  
; CITY: Portland  
; STATE: Oregon  
; COUNTRY: United States of America  
; ZIP: 97204  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Disk, 3-1/2 inch  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,981  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/323,449  
; FILING DATE: October 14, 1994  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Alan. E.  
; REGISTRATION NUMBER: 35,123  
; REFERENCE/DOCKET NUMBER: 4630-42933  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (503) 226-7391  
; TELEFAX: (503) 228-9446  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 945 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
; US-08-485-981-9

Alignment Scores:  
Pred. No.: 4.15e-29 Length: 945  
Score: 321.50 Matches: 80  
Percent Similarity: 56.19% Conservative: 47  
Best Local Similarity: 35.40% Mismatches: 74  
Query Match: 29.15% Indels: 25  
DB: 2 Gaps: 6

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Db 16 ATGGGAGGGGTAGGGTTGACCTTAAGAGATACAGAACAGATCAACAGCGCAAGTGACC 75  
Qy 21 TyrSerLysArgArgAsnGlyIleIleLysLysAlaLysGluIleThrValLeuCysAsp 40  
Db 76 TTCGCTAAGAGAGAAATGGACCTTTTGAAAAAGCCTTATGAGCTTTCTGTTCTTTGTGAT 135  
Qy 41 AlaLysValSerLeuIleThrSerSerGlyLysMetValGluTyrCysSerPro 60  
Db 136 GCTGAGGTGCTCTCACTCTCTCCCAATAGGGGAAACTGTACAGAGTTCTGCAGT--- 192  
Qy 61 SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80

Db 193 AGCTCTAGCATGCTCAAGACATTAGAGAGGTACCAG-----AAGTGCACACTAC 240  
Qy 81 AspalalysHisGluAsnLeuSer-----AsnGlu 90  
Db 241 GGAGCACACAGAGACCAATATATCCACACGAGAAACACTGGAAATAAGTAGCAACACAGAA 300  
Qy 91 ValAspArgValLysLysAspAsnAspSerMetGlnValGluLeuArgHisLeuLysGly 110  
Db 301 TACTTGAAGCTTAAAGCAGCTTACGAGCATTCACGCGATCACAGAGAAATCTTCTTGGT 360  
Qy 111 GluAspIleThrSerLeuAsnHisValGluLeuMetAlaLeuGluGluAlaLeuGluAsn 130  
Db 361 GAAGATCTTGGCCCTTTTGATAGCAAGAACTTGAATCCTTGTAGAGCGCAGCTTGATG 420  
Qy 131 GlyLeuThrSerIleArgAspLysGlnSerLys---PheValAspMetMetArgAsp--- 148  
Db 421 TCACGTGAACACAGATTCGATCACTCGGACTCAGTTAATGTTGGATCACTTACAGATCTT 480  
Qy 149 -----AsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrTyrGluLeuGlnLys 166  
Db 481 CAGAGAAAGGAACATGCATTAAACGAGCAACACAGAACCTTTGAAACAAAGGTTGATGAA 540  
Qy 167 GlnGlnGluMetLysIleLysGluAsnValArgAsnMetGluAsnGlyTyrHisGlnArg 186  
Db 541 GGAAGCCCAACTAAATCTGCGTGGCAACAAATGCAACAGATATGGCTACGGCGGCA 600  
Qy 187 GlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPheAlaPheArgValGlnPro 206  
Db 601 -----ACAACTCAAACTCAGGGCGATGGCTTTTTCATCCTTTTGAA 642  
Qy 207 IleGlnProAsnLeuGln 212  
Db 643 TGTGAACCCACTTTTGCAA 660

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Job time : 69.8568 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 26, 2004, 04:52:23 ; Search time 3674.24 Seconds  
(without alignments)  
2536.240 Million cell updates/sec

Title: US-10-069-527-2  
Perfect score: 1103  
Sequence: 1 MGRGKVEIKRIENSNRQVT.....QQIPFAPRVQIPNLQERI 215

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Ygapop 10.0 , Ygapext 0.5  
Rgapop 6.0 , Rgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2/1/USPRO\_spoor/US10069527/runat\_23092004\_163623\_5742/app\_query.fasta\_1.782  
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10069527 @CGN 1.1 3998 @runat\_23092004\_163623\_5742 -NCPU=6 -ICPU=3  
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-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb.htg.\*  
3: gb.in.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
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19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
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33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sv.\*  
39: em.tgo.hum.\*  
40: em.tgo.mus.\*  
41: em.tgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1103	100.0	868	8	MDO291490	AJ291490 Malus dom
2	975	88.4	890	8	AB081092	AB081092 Malus x d
3	824	74.7	845	8	AF043255	AF043255 Cucumis s
4	811	73.5	967	8	AB038462	AB038462 Rosa rugo
5	740.5	67.1	971	8	PHFMADS2	X69947 P.hybrida m
6	739.5	67.0	904	8	PHFBP3	X71417 P.hybrida f
7	720	65.3	875	8	BPE488589	AJ488589 Betula p
8	707	64.1	768	8	NTGLOBOSA	B67959 N.tabacum G
9	701.5	63.6	822	8	AB071379	AB071379 Lilium re
10	698.5	63.3	761	8	AP230711	AP230711 Hydrangea
11	698.5	63.3	807	8	AB079259	AB079259 Agapanthu
12	696	63.1	876	8	AB094967	AB094967 Tulipa ge
13	691	62.6	810	8	GHY9726	AJ009726 Gerbera h
14	685.5	62.1	814	8	AY173061	AY173061 Chrysanth
15	684.5	62.1	780	6	A36587	A36587 Sequence 1
16	684.5	62.1	780	8	PRTTNSPA	M91190 Petunia tra
17	684	62.0	896	8	SLSLM2	X80489 S.latifolia
18	669.5	60.7	920	8	AF029976	AF029976 Eucalyptu
19	666	60.4	888	8	AF134114	AF134114 Hyacinthu
20	664	60.2	894	8	AF052857	AF052857 Dicentra
21	664	60.2	907	8	AB094985	AB094985 Orchis it
22	663.5	60.2	959	8	AF230710	AF230710 Chloranth
23	660.5	59.9	848	8	AY173069	AY173069 Helianthu
24	660.5	59.9	896	8	ATHMADSBOX	D30807 Arabidopsis
25	647	58.7	802	8	AF052862	AF052862 Delphinu
26	643	58.3	801	8	AB071380	AB071380 Lilium re
27	642.5	58.3	1101	8	ZMA292961	AJ292961 Zea mays
28	641.5	58.2	1034	8	ZMA292960	AJ292960 Zea mays
29	638	57.8	879	8	AF134115	AF134115 Hyacinthu
30	633	57.4	744	8	AP230708	AP230708 Calycanth
31	633	57.4	842	8	DCA271148	AJ71148 Daucus ca
32	632.5	57.3	909	8	AY089002	AY089002 Arabidops
33	625	56.7	791	8	AF052863	AF052863 Michelia
34	623	56.5	1000	8	ZMA292959	AJ292959 Zea mays
35	623	56.5	1089	6	AX478037	AX478037 Sequence
36	620.5	56.3	978	8	RICOSMAA	L37527 Oryza sativ
37	618.5	56.1	784	8	AY162865	AY162865 Cimicifug
38	617	55.9	1036	8	RICOSMA	L37526 Oryza sativ
39	617	55.9	1057	8	AK070894	AK070894 Oryza sat
40	615.5	55.8	733	8	AF052864	AF052864 Liriodend
41	611.5	55.4	759	8	AF052861	AF052861 Syringa v
42	611.5	55.4	801	8	AF335473	AF335473 Medicago
43	610	55.3	1027	8	AK100233	AK100233 Oryza sat
44	608.5	55.2	786	8	AY162836	AY162836 Akebia qu
45	608.5	55.2	800	8	AF230713	AF230713 Tacca cha

## ALIGNMENTS

RESULT 1

MDO291490  
 LOCUS MDO291490 868 bp mRNA linear PLN 02-FEB-2001  
 DEFINITION Malus domestica mRNA for Pistillata MADS-box protein (pi gene).  
 ACCESSION AJ291490  
 VERSION AJ291490.1 GI:12666532  
 KEYWORDS PI gene; Pistillata MADS-box protein.  
 SOURCE Malus x domestica (apple tree)  
 ORGANISM Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 REFERENCE 1  
 AUTHORS Yao, J., Dong, Y. and Morris, B.A.  
 TITLE Parthenocarpic apple fruit production conferred by transposon  
 insertion mutations in a MADS-box transcription factor  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)  
 MEDLINE 21107711  
 PUBMED 11158635  
 REFERENCE 2 (bases 1 to 868)  
 AUTHORS Yao, J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-OCT-2000) Yao J.L., Plant Health and Development  
 Group, Horticulture and Food Research Institute of New Zealand, 120  
 Mc Albert Road, Auckland, Private Bag 92169, NEW ZEALAND  
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 /dev\_stage="flowering"  
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 /gene="pi"  
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 /function="flower and fruit development"  
 /codon\_start=1  
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 VELRHUKGEDITSLNHELMALEENGLTSIRDKOSKFDVMDRNGKALEDNKRL  
 TYELQKQEMKIKENVRNMENGYHQHQLGNYNNOQIIPFAPRVQPIQPNLQERI"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,07e-84 Length: 868  
 Score: 1103.00 Matches: 215  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-069-527-2 (1-215) x MDO291490 (1-868)  
 Qy 1 MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20  
 Db 1 ATGGGACGTGGGAGGTGTGATCAAGAGGATTGAGAATCAAGTAAACAGCGGAGGCC 60  
 Qy 21 TyrSerLysArgAsnGlyLleLleLysLysAlaLysGluIleThrValLeuCyAsp 40  
 Db 61 TACTCCAGAGGAGGATGGATATCAAGAGGCAAGAGGAGATCACTGTTCTATGTAT 120  
 Qy 41 AlaLysValSerLeuIleLleTyrSerSerSerGlyLysMetValGluTyrCysSerPro 60  
 Db 121 GCTAAGATATCTCTATATCTATCTATCTAGCTCTGGGAAGATGTTGAATCTGCAGCC 180  
 Qy 61 SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLeuTyr 80

Db 181 TCAACTACGCTGACAGAAATCTTTGGACAAATACCATGGACAATCTGGGAAGAAGTTGTGG 240  
 Qy 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100  
 Db 241 GATGCTAAGCATGAGAACCTTCAGCAATCAAGTGGATAGAGTCAAGAAAGACATGACAGC 300  
 Qy 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120  
 Db 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGAGATATCATCATTCATGAACCATGTAGAG 360  
 Qy 121 LeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140  
 Db 361 CTGATGCGCTTAGAGGAGGACATGAAAATGGCTTACAAGTATCCGGCAAGCAGTCC 420  
 Qy 141 LysPheValAspMetMetA:GAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160  
 Db 421 AAGTTCTCGACATGATGAGAGACAATGGAAGGCACTGGAGATGAGAGATAAAGCGCTC 480  
 Qy 161 ThrTyrGluLeuGlnLysGlnGlnMetLysIleLysGluAsnValAlaArgAsnMetGlu 180  
 Db 481 ACTTATGAGCTGCAAAAACAACAGGAGATGAAAATAAAGAGAAATGTGAGAAACATGGAA 540  
 Qy 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnGlnIleProPhe 200  
 Db 541 AATGGGTATCATCAGAGGAGCTGGGGAAGTCAACAACAACCAACAGCAGCAGATACCTTT 600  
 Qy 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle 215  
 Db 601 GCCTTCGCGTGCAGCGCTATTTCAGCCAAATCTCCAGGAGAGAAATC 645  
 RESULT 2  
 LOCUS AB081092 890 bp mRNA linear PLN 06-SEP-2002  
 DEFINITION Malus x domestica Mdipi mRNA for MADS-box protein, partial cds.  
 ACCESSION AB081092  
 VERSION AB081092.1 GI:22775405  
 KEYWORDS Malus x domestica (apple tree)  
 SOURCE Malus x domestica  
 ORGANISM Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 REFERENCE 1  
 AUTHORS Matsumoto, S., Ohtsubo, T. and Soejima, J.  
 TITLE Cloning and sequencing of apple MADS-box genes 'Mdipi', 'MDTM6', and  
 'MdMADS13'  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 890)  
 AUTHORS Ohtsubo, T. and Matsumoto, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,  
 Department of Biology, Faculty of Education, 1-1, Yanagido, Gifu,  
 Gifu 501-1193, Japan (E-mail:shmatsumo@gifu-u.ac.jp,  
 Tel:81-58-293-2257, Fax:81-58-293-2207)  
 FEATURES  
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 /location=Qualifiers  
 /organism="Malus x domestica"  
 /mol\_type="mRNA"  
 /cultivar="Indo"  
 /db\_xref="taxon:3750"  
 /tissue\_type="young floral parts"  
 1..890  
 /gene="Mdipi"  
 <1..574  
 /gene="Mdipi"  
 /codon\_start=2  
 /product="MADS-box protein"  
 /protein\_id="BAC1196.1"  
 /db\_xref="GI:22775406"  
 /translation="NGIIKKAKKAITVLCDKAVSLIYSSGKRVFYCSPTILTEILD  
 KYHQSCKLWDKHNLSNEVDKVDNDSMQVELRHUKGEDITSLNHELMALEENGLTSIRDKOSKFDVMDRNGKALEDNKRLTYELQKQEMKIKENVRNMENGYHQHQLGNYNNOQIIPFAPRVQPIQPNLQERI"  
 gene  
 CDS

## ORIGIN

## Alignment Scores:

Pred. No.: 1.36e-73 Length: 890  
 Score: 975.00 Matches: 189  
 Percent Similarity: 100.00% Conservatives: 1  
 Best Local Similarity: 99.47% Mismatches: 0  
 Query Match: 88.40% Indels: 0  
 DB: 8 Gaps: 0

US-10-069-527-2 (1-215) x AB081092 (1-890)

QY 26 AsnGlyIleLeuLysLysAlaLysGluIleThrValLeuCysAspAlaLysValSerLeu 45  
 Db 2 AATGGGATTATCAAGAAAGCAAGAGATCACTGTTCTATGATGCTTAAGTATCTCTT 61  
 QY 46 IleIleTySerSerSerGlyLysMetValGluTyTyCysSerProSerThrThrLeuThr 65  
 Db 62 ATCATTTATTTCTAGCTCTGGAGATGGTTGATATCTGAGGCCCTTCAACTAGCTGACA 121  
 QY 66 GluIleLeuAspLysTyTrHisGlyGlnSerGlyLysLeuLeuTrAspAlaLysHisGlu 85  
 Db 122 GAATCTTGGACAAATACCATGACAACTCTGGAGAAAGTTGTGGATGCTAAGCATGAG 181  
 QY 86 AsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeu 105  
 Db 182 AACCTCAGCAATGAAGTGGATAGATCAAGAAAGCAATCAGCATGCAAGTAGAGCTC 241  
 QY 106 ArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGluLeuMetAlaLeuGlu 125  
 Db 242 AGGCATCTGAGGAGAGAGATATCATCATTTGAACCATGTAGAGCTGATGCCCTTAGAG 301  
 QY 126 GluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSerLysPheValAspMet 145  
 Db 302 GAAGCACTTGAAATGGCTTACAGTATCCGGACCAACAGCTCCAAGTTGCTGCACATG 361  
 QY 146 MetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeuThrTyrgluLeuGln 165  
 Db 362 ATGAGAGCAATGGAAGGACCTGGAGATGAGATGAATGAAGCGCTCATCTTATGAGCTGCAA 421  
 QY 166 LysGlnGlnGluMetLysLysLysGluAsnValArgAsnMetGluAsnGlyTyTrHisGln 185  
 Db 422 AAACACAGAGATGAATAGAGAGATGTGAGAAACATGGAAATGGGTATCATG 481  
 QY 186 ArgGlnLeuGlyAsnTyTrAsnAsnAsnGlnGlnGlnIleProPheAlaPheArgValGln 205  
 Db 482 AGGCAGCTGGGAACTACAAACCAACAGCAGCAGATACCTTTTGGCTTCCGCGTGCAG 541  
 QY 206 ProIleGlnProAsnLeuGlnArgIle 215  
 Db 542 CCTATTTCAGCAAAATCTCCAGGAGAGATC 571

## RESULT 3

AF043255 845 bp mRNA linear PLN 05-JAN-1999  
 LOCUS Cucumis sativus MADS box protein 26 (CUM26) mRNA, complete cds.  
 DEFINITION Cucumis sativus  
 ACCESSION AF043255  
 VERSION AF043255.1 GI:4105096

## KEYWORDS

Cucumis sativus (cucumber)

Cucumis sativus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

1 (bases 1 to 845)

Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and

Angenent,G.C.

Class C homeotic genes are required for whorl specific sex

determination in unisexual flowers

Unpublished

2 (bases 1 to 845)

Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and

Angenent,G.C.

## TITLE

## JOURNAL

## FEATURES

## Source

## gene

## CDS

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-069-527-2 (1-215) x AF043255 (1-845)

## QY

## Db

## QY

## Db

## QY

## Db

## QY

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## Direct Submission

## Submitted (15-JAN-1998)

## Developm. Biology, CPRO-DLO,

## Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands

## Location/Qualifiers

## 1. 845

## /organism="Cucumis sativus"

## /mol\_type="mRNA"

## /db\_xref="taxon:3659"

## /sex="female"

## 1. 845

## /gene="CUM26"

## /note="class B MADS box gene"

## 6. 641

## /gene="CUM26"

## /function="involved in the determination of the identity

## of petals and stamens"

## /note="transcription factor"

## /codon\_start=1

## /product="MADS box protein 26"

## /protein\_id="AAD02250.1"

## /db\_xref="GI:4105097"

## /translation="MGRGKIEIKRIENSSNROVITYSKRNGIILKKAKEITVLCDQAVS

## LVIPASSGKMHYCSPTPLVIDDKTKHOSGKRLMDAKHENSMDRVRKENDNQ

## IEURHLRGEDITSLNYKELMALBEALENGITVREKQSEFMKMTTRHMEEBENKEL

## NYELYQKEMVAMGDSVRENDIGYNQMRDFNSQMPFAFRVQPIQPNLQERS"

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-069-527-2 (1-215) x AF043255 (1-845)

## QY

## Db

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## QY

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45..683
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ORIGIN
Alignment Scores:
Pred. No.: 9,35e-54 Length: 971
Score: 740.50 Matches: 145
Percent Similarity: 81.86% Conservative: 31
Best Local Similarity: 67.44% Mismatches: 36
Query Match: 67.14% Indels: 3
DB: 8 Gaps: 1

US-10-069-527-2 (1-215) x PHPMADS2 (1-971)

Qy 1 MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 45 ATGGGAGAGGAAGATAGAGATAAAGAGAAATAGAGAACTCTAGCAACAGCAAGTACT 104
Qy 21 TyrSerLysArgArgAsnGlyIleLysLysAlaLysGluIleThrValLeuCysAsp 40
Db 105 TACTCCAGAGAGAAATGGGATATCAAGAAAGCTAAGAAATCACTGTTCTTTGTGAT 164
Qy 41 AlaLysValSerLeuIleLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 165 GCTAAGGTTTCCCTTATCATCTTGTGTAATCTCGCAAGATGATGAATATTGTAGCCT 224
Qy 61 SerThrThrLeuThrGluIleLysAspLysTyrHisGlyGlnSerGlyLysLeuTyr 80
Db 225 TCTACTACGTTACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 284
Qy 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnSper 100
Db 285 GATGCTAAGCATCAGAACTTGACCAATGAATCGATAGATCAAGAAAGAGACGACAT 344
Qy 101 MetGlnValGluLeuArgHisLeuLysGlyLysGluAspIleThrSerLeuAsnHisValGlu 120
Db 345 ATGCAAGTTAAGCTCAGGCACCTCAAGAGGAGAGATATCAATTCTTTGAACCAAGAG 404
Qy 121 LeuMetAlaLeuGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
Db 405 CTATGTTTTCGAGAGAGGCTTAACAATGGACTTCTAGTATCATGTCGACAGAGTCG 464
Qy 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
Db 465 GAGATCTTGAGGATGCTGAGGAAATATGATCAAAATCTCGAGGAGGAGAACACAGCAACT 524
Qy 161 ThrTyrGluLeuGlnLysGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
Db 525 CAAATGCTTTGACCAAGAGGAGATGGCAGCCATGGTGGGAAATATGATGATGATGAA 584
Qy 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnIleProPhe 200
Db 585 GAAGTGATCATCAAGA-----GACAGGGATTTACCAATACCAGCAGATGCCATT 635
Qy 201 AlaPheArgValGlnProLeuGlnProAsnLeuGlnGluArgIle 215
Db 636 GCCCTTCGAGTTTCAGCCAAATGAGCCAAATCTACATGAAGAAGATG 680

P.hybriida fbp3 mRNA.
X71417
VERSION X71417.1 GI:454264
KEYWORDS fbp3 gene; MADS-box protein.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Petunia.
1
Angenent,G.C., Franken,J., Busscher,M., Weiss,D. and van Tunen,A.J.
Co-suppression of the petunia homeotic gene fbp2 affects the
identity of the generative meristem
Plant J. 5 (1), 33-44 (1994)
94177174
PUBMED 7907515
REFERENCE 2 (bases 1 to 904)
AUTHORS Angenent,G.C.
TITLE Direct Submision
JOURNAL Submitted (30-MAR-1993) G.C. Angenent, CPRO-DLO, Droevendaalsesteeg
1, Wageningen, THE NETHERLANDS
FEATURES
Location/Qualifiers
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/organism="Petunia x hybrida"
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46..684
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/protein_id="CAA50549.1"
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/db_xref="SPTREMBL:Q40883"
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ORIGIN
Alignment Scores:
Pred. No.: 1.05e-53 Length: 904
Score: 739.50 Matches: 145
Percent Similarity: 81.86% Conservative: 31
Best Local Similarity: 67.44% Mismatches: 36
Query Match: 67.04% Indels: 3
DB: 8 Gaps: 1

US-10-069-527-2 (1-215) x PHFBP3 (1-904)

Qy 1 MetGlyArgGlyLysValGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20
Db 46 ATGGGAGAGGAAGATAGAGATAAAGAGAAATAGAGAACTCTAGCAACAGCAAGTACT 105
Qy 21 TyrSerLysArgArgAsnGlyIleLysLysAlaLysGluIleThrValLeuCysAsp 40
Db 106 TACTCCAGAGAGAAATGGGATATCAAGAAAGCTAAGAAATCACTGTTCTTTGTGAT 165
Qy 41 AlaLysValSerLeuIleLysTyrSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 166 GCTAAGGTTTCCCTTATCATCTTGTGTAATCTTGCAAGATGATGAATATTGTAGCCT 225
Qy 61 SerThrThrLeuThrGluIleLysAspLysTyrHisGlyGlnSerGlyLysLeuTyr 80
Db 226 TCTACTACGTTACTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 285
Qy 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnSper 100
Db 286 GATGCTAAGCATCAGAACTTGAGCAATGAATCGATAGATCAAGAAAGAGACGACAT 345

RESULT 6
PHFBP3
LOCUS

```



TITLE Direct Submission  
JOURNAL Submitted (03-AUG-1992) G. Hansen, Max-Planck Inst. fuer  
Zuchtungsforchung, Carl-von-Linne Weg, 10, 5000 Koeln 30, FRG  
FEATURES Location/Qualifiers  
source 1..768  
/organism="Nicotiana tabacum"  
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/tissue\_type="flower"  
/clone\_lib="lambda gt10"  
/dev\_stage="mature"  
1..768  
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/codon\_start=1  
/protein\_id="CAA48142.1"  
/db\_xref="GI:19871"  
/db\_xref="GOA:Q03416"  
/db\_xref="SWISS-PROT:Q03416"  
/translations="MGRGKIEIKRIENSTNRQVTSKRRNGILKKAKEISVLCDARVS  
VIFASGKMHFESSLVLDIDQYHKLTRRLNDKADHENLDNEINKVKKNDNNQIE  
LRLKGEDITSLNRELMLELDLNGLTSIRNKQNDLLRMKTKTQSMEEBQDLNW  
QLRQLEIASNNRMNGEIGVFHORENEYQTOMPFAPRVQPMQPNLQER"

ORIGIN  
Alignment Scores:  
Pred. No.: 4,83e-51 Length: 768  
Score: 707.00 Matches: 136  
Percent Similarity: 82.71% Conservative: 41  
Best Local Similarity: 63.55% Mismatches: 31  
Query Match: 64.10% Indels: 6  
DB: 8 Gaps: 2

US-10-069-527-2 (1-215) x NTGLOBOSA (1-768)

QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20  
Db 1 ATGGGAAGAGGAAGATAGAGATCAAAAGAAATAGAGAACTCAAGCAACAGGCGAGTCACT 60  
QY 21 TyrSerLysArgGlyLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40  
Db 61 TACTCAAAAGAAAGAAATGGGATCTTGAAGAAAGCTAAGCAAAATCAAGTCTCTTTGTGAT 120  
QY 41 AlaLysValSerLeuLeuLysSerSerSerSerSerSerSerSerSerSerSerSerSerPro 60  
Db 121 GCTCGTTCGTCTCATCTTTTGTCTAGTCTTGGCAAGATGCATGATCTC-----TCC 174  
QY 61 SerThrThrLeuThrGluLeuLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 80  
Db 175 TCTACTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGTTCGT 234  
QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysLysLysLysLysLys 100  
Db 235 GATGCTAAGCATGAGAACTTGGCAATGAATCAAAAGTCAAGAAAGCAATGACAAAC 294  
QY 101 MetGlnValGluLeuLeuArgHisLysLysLysLysLysLysLysLysLysLysLysLysLys 120  
Db 295 ATGCAAAATTCAGTCAAGGCACTTAAAGGTGAAGACATCACATCTTTTGAACCAAGAGAG 354  
QY 121 LeuMetAlaLeuCluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140  
Db 355 CTATGATGTGGAAAGTCCCTTGATAATGGACTCCTAGTATCGGTAAACAGAGAAAT 414  
QY 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160  
Db 415 GACCTTCAGGATGATGAGAAAGAACTCAAGTATGAGAGGAGGAGCAAGCAACTT 474  
QY 161 ThrTyrGluLeuGlnLysGlnGluMetLysLysLysLysLysLysLysLysLysLysLysLys 180  
Db 475 AATTGGCAATTGGGCAACTAGAGATAGCAAGCATGATAGGAATATGGGAATATGGG 534

QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnGlnIleProPhe 200  
Db 535 GAAGTGTTCACCAAGGGAG-----AATGAATACCAAACTCAGATGCCTTTT 582  
QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArg 214  
Db 583 GCCTCCGAGTTCAGCAATCAGCCTAATTCAGGAGAGA 624  
RESULT 9  
AB071379 Liliu regale LRGLOA mRNA for MADS-box transcription factor,  
LOCUS complete cds.  
DEFINITION  
AB071379 AB071379.1 GI:20513261  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Liliu regale  
Liliu regale  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;  
Liliu.  
1  
REFERENCE  
AUTHORS  
Winter,K.U., Weiser,C., Kaufmann,K., Bohne,A., Kirchner,C.,  
Kanno,A., Saedler,H. and Theissen,G.  
Evolution of class B floral homeotic proteins: obligate  
heterodimerization originated from homodimerization  
Mol. Biol. Evol. 19 (5), 587-596 (2002)  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
Kanno,A., Bohne,A., Saedler,H. and Theissen,G.  
Direct Submission  
TITLE  
JOURNAL  
SUBMITTED (11-SEP-2001) Akira Kanno, Tohoku University, Graduate  
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi  
980-8577, Japan (E-mail:kanno@ige.tohoku.ac.jp,  
Tel:81-22-217-5725(ex.5725), Fax:81-22-217-5725)  
FEATURES  
Location/Qualifiers  
source 1..822  
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/mol\_type="mRNA"  
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/tissue\_type="flower"  
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14..646  
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Alignment Scores:  
Pred. No.: 1.52e-50 Length: 822  
Score: 701.50 Matches: 132  
Percent Similarity: 83.10% Conservative: 45  
Best Local Similarity: 61.97% Mismatches: 31  
Query Match: 63.60% Indels: 5  
DB: 8 Gaps: 3

US-10-069-527-2 (1-215) x AB071379 (1-822)

QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20  
Db 14 ATGGCCCGCGCAAGATCGAGATCAAGCGATCGAACATCGACCATCGCGATCACC 73  
QY 21 TyrSerLysArgGlyAsnGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40  
Db 74 TTCTCCAAGCCCGCAAGCGATCATCAAGAAACCGGTGAGATCAGCGTCTCTGTGAG 133

KYHTSGKRLWDKAKHENLSNIDRIKKENDNMQIELRLHLKGBDVTSLNHKELMALELA  
LENGLASIDRDKDEVEFMKKVKIOALDDNKKRLIYELHQQBMNMCNVRMENGYYQ  
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ORIGIN
Alignment Scores: 2.49e-50 Length: 761
Pred. No.: 698.50 Matches: 137
Score: 86.46% Conservative: 29
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Best Local Similarity: 71.35% Indels: 7
Query Match: 63.33% Gaps: 4
DB: 8

US-10-069-527-2 (1-215) x AF230711 (1-761)
QY 26 AsnGlyTlelelelyslsyalysGluileThrValleuCysAspAlalysValserLeu 45
Db 1 AATGGGATCTTGAAGAGGCTAAGGAGATCACTGTTCTGTGTGATGCTAGTGTCTCTC 60
QY 46 IleileTyrSerSerGlyLysMetValGluTyrCysSerProSerThrThrLeuThr 65
Db 61 ATTGCTTTCTAGCTCTGCAAGATGCATGACTACTGTAGCCCCCAAAACCACTTGATT 120
QY 66 GluileleuAspLysTyrHisGlyGlnSerGlyLysLeuThrAspAlalysHisGlu 85
Db 121 GACATATTACAAAATATCACTCACTCTGGAAGAGGTTGTGGATGCTAAGCATGAG 180
QY 86 AsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSerMetGlnValGluLeu 105
Db 181 AATCTAGCAATGAATTTAGATGATCAAGAAAGAGACGATACATGACATGAGTTAGCTA 240
QY 106 ArgHisLeuLysGlyGluAspLysThrSerLeuAsnHisValGlnLeuMetAlaLeuGlu 125
Db 241 AGGCACCTGAAGGGGGAAGATGTCACTCTTTGAACCAAGAGATCATGGCTTTGGAG 300
QY 126 GluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSerLysPheValAspMet 145
Db 301 CTAGCCCTTGAGAAATGGCTTGTAGTATTCTGTGACAGAAAGATGAGTCTTCGAGATG 360
QY 146 MetArgAspAsnGlyLys-----AlaLeuGluAspGluAsnLysArgLeuThrTyrGlu 163
Db 361 ATTAAGAAAAAATGTGAAAATTCAGACCACTTGAGGATGACAAAGCGCCCTTATTACGAG 420
QY 164 LeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGluAsnGlyTyr 183
Db 421 TTGCAC---CAGCAAGAGATGAATATGGATGCAATGTAAAGAAATGGAAATGGGTAT 477
QY 184 HisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnGlnIleProPheAlaPheArg 203
Db 478 -----CAAAGGGTGGGAGACTACCACTCTCAT-----CAGATGGCTTTGGCTTCAGG 525
QY 204 ValGlnProLeuGlnProAsnLeuGlnGluArgIle 215
Db 526 GTGCAGCAATTCAGCAAACTTACAGGAGAGATG 561

RESULT 11
LOCUS AB079259 807 bp mRNA linear PLN 02-APR-2003
DEFINITION Agapanthus praecox ApMADS1 mRNA for MADS-box transcription factor
ACCESSION AB079259
VERSION AB079259.1 GI:29467045
KEYWORDS
SOURCE Agapanthus praecox
ORGANISM Agapanthus praecox
REFERENCE 1
AUTHORS Nakamura, T. and Nakano, M.
TITLE The MADS-box gene which expressed in floral organs of Agapanthus praecox
JOURNAL Published Only in Database (2003)

QY 41 AlaLysValserLeuIleleTyrSerSerGlyLysMetValGluTyrCysSerPro 60
Db 134 GCCAGGCTCTCGTCTCATCTCTCCAGCTCTGCAAGATGCTCCGAGTACTGCGAGCCCC 193

QY 61 SerThrThrLeuThrGluLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTyr 80
Db 194 TCACCTCTCTACCGAAGATCTCTGAGAGTATCAGTCAACTGCGGCAGAGATCTTGG 253

QY 81 AspAlaLysHisGlnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
Db 254 GATCCCAAGCATGAGCACCTGAGCGCGGAGATTGATGATCAAGAAGAGAGATGATAAT 313

QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
Db 314 ATGCAGATCCAGTCTGAGGATCTGAAGGAGAGGATCTGAATCTGCTGCGCCGAGAGAG 373

QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
Db 374 CTGATCCCAATCGAGGAGCGCTGGAGAACGCGATCCGGGCGGAGAGCAGAAAT 433

QY 141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
Db 434 GATTCTTCTGAGGATGCTCAAGAGAACGAGAGGATGCTGGAAGAGATGAACAAACGGTTA 493

QY 161 ThrTyrGluLeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
Db 494 ACTTATATCTGACCATCAGCAA---CTGGCAATGGATGAATATGAGGAACCTGGAA 550

QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPhe 200
Db 551 TTTGCATATCATATAAAGAT---GGGATTTTCAGTTCC-----CAGATGCCAATG 598

QY 201 AlaPheArgValGlnProLeuGlnProAsnLeuGlnGlu 213
Db 599 GCCTTTCTGTGCGCAATTCAGCCTAATTACATGAG 637

RESULT 10
AF230711 761 bp mRNA linear PLN 02-JUN-2000
LOCUS Hydrangea macrophylla MADS box containing protein PI mRNA, partial cds
DEFINITION
ACCESSION AF230711 GI:8163963
KEYWORDS Hydrangea macrophylla
SOURCE Hydrangea macrophylla
ORGANISM Hydrangea macrophylla
REFERENCE 1
AUTHORS Kramer, E.M. and Irish, V.F.
TITLE Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
JOURNAL Int. J. Plant Sci. (2000) In press
DEFINITION 2 (bases 1 to 761)
AUTHORS Kramer, E.M. and Irish, V.F.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2000) MCDB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
FEATURES
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CDS

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REFERENCE
2 (bases 1 to 807)
AUTHORS
Nakamura,T. and Nakano,M.
TITLE
Direct Submission
JOURNAL
Submitted (02-FEB-2002) Toru Nakamura, Niigata University, Fac. of
Agriculture; 2-8050 Ikarashi, Niigata, Niigata 950-2181, Japan
(E-mail:f01e402k@mail.cc.niigata-u.ac.jp, Tel:81-25-262-6598,
Fax:81-25-262-6858)
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41..673
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TYILRHQQLAMEGNVRQLDIGHQREEREFAPQMPAFRVQPIHPNLQNK"
ORIGIN
Alignment Scores:
Pred. No.: 2,66e-50 Length: 807
Score: 698.50 Matches: 132
Percent Similarity: 81.22% Conservative: 41
Best Local Similarity: 61.97% Mismatches: 35
Query Match: 63.33% Indels: 5
DB: 8 Gaps: 2
US-10-069-527-2 (1-215) x AB079259 (1-807)
QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
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QY 21 TyrSerLysArgArgAsnGlyLleLysLysAlaLysGluLeuThrValLeuCysAsp 40
Db 101 TTCGGAAGCGCGGATGCGCATCATCAAGAAAGCTAGAGATGACGCTCTTTTCGAA 160
QY 41 AlaLysValSerLeuLleLysSerSerSerGlyLysMetValGluTyrCysSerPro 60
Db 161 TCACAGTCTCTCTGATCTCTCTAGCTGTGGGAGATGTCGAGTATTCGACCCCA 220
QY 61 SerThrThrLeuThrGluLleLysLysLysLysLysLysLysLysLysLysLysLys 80
Db 221 AACACCTCGTTTCGAGGATATTGGAGAGTACCAGCAACTGTGGGAAGAGCTATGG 280
QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
Db 281 GATGCTAAGCATGAGATCTAATATGCCAGATCGATCGGTTAAGAAAGATGATAAC 340
QY 101 MetGlnValGluLeuArgHisLysLysGlyLysGlyLysLysLysLysLysLysLys 120
Db 341 ATGCMAATGAGTCTAGGCAATTTGAAAGGGAGGATTTGAACCTCTGTAATCCAAAGAA 400
QY 121 LeuMetAlaLeuGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 140
Db 401 CTGATCCGATCGAAGAGCTCGAGAACGGACTCAATGGTGTCCGAGCTAAGCAGATG 460
QY 141 LysPheValAspMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
Db 461 GAATACTTGAAGATGTTGAAAGAGATGAAGGCTTCTGGAAGAGGAGAAATAGAGATTG 520
QY 161 ThrTyrGluLeuGlnLysGlnGlnMetLysLysLysLysLysLysLysLysLysLysLys 180
Db 521 ACTTATATCCTGGCCATCAGCAA--TTGGCGATGAGGAGAAATGTAGGCAATTGGAT 577

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QY 181 AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnGlnLeuProPhe 200
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QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGlu 213
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RESULT 12
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LOCUS
AB094967 876 bp mRNA linear PLN 31-OCT-2003
DEFINITION
Tulipa gesneriana TGGLO mRNA for MADS-box transcription factor,
complete cds.
ACCESSION
AB094967
VERSION
AB094967.1 GI:30172224
KEYWORDS
Tulipa gesneriana
SOURCE
Tulipa gesneriana
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Tulipa.

```

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REFERENCE
1
AUTHORS
Kanno,A., Saeki,H., Kameya,T., Saedler,H. and Theissen,G.
TITLE
Heterotopic expression of class B floral homeotic genes supports a
modified ABC model for tulip (Tulipa gesneriana)
JOURNAL
Plant Mol. Biol. 52 (4), 831-841 (2003)
MEDLINE
22856392
PUBMED
13677470
REFERENCE
2 (bases 1 to 876)
AUTHORS
Kanno,A.
TITLE
Direct Submission
JOURNAL
Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail:kanno@ige.tohoku.ac.jp, Tel:81-22-217-5725,
Fax:81-22-217-5725)

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gene
CDS

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ORIGIN
Alignment Scores:
Pred. No.: 4,75e-50 Length: 876
Score: 696.00 Matches: 131
Percent Similarity: 77.93% Conservative: 35
Best Local Similarity: 61.50% Mismatches: 43
Query Match: 63.10% Indels: 4
DB: 8 Gaps: 1
US-10-069-527-2 (1-215) x AB094967 (1-876)

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QY 1 MetGlyArgGlyLysValGluLeuLysArgIleGluAsnSerSerAsnArgGlnValThr 20
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QY 21 TyrSerLysArgArgAsnGlyLysLysLysLysLysLysLysLysLysLysLysLys 40

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80	TTCCTCAAGCCGCGAATCATCAAGAAGCAGGAGATCAGCGTGTGGAC	139
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140	GCTGGGTCTCTGTCGTCATATTCTCCAGCTCCGGGAAGATGTCCGAGTACTGCAGCCCC	199
QY	SerThrThrLeuThrGluLeuAspLysTyrThiSgLYnSerGlyLysLysLysTrp	80
Db	:: :: :	
200	ACCATPCAGCGTACCAGAAAGATCTCGACAAGTACACAGAACCTGCCGGGAACAGCTCTGG	259
QY	AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnSer	100
Db	: : : : :       : : : : :       : : : : :       : : : : :	
260	GACGCCAAGCACCCAGATCTGAGCAGGAGATTGTATAGGATCAGNAGGAGAACGACAC	319
QY	MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu	120
Db	: : : : :       : : : : :       : : : : :       : : : : :	
320	ATGCAGATAGAGCTGAGGCATCTCAAGGGGAGAGATCTGAATCTCGTCGAGCCCAGGAG	379
QY	LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer	140
Db	: : : : :       : : : : :       : : : : :       : : : : :	
380	CTGATCCCGATTGAGAGCGCTGAGAACCGTTTCAGGAGGCTGAGGAGAGCAGGAT	439
QY	LysPheValaspMetMetArgAspAsnGlyLysAlaLeuGluAspLysLysArgLeu	160
Db	:: :: :	
440	GATGTGCTGATGACGAGGAAGAATAATGACGCTGATGAGGAGGATAAACAACGGCTG	499
QY	ThrTyrGluLeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGlu	180
Db	: : : : :       : : : : :       : : : : :       : : : : :	
500	AATATGTACTGCATCCACGACAAACAGCGAATGGATGAAATATAAGGAGCATGGAG	559
QY	AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnGlnGlnGlnIleProPhe	200
Db	: : : : :       : : : : :       : : : : :       : : : : :	
560	CTTGCTATCATCAAAA-----CATAGGGAATTCATTCCCAGATGCCAATG	607
QY	AlaPheArgValGlnProIleGlnProAsnLeuGlnGlu	213
Db	: : : : :       : : : : :       : : : : :       : : : : :	
608	AGGTTCCGTGTGCACCAANTTCAGCCTAATTTGCATGAG	646
GHY9726	Gerbera hybrida cv. 'Terra Regina' mRNA linear	PLN 02-APR-2003
LOCUS	GGLO1.	
DEFINITION	gglol gene; MADS-box protein.	
ACCESSION	AJ009726	
VERSION	AJ009726.1 GI:4218172	
KEYWORDS	Gerbera hybrid cv. 'Terra Regina'	
SOURCE	Gerbera hybrid cv. 'Terra Regina'	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterids; campanulids; Asterales; Asteraceae; Mutisioideae; Mutisieae; Gerbera.	
REFERENCE	1 Yu, D., Korilainen, M., Pollanen, E., Mehto, M., Elomaa, P., Helariutta, Y., Albert, V.A. and Teeri, T.H. Organ identity genes and modified patterns of flower development in Gerbera hybrida (Asteraceae) Plant J. 17 (1), 51-62 (1999)	
JOURNAL MEDLINE	99168221	
PUBMED	10069067	
REFERENCE	2 (bases 1 to 810) Teeri, T.H. Direct Submission Submitted (21-JUL-1998) Teeri T.H., Institute of Biotechnology, University of Helsinki, P.O. Box 56, FIN-00014 Univ. Helsinki, FINLAND	
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source	1..810 /organism="Gerbera hybrid cv. 'Terra Regina'" /mol_type="mRNA" /cultiivar="Terra Regina" /db_xref="taxon:226891"	
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Qy      141 LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
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Qy      161 ThrTyrgluLeuGlnLysGlnGlnGluMetLysIleLysGluAsnValArgAsnMetGlu 180
Db      517 ATGTAT---TTAGTGCAACAAGTGAATG----- 543
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Db      544 -----GCAGCGATGGGAGATATC-----CAAGCTCATGAACCCCTTT 579

RESULT 15
A36587 LOCUS A36587 780 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 1 from Patent WO9400582.
ACCESSION A36587
VERSION A36587.1 GI:2293891
KEYWORDS
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamiales; Solanales; Solanaceae; Petunia.
JOURNAL 1 (bases 1 to 780)
FOR PLANT BREEDING AND REPRODU (NL)
FEATURES Location/Qualifiers
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ORIGIN
Alignment Scores: 3.89e-49 Length: 780
Pred. No.: 684.50 Matches: 134
Score: 684.50
Percent Similarity: 82.33% Conservative: 43
Best Local Similarity: 62.33% Mismatches: 33

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Query Match:	62.06%	Indels:	5
DB:	6	Gaps:	2
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DB	8	ATGGGGAGAGGAAGATAGAGTAAAGAATAGAAACTCAAGCAACAGACAGATTA	67
QY	21	TyrSerLysArgArgAsnGlyLeuLeuLysLysAlaLysGluLeuThrValLeuCysAsp	40
DB	68	TACTCAAAAGAGAAATGGGATCTTGAATAAAGCTAAGGAAATTAGTGTCTTGTGAT	127
QY	41	AlaLysValSerLeuIleTyrSerSerGlyLysMetValGluTyrCysSerPro	60
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QY	61	SerThrThrLeuThrGluIleLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp	80
DB	182	TCTACTCGTTGGTTGATATTGGATCAATATCACAAAGCTTACTGTTAGAAGATTGTTG	241
QY	81	AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValLysLysAspAsnAspSer	100
DB	242	GATGCTAAGCATGAGAACTTGGACAATGAAATCAACAAAGTCAAGAAAGACATGACAAC	301
QY	101	MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu	120
DB	302	ATGCAAAATGAACCTCAGCGACTTGAGGGTGAAGATATCATCTTTGAACCATAGAGAG	361
QY	121	LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer	140
DB	362	CTCATGATATTGGAAGATGCCCTTGAAATGGACTCACTAGTATTCGTAAACAAACAAAT	421
QY	141	LysPheValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu	160
DB	422	GAGGTTCTGAGGATGATGAGGAAAAGACTCAAAAGTATGGAGGAGGAGCAAGACCACTT	481
QY	161	ThrTyrGluLeuGlnLysGlnGlnLeuMetLysLysGluAsnValArgAsnMetGlu	180
DB	482	AATTGCAATTCGCGCAACTTGAGATAGCAACCATGAATAGGAATATGGGAGAAATGGCG	541
QY	181	AsnGlyTyrHisGlnArgGlnLeuGlyAsnTyrAsnAsnAsnGlnGlnIleProPhe	200
DB	542	GAAGTGTTTCACGAGGGGAATCATGATACCAAAACCAT-----ATGCCTTTT	592
QY	201	AlaPheArgValGlnProIleGlnProAsnLeuGlnGluArgIle	215
DB	593	GCCTTCGAGTACAAACCAATGAGCCAAATTTGAGGAGAGGTTG	637

Search completed: September 26, 2004, 09:11:12  
Job time : 3677.24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:18:34 ; Search time 69.2617 Seconds  
(without alignments)  
979.421 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGSKVEIKRIENSRQVT.....QQIPFAFRVQIPNLQERI 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_25:

1: sp\_archaea:

2: sp\_bacteria:

3: sp\_fungi:

4: sp\_human:

5: sp\_invertebrate:

6: sp\_mammal:

7: sp\_mhc:

8: sp\_organelle:

9: sp\_phase:

10: sp\_plant:

11: sp\_rodent:

12: sp\_virus:

13: sp\_vertebrate:

14: sp\_unclassified:

15: sp\_rvirus:

16: sp\_bacteriap:

17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	215	10 Q9AVU7	Q9avv7 malus domes
2	1099	99.6	215	10 Q9AVU6	Q9avv6 malus domes
3	975	88.4	190	10 Q8LSM9	Q8l5m9 malus domes
4	824	74.7	211	10 Q9ZTQ9	Q9ztq9 cucumis sat
5	811	73.5	203	10 Q9FZNI	Q9fzni rosa rugosa
6	739.5	67.0	212	10 Q40883	Q40883 petunia hyb
7	720	65.3	211	10 Q84L10	Q84l10 betulia verr
8	701.5	63.6	210	10 Q84L10	Q84l10 lilium rega
9	698.5	63.3	187	10 Q9LL94	Q9ll94 hydrangea m
10	698.5	63.3	210	10 Q84L87	Q84l87 agapanthus
11	696	63.1	211	10 Q84M20	Q84m20 tulipa gesn
12	691	62.6	197	10 Q9ZS26	Q9zs26 gerbera hyb
13	685.5	62.1	196	10 Q84LC9	Q84lc9 chrysanthem
14	684	62.0	213	10 Q41353	Q41353 silene lati
15	669.5	60.7	208	10 Q64934	Q64934 eucalyptus
16	666	60.4	202	10 Q9XF83	Q9xf83 hyacinthus

17	664	60.2	209	10 Q8GTP3	Q8gtp3 orchis ital
18	664	60.2	229	10 Q65124	Q65124 dicentra ex
19	663.5	60.2	200	10 Q9LL95	Q9ll95 chloranthus
20	663.5	60.2	208	10 Q9SEF9	Q9sef9 arabidopsis
21	660.5	59.9	196	10 Q84LC2	Q84lc2 helianthus
22	647	58.7	196	10 Q65129	Q65129 delphinium
23	642.5	58.3	212	10 Q9AR49	Q9ar49 zea mays (m
24	641.5	58.2	212	10 Q9AR50	Q9ar50 zea mays (m
25	638	57.8	202	10 Q9XF84	Q9xf84 hyacinthus
26	633	57.4	186	10 Q9LL97	Q9ll97 calycanthus
27	633	57.4	216	10 Q8LSF6	Q8lsf6 daucus caro
28	625	56.7	186	10 Q65130	Q65130 michelia fi
29	623	56.5	209	10 Q9AR51	Q9ar51 zea mays (m
30	620.5	56.3	210	10 Q40703	Q40703 oryza sativ
31	618.5	56.1	187	10 Q84V60	Q84v60 cimicifuga
32	617	55.9	209	10 Q40702	Q40702 oryza sativ
33	615.5	55.8	185	10 Q65131	Q65131 liriodendro
34	611.5	55.4	212	10 Q94FT9	Q94ft9 medicago sa
35	609	55.2	200	10 Q65128	Q65128 syringa vul
36	608.5	55.2	186	10 Q9LL92	Q9ll92 tacca chant
37	608.5	55.2	187	10 Q84Y89	Q84y89 akebia quin
38	607.5	55.1	187	10 Q84Y59	Q84y59 cimicifuga
39	606	54.9	231	10 Q65122	Q65122 papaver nud
40	605.5	54.9	187	10 Q84Y88	Q84y88 akebia quin
41	597.5	54.2	185	10 Q84Y64	Q84y64 berberis gi
42	596.5	54.1	208	10 Q9LL93	Q9ll93 sagittaria
43	595	53.9	167	10 Q8GT92	Q8gt92 helianthus
44	593.5	53.8	170	10 Q84Y29	Q84y29 trolius la
45	593.5	53.8	181	10 Q8LT08	Q8lt08 lilium rega

#### ALIGNMENTS

RESULT 1

Q9AVU7	PRELIMINARY;	PRT;	215 AA.
ID Q9AVU7			
AC Q9AVU7			
DT 01-JUN-2001 (TREMELrel. 17, Created)			
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)			
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)			
DE Pistillata MADS-box protein.			
GN Pi.			
OS Malus domestica (Apple) (Malus sylvestris).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.			
OX NCBI_TaxID=3750;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=cv. Granny Smith; TISSUE=Flower;			
RX MEDLINE=21107711; PubMed=11158635;			
RA Yao J.L., Dong Y.H., Morris B.A.;			
RT "Parthenocarpic apple fruit production conferred by transposon			
RT insertion mutations in a MADS-box transcription factor.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:1306-1311(2001).			
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION			
CC FACTORS.			
CC EMBL; AJ291490; CAC28021.1; -.			
DR HSSP; P11746; IMNM.			
DR TRANSFAC; T05238; -.			
DR GO; GO:0005634; C:nucleus; IEA.			
DR GO; GO:0003700; F:transcription factor activity; IEA.			
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR GO; GO:0006350; P:transcription; IEA.			
DR InterPro; IPR002487; TF_Kbox.			
DR InterPro; IPR002100; TF_MADSbox.			
DR Pfam; PF01486; K-box; 1.			
DR Pfam; PF00319; SRP-TF; 1.			
DR PRINTS; PR00404; MADSDOMAIN.			
DR SMART; SM00432; MADS; 1.			
DR PROSITE; PS00350; MADS_BOX_1; 1.			

DR PROSITE; PS00066; MADS BOX 2; 1.  
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 215 AA; 24999 MW; 51F6E2B849ADB26C CRC64;

Query Match 100.0%; Score 1103; DB 10; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-64;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60  
 DB 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60  
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 DB 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 QY 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215  
 DB 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215

RESULT 2  
 Q9AVU6 PRELIMINARY; PRT; 215 AA.  
 ID Q9AVU6  
 AC Q9AVU6  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Placillata MADS-box protein.  
 GN PI.  
 OS Malus domestica (Apple) (Malus sylvestris).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 OX NCBI\_TaxID=3750;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Granny Smith; TISSUE=Leaf;  
 RX MEDLINE=21107711; PubMed=1158635;  
 RT Yao J.L., Dong Y.H., Morris B.A.;  
 RT "Parthenocarpic apple fruit production conferred by transposon  
 RT insertion mutations in a MADS-box transcription factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1306-1311(2001).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL; AJ291491; CAC28022.1; -;  
 DR HSSP; P11746; 1MNW.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRP-TF; 1.  
 DR PRINTS; PR00404; MADSDOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 215 AA; 25000 MW; 51F6EFD5F7B26C CRC64;

Query Match 99.6%; Score 1099; DB 10; Length 215;  
 Best Local Similarity 99.5%; Pred. No. 1.4e-63;  
 Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60  
 DB 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60  
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 DB 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 QY 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215  
 DB 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215

DB 1 MGRGKVEIKRIENSSNRQVTSYKRRNGIIKKAKEITVLCDKAVSLIIYSSSGKMWVCSP 60  
 QY 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 DB 61 STLTTEILDYKHGSGKKLWDAKHENLSNEVDYKNDNSMQVELRHLKGEDITSLNHVE 120  
 QY 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEAEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
 QY 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215  
 DB 181 NGYHQRLGNYNQOQIIPFAFRVQPIQPNLQERI 215

RESULT 3  
 Q8L5M9 PRELIMINARY; PRT; 190 AA.  
 ID Q8L5M9  
 AC Q8L5M9  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE MADS-box protein (Fragment).  
 GN MDPI.  
 OS Malus domestica (Apple) (Malus sylvestris).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 OX NCBI\_TaxID=3750;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Indo; TISSUE=Young floral parts;  
 RA Matsumoto S., Ohtsubo T., Soejima J.;  
 RT "Cloning and sequencing of apple MADS-box genes 'MdPI', 'MdTM6' and  
 RT 'MdMADS13'.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL; AB081092; BAC11906.1; -;  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRP-TF; 1.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 FT NON TER 1  
 SQ SEQUENCE 190 AA; 22025 MW; 9D6DED732D01B5D9 CRC64;

Query Match 88.4%; Score 975; DB 10; Length 190;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-55;  
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 26 NGIIRKAKEITVLCDKAVSLIIYSSSGKMWVCSPSTTLTEILDYKHGSGKKLWDKAKEH 85  
 DB 1 NGIIRKAKEITVLCDKAVSLIIYSSSGKMWVCSPSTTLTEILDYKHGSGKKLWDKAKEH 85  
 QY 86 NLSNEVDYKNDNSMQVELRHLKGEDITSLNHVELMALEAEALENGLTSIRDKQSKFVDM 145  
 DB 61 NLSNEVDYKNDNSMQVELRHLKGEDITSLNHVELMALEAEALENGLTSIRDKQSKFVDM 120  
 QY 146 MRDNGKALEDENKRLTYELQKQEMKIKENVRNMGYHQRLGNYNQOQIIPFAFRVQ 205  
 DB 121 MRDNGKALEDENKRLTYELQKQEMKIKENVRNMGYHQRLGNYNQOQIIPFAFRVQ 180  
 QY 206 PIQPNLQERI 215  
 DB 181 PIQPNLQERI 190

RESULT 4  
Q92TQ9 PRELIMINARY; PRT; 211 AA.  
ID Q92TQ9  
AC Q92TQ9  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE MADS-box protein 26.  
GN CUM26.  
OS Cucumis sativus (Cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid1; Cucurbitales; Cucurbitaceae; Cucumis.  
OX NCBI\_TaxID=3659;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kater M.M., Franken J., Carney K., van Lookeren Campagne M.M.,  
RA Angenent G.C.;  
RT "class C homeotic genes are required for whorl specific sex  
determination in unisexual flowers";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
FACTORS.  
DR EMBL: AF043255; AAD02250.1; -.  
DR HSSP: P11746; 1NMN.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription; IEA.  
DR GO: GO:0006350; P:transcription; IEA.  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box; 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS; 1.  
DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
SQ SEQUENCE 211 AA; 24904 MW; D89FD0D1A879C03 CRC64;

Query Match 74.7%; Score 824; DB 10; Length 211;  
Best Local Similarity 73.8%; Pred. No. 7.5e-46;  
Matches 158; Conservative 34; Mismatches 18; Indels 4; Gaps 2;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIKKAKETIVLADAKVSLIIYSSSGKWEYCSF 60  
DB 1 MGRGKVEIKRIENSSNQVYTSKRNGIIKKAKETIVLADAKVSLIIYSSSGKWEYCSF 60  
QY 61 STLTLEILDKYHGSGKKLWDAKHENLSNEVDYKNDKNDMOVELRLKGEDITSLNHV 120  
DB 61 STLTLEILDKYHGSGKKLWDAKHENLSNEVDYKNDKNDMOVELRLKGEDITSLNHV 120  
QY 121 LMALEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 180  
DB 121 LMALEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 180  
QY 121 LMALEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 180  
DB 121 LMALEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 180  
QY 181 NGYHQRQLGYNVNNQOQIPFAFRVQPIQPIQLQER 214  
DB 181 NGYHQRQLGYNVNNQOQIPFAFRVQPIQPIQLQER 214  
QY 181 IGYNR-MRDPNS---QMPFAFRVQPIQPIQLQER 210  
DB 181 IGYNR-MRDPNS---QMPFAFRVQPIQPIQLQER 210

RESULT 5  
Q9FZNI PRELIMINARY; PRT; 203 AA.  
ID Q9FZNI  
AC Q9FZNI  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE MADS-box protein.  
GN MASAKO Bp.

OS Rosa rugosa (Rugosa rose).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid1; Rosales; Rosaceae; Rosoideae; Rosa.  
OX NCBI\_TaxID=74645;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tissue-flower.  
RA Matsumoto S., Kitahara K., Hirai S., Wada K., Fukui H.;  
RT "Rose MADS-box gene 'MASAKO Bp' homologous to class B floral identity  
genes";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
FACTORS.  
DR EMBL: AB038462; BAB11939.1; -.  
DR HSSP: P11746; 1NMN.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription; IEA.  
DR GO: GO:0006350; P:transcription; IEA.  
DR InterPro: IPR002487; TF\_Kbox.  
DR InterPro: IPR002100; TF\_MADSbox.  
DR Pfam: PF01486; K-box; 1.  
DR PRINTS: PR00404; MADSDOMAIN.  
DR SMART: SM00432; MADS; 1.  
DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
DR PROSITE: PS50066; MADS\_BOX\_2; 1.  
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
SQ SEQUENCE 203 AA; 23573 MW; C577C9A497FBEBC CRC64;

Query Match 73.5%; Score 811; DB 10; Length 203;  
Best Local Similarity 75.0%; Pred. No. 4.9e-45;  
Matches 162; Conservative 20; Mismatches 20; Indels 14; Gaps 4;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIKKAKETIVLADAKVSLIIYSSSGKWEYCSF 59  
DB 1 MGRGKVEIKRIENSSNQVYTSKRNGIIKKAKETIVLADAKVSLIIYSSSGKWEYCSF 60  
QY 60 PSTTLEILDKYHGSGKKLWDAKHENLSNEVDYKNDKNDMOVELRLKGEDITSLNHV 119  
DB 61 PSTTLEILDKYHGSGKKLWDAKHENLSNEVDYKNDKNDMOVELRLKGEDITSLNHV 120  
QY 120 ELMLEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 179  
DB 121 ELMLEELNGLTISIRKQSKFVDMKEDNGKALDENKRLTYELQKQCKEIKENRANE 179  
QY 180 ENGYHQRQLGYNVNNQOQIPFAFRVQPIQPIQLQER 215  
DB 179 -----NYYNN-TQIPFALRVQNPQVNLHDM 203

RESULT 6  
Q40883 PRELIMINARY; PRT; 212 AA.  
ID Q40883  
AC Q40883  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE FBP3.  
GN FBP3.  
OS Petunia hybrida (Petunia).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiales; Solanales; Solanaceae; Petunia.  
OX NCBI\_TaxID=4102;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=R27; TISSUE=Petal;  
RX MEDLINE=94177174; PubMed=7907515;  
RA Angenent G.C., Franken J., Buscher M., Weiss D., van Tunen A.J.;  
RT "Co-suppression of the Petunia homeotic gene fbp2 affects the identity

RT of the generative meristem."  
 RL Plant J 5:33-44(1994).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL; X71417; CAA50549.1; -.  
 DR PIR; S60288; S60288.  
 DR HSSP; P11746; 1MNW.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR PRINTS; PR00404; MADSOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS0066; MADS\_BOX\_2; 1.  
 KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 212 AA; 24740 MW; 712351a6c8369f CRC64;  
 Query Match 67.0%; Score 739.5; DB 10; Length 212;  
 Best Local Similarity 67.4%; Pred. No. 2.1e-40;  
 Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;  
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60  
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60  
 QY 61 STTLEILDKYHGQSGKLMADAKHENSNEVDVRKKNDSQWVELRLHKGEDITSLNHVE 120  
 DB 61 STTLEILDKYHGQSGKLMADAKHENSNEVDVRKKNDSQWVELRLHKGEDITSLNHVE 120  
 QY 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 QY 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 QY 181 NGYHQRGLGNVNNQOQIPPAFRVOPICPNLOERI 215  
 DB 181 EYVHQR---DRDYEQVQMFALRVQPMQNLHERM 212  
 RESULT 7  
 Q84L10 PRELIMINARY; PRT; 211 AA.  
 ID 084L10;  
 AC 084L10;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-OCT-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Pistillata homologue.  
 GN MADS2.  
 OS Betula verrucosa (White birch) (Betula pendula).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fagales; Betulaceae; Betula.  
 OC NCBI\_TaxID=3505;  
 RN (1)  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=flower;  
 RA Jaervinen P.L.H., Lemmetyinen J., Savolainen O., Sopanen T.;  
 RT "DNA sequence variation in BpmMDS2 gene in two populations of Betula  
 RT pendula.";  
 RL Mol. Ecol. 12:369-384 (2003).  
 DR EMBL; AJ488589; CAD32764.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRP-TF; 1.

DR PRINTS; PR00404; MADSOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS0066; MADS\_BOX\_2; 1.  
 SQ SEQUENCE 211 AA; 24930 MW; F9B96C504C1E26DC CRC64;  
 Query Match 65.3%; Score 720; DB 10; Length 211;  
 Best Local Similarity 66.0%; Pred. No. 3.8e-39;  
 Matches 142; Conservative 31; Mismatches 38; Indels 4; Gaps 2;  
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60  
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60  
 QY 61 STTLEILDKYHGQSGKLMADAKHENSNEVDVRKKNDSQWVELRLHKGEDITSLNHVE 120  
 DB 61 STTLEILDKYHGQSGKLMADAKHENSNEVDVRKKNDSQWVELRLHKGEDITSLNHVE 120  
 QY 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 QY 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 DB 121 LMALEALENGSLTIRDKOSKEVDMWRDNGKALEDENRKLTYELQKQEMKIKENVRNME 180  
 QY 181 NGYHQRGLGNVNNQOQIPPAFRVOPICPNLOERI 215  
 DB 181 DYVEQR-VRDYNS---QMPFAFRVOPICPNLOERI 211  
 RESULT 8  
 Q8LT09 PRELIMINARY; PRT; 210 AA.  
 ID 08LT09;  
 AC 08LT09;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE MADS-box transcription factor.  
 GN LRGLOX.  
 OS Lilium regale (Regal lily).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
 OC NCBI\_TaxID=82328;  
 RN (1)  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=flower;  
 RA MEDLINE=21959322; PubMed=11961093;  
 RA Winter K.U., Weiser C., Kaufmann K., Bohne A., Kirchner C., Kanno A.,  
 RA Saedler H., Theissen G.;  
 RT "Evolution of Class B Floral Homeotic Proteins: Obligate  
 RT Heterodimerization Originated from Homodimerization.";  
 RL Mol. Biol. Evol. 19:587-596(2002).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL; AB071379; BAB94551.1; -.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003700; P:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRP-TF; 1.  
 DR PRINTS; PR00404; MADSOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS0066; MADS\_BOX\_2; 1.  
 KM DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 210 AA; 24621 MW; F2F3262F364EBB4E CRC64;  
 Query Match 63.6%; Score 701.5; DB 10; Length 210;  
 Best Local Similarity 62.0%; Pred. No. 6e-38;  
 Matches 122; Conservative 45; Mismatches 31; Indels 5; Gaps 3;  
 QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60  
 DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLCDAKVSIIYSSGKMYEYCSF 60

ID	Sequence	Score	Length	DB	Match	Conservative	Mismatches	Indels	Gaps
Db	1 MORGIEIETRIENSTNRQVTFEKRNGGIIKKAREISVLCQAVSVIIFSSSGKSEYCS	63.3%	698.5	DB 10	187	29	19	7	4
Qy	61 STLTLEIIIDKHGSGGKLMADKHNLSNEVVRVKKDNDNQVLEIRHKGEDITSLNVE	71.4%	82	DB 10	187	29	19	7	4
Db	61 STSLPKRIETRVQNGCKIWDPRHSHLSAIDRIKENDNQIQLRHKGEDLSNLOPE	71.4%	82	DB 10	187	29	19	7	4
Qy	121 LMALAEALENGSLTIRDSKSFVDMDKNGKALBEDENKRLTYELQKQEMKIKENVRNE	71.4%	82	DB 10	187	29	19	7	4
Db	121 LIPIREALENGIRGVRKENDPRLTKKVERILLEEDNKRLTYILHQQ-LAMDENRMLE	71.4%	82	DB 10	187	29	19	7	4
Qy	181 NGYHORLGNNVNNQOQIPFARVQPIQNLQE	71.4%	82	DB 10	187	29	19	7	4
Db	180 PAYHKKD-GDFSS--QMPAFRRVQPIQNLQE	71.4%	82	DB 10	187	29	19	7	4
RESULT 9									
Q9LL94	PRELIMINARY:	PRT:	187 AA.						
Q9LL94	Q9LL94:	Q9LL94:	Q9LL94:						
AC	01-OCT-2000 (TREMBLrel. 15, Created)								
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)								
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)								
DE	MADS box containing protein PI (Pfam02487).								
DE	Hydangea macrophylla.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spematiophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;								
OC	Cornales; Hydrangeaceae; Hydrangea.								
NCBI	taxid=23110;								
RP	SEQUENCE FROM N.A.								
RA	Kramer E.M., Irish V.F.;								
RT	"Evolution of the petal and stamen developmental programs: Evidence								
RT	from comparative studies of the lower eudicots and basal								
RT	angiosperms.";								
RL	Int. J. Plant Sci. 0:0-0(2000).								
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).								
CC	-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION								
CC	FACTORS.								
EMBL	AF230711; AAF73940.1; -;								
DR	GO; GO:0005634; C:nucleus; IEA.								
DR	GO; GO:0003700; F:transcription factor activity; IEA.								
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.								
DR	GO; GO:0006350; P:transcription; IEA.								
DR	InterPro: IPR002487; Trf_Kbox.								
DR	InterPro: IPR002100; Trf_MADSbox.								
DR	Pfam: PF01486; K-box; 1.								
DR	Pfam: SM00432; SRF-Trf; 1.								
DR	SMART; SM00432; MADS; 1.								
DR	PROSITE; PS50066; MADS_BOX_2; 1.								
KW	DNA-binding; Nuclear protein; Transcription; Transcription regulation.								
FT	NON_TER								
FT	1								
SEQUENCE	187 AA; 21844 MW; C7CE02871F635034 CRC64;								
Query Match	63.3%; Score 698.5; DB 10; Length 187;								
Best Local Similarity	71.4%; Pred. No. 82=38;								
Matches	137; Conservative 29; Mismatches 19; Indels 7; Gaps 4								
Qy	26 NGIIRKAKETIVLCAKASLLIYSSSGKAVEXCSPSTLTITLIDKHGSGGKLMADKHE								
Db	1 NGIILKAKETIVLCPDASVSLIVFASGKHEVCSPSTLTITLIDKHGSGGKLMADKHE								
Qy	86 NISNVDRVKKDNDNQVLEIRHKGEDITSLNHVELMALAEALENGSLTIRDSKSFVDM								
Db	61 NISNLEIDRIKKENDNQIQLRHKGEDVSLNHKEIMALEALENGSLTIRDSKSEVFEEM								
Qy	146 MKDNGK-ALBEDENKRLTYELQKQEMKIKENVRNNENGYHORLGNNVNNQOQIPFAR								
Db	121 IKRYVYIQLALEDNKRLTYELH-QQEMNNECVREWENGY--QVADYQSH--QMPAFRR								
Qy	204 VQPIQNLQERI 215								
Db	176 VQPIQNLQERM 187								

RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;  
RT "Heterotopic expression of class B floral homeotic genes supports a  
RT modified ABC model for tulip (*Tulipa gesneriana*).";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB094967; BAC75972.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR002487; TF\_Box.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1.  
DR Pfam; PF00319; SRP-TF; 1.  
DR PRINTS; PRO0404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
SQ SEQUENCE 211 AA; 25022 MW; A785CD6275573692 CRC64;

Query Match 63.1%; Score 696; DB 10; Length 211;  
Best Local Similarity 61.5%; Pred. No. 1.4e-37;  
Matches 131; Conservative 35; Mismatches 43; Indels 4; Gaps 1;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120  
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120  
QY 121 LMALEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
DB 121 LMALEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
QY 121 LPIEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
DB 121 LPIEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
QY 181 NGYHOROGLNYYNNQOIPPAFVQPIOPNLOE 213  
DB 181 NGYHOROGLNYYNNQOIPPAFVQPIOPNLOE 213  
QY 181 LAHQK---HRENSQWPMTRVQPIOPNLE 209  
DB 181 LAHQK---HRENSQWPMTRVQPIOPNLE 209

## RESULT 12

092S26 PRELIMINARY; PRT; 197 AA.

AC 092S26; 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE MADS-box protein, GGIOL.  
OS Gerbera hybrida.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Campanulids; Asterales; Asterales; Mutilisoidae; Mutilisae; Gerbera.  
OC NCBI\_Taxid=18101;  
RN [1] \_SEQUENCE FROM N.A.  
RC STRAIN=cy. Terra Regina;  
RX MEDLINE=99168221; PubMed=10069067;  
RA Yu D., Kotliainen M., Poellänen B., Mehto M., Elomaa P.,  
RT Helariutta Y., Albert V.A., Teeri T.H.;  
RT "Organ identity genes and modified patterns of flower development in  
RT Gerbera hybrida (Asteraceae).";  
RL Plant J. 17:51-62(1999).  
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
CC FACTORS.  
DR EMBL; AJ009726; CA08804.1; -;  
DR HSP; P11746; INNM.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR GO; GO:0006355; P:transcription; IEA.  
DR InterPro; IPR002487; TF\_Box.  
DR InterPro; IPR002100; TF\_MADSbox.

DR Pfam; PF01486; K-box; 1.  
DR Pfam; PF00319; SRP-TF; 1.  
DR PRINTS; PRO0404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
SQ SEQUENCE 197 AA; 23133 MW; DDDIC2B2E01C5A2A CRC64;

Query Match 62.6%; Score 691; DB 10; Length 197;  
Best Local Similarity 63.3%; Pred. No. 2.6e-37;  
Matches 136; Conservative 30; Mismatches 31; Indels 18; Gaps 3;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120  
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120  
QY 121 LMALEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
DB 121 LMALEBALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 180  
QY 121 LIAYEDALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 169  
DB 121 LIAYEDALENGTLTIRDKOSKFLVDMWRDNGKALEDENRLEYLQKQEMKIKENVRNME 169  
QY 181 NGYHOROGLNYYNNQOIPPAFVQPIOPNLOE 215  
DB 181 NGYHOROGLNYYNNQOIPPAFVQPIOPNLOE 215  
QY 170 ----AAGDYQAAHE--PFSFVQPMOENLHERM 197  
DB 170 ----AAGDYQAAHE--PFSFVQPMOENLHERM 197

## RESULT 13

084LC9 PRELIMINARY; PRT; 196 AA.

AC 084LC9; 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE MADS-box transcription factor CDM86.  
GN CDM86.  
OS Chrysanthemum x morifolium.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Campanulids; Asterales; Asterales; Anthemideae; Anthemideae;  
OC Chrysanthemum.  
OC NCBI\_Taxid=41568;  
RN [1] \_SEQUENCE FROM N.A.  
RC STRAIN=cy. Parliament; TISSUE=flower;  
RA Shchemnikova A.V., Shulga O.A., Skryabin K.G., Angenent G.C.;  
RT "Chrysanthemum MADS-box transcription factor CDM86.";  
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AY173061; AA022986.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR002487; TF\_Box.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1.  
DR Pfam; PF00319; SRP-TF; 1.  
DR PRINTS; PRO0404; MADSDOMAIN.  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
SQ SEQUENCE 196 AA; 22593 MW; 84D0035B13E121D0 CRC64;

Query Match 62.1%; Score 685.5; DB 10; Length 196;  
Best Local Similarity 63.3%; Pred. No. 6e-37;  
Matches 136; Conservative 28; Mismatches 32; Indels 19; Gaps 3;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIITKAKETITVLDKAVSLIYSSSGKMYEYCS 60  
QY 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120  
DB 61 STLTLEILDYKYGSGKGLMDAKHENTLSNEVDKNDSDMOVELRHLKGEDITSINHYE 120



Db 61 KTVLIDRLDRYQSLGSKLMDAKHENTLQNEIDRIKKNESMQLEHLKGEDITSINYE 120  
 QY 121 LMALEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 180  
 Db 121 LIAVEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 169  
 QY 181 NGYHQRQLGNYNNNOQIIPFAFRVOPIDPNIQERI 215  
 Db 170 -----AAMGDY-----QNHPRSPFRVQMPNHLHERM 196

RESULT 14  
 Q41353 PRELIMINARY; PRT; 213 AA.  
 AC Q41353;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
 DE SLM2 protein.  
 GN SLM2.  
 OS Silene lactifolia (White campion).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OC NCBI\_TaxId=37657;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Petal, and Stamen;  
 RX MEDLINE=95170282; PubMed=7866023;  
 RA Hardenack S., Ye D., Saedler H., Grant S.;  
 RT "Comparison of MADS-box gene expression in developing male and female  
 RT flowers of the dioecious plant white campion.";  
 RL Plant Cell 6:1175-1187(1994).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL: X80489; CAA56656.1; -.  
 DR HSSP: P11746; 1MMN.  
 DR TRANSPAC: T03174; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO: GO:0006350; P:transcription; IEA.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR PRINTS: PR00404; MADSDOMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_2; 1.  
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 213 AA; 24938 MW; 807C33859646ECB CRC64;

Query Match 62.0%; Score 684; DB 10; Length 213;  
 Best Local Similarity 63.4%; Pred. No. 8.2e-37;  
 Matches 137; Conservative 31; Mismatches 44; Indels 4; Gaps 2;

QY 1 MGRGKVEIKRIENSNFQVYTSKRNGIIRKAKETITVLCDAKVSIIYSSSGKWEYCSF 60  
 Db 1 MGRKIKIKRIENSTNQVYTSKRNGIIRKAKETITVLCDAKVSIIYSSSGKWEYCSF 60  
 QY 61 STTLEILDKYHGSGKLLMDAKHENTLNEVDKYNKDSNOVELRHLKGEDITSINYE 120  
 Db 61 ETAVEDILDOYHKISGRLMDAKHENTLNEVDKYNKDSNOVELRHLKGEDITSINYE 120  
 QY 121 LMALEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 180  
 Db 121 LMALEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 180  
 QY 181 NGYHQRQLGNYNNNOQIIPFAFRVOPIDPNIQERI 215  
 Db 181 NGYHQRQLGNYNNNOQIIPFAFRVOPIDPNIQERI 215

Db 178 AGVCSNPSDRDYHYQNPPIPPYGFVQMPNLODM 213

RESULT 15  
 ID 064934 PRELIMINARY; PRT; 208 AA.  
 AC 064934;  
 DT 01-AUG-1998 (TRENBLREL. 07, Created)  
 DT 01-AUG-1998 (TRENBLREL. 07, Last sequence update)  
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
 DE MADS box protein.  
 GN EGM2.  
 OS Eucalyptus grandis (Flooded gum).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Myrtaceae; Eucalyptus.  
 OC NCBI\_TaxId=71139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=flower;  
 RX MEDLINE=98440658; PubMed=9765522;  
 RA Southerton S.G., Marshall H., Mouradov A., Teasdale R.D.;  
 RT "Eucalypt MADS-Box genes expressed in developing flowers.";  
 RL Plant Physiol. 118:365-372(1998).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION  
 CC FACTORS.  
 DR EMBL: AF029976; AAC78283.1; -.  
 DR HSSP: P11746; 1MMN.  
 DR TRANSPAC: T03086; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR GO: GO:0006350; P:transcription; IEA.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR PRINTS: PR00404; MADSDOMAIN.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_2; 1.  
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.  
 SQ SEQUENCE 208 AA; 24171 MW; 24EA75AF5305F09C CRC64;

Query Match 60.7%; Score 669.5; DB 10; Length 208;  
 Best Local Similarity 60.7%; Pred. No. 6.9e-36;  
 Matches 130; Conservative 37; Mismatches 40; Indels 7; Gaps 2;

QY 1 MGRGKVEIKRIENSNFQVYTSKRNGIIRKAKETITVLCDAKVSIIYSSSGKWEYCSF 60  
 Db 1 MGRKIKIKRIENSTNQVYTSKRNGIIRKAKETITVLCDAKVSIIYSSSGKWEYCSF 60  
 QY 61 STTLEILDKYHGSGKLLMDAKHENTLNEVDKYNKDSNOVELRHLKGEDITSINYE 120  
 Db 61 STTLEILDKYHGSGKLLMDAKHENTLNEVDKYNKDSNOVELRHLKGEDITSINYE 120  
 QY 121 LMALEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 180  
 Db 121 LMALEALENGSLTIRDKOSKFDVMDKNDKALJEDENKLTLYELQKQOEMKIKENVRNME 180  
 QY 181 NGYHQRQLGNYNNNOQIIPFAFRVOPIDPNIQERI 214  
 Db 181 NGYHQRQLGNYNNNOQIIPFAFRVOPIDPNIQERI 214

Search completed: September 27, 2004, 09:28:15  
 Job time : 72.2617 secs



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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:11:24; Search time 14.4295 Seconds  
(without alignments)  
775,845 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103  
Sequence: 1 MGRGVEIKRINSSNRQVT.....QQIPPAFVQPIQPLQERI 215

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740.5	67.1	212	1	MAD2_PETHY 007474 petunia hyb
2	713	64.6	215	1	GLOB_ANTMA 003378 antirrhinum
3	707	64.1	210	1	GLOB_TOBAC 003416 nicotiana t
4	684.5	62.1	210	1	FBP1_PETHY 003488 petunia hyb
5	660.5	59.9	208	1	PIST_PETHY 048007 arabidopsis
6	421	38.2	237	1	M13_GNEGN 09xg14 gnetum gne
7	384.5	34.9	259	1	M17_MAZE 08vwm8 zea mays (m
8	377.5	34.2	231	1	MAD1_PETHY 007472 petunia hyb
9	373.5	33.9	217	1	DEB1_ANTMA 08r14 antirrhinum
10	360.5	32.7	268	1	FB24_PETHY 09ates petunia hyb
11	356.5	32.3	222	1	AP3_ARATH 035632 arabidopsis
12	349	31.6	227	1	DEP1_ANTMA 08ryd9 antirrhinum
13	342	31.0	252	1	TT16_ARATH 08ryd9 arabidopsis
14	335	30.4	251	1	SEB3_ARATH 02456 arabidopsis
15	334	30.3	265	1	JOIN_LYCES 09fiv6 lycopersico
16	332	30.1	214	1	CMB2_DIACA 042498 dianthus ca
17	330	29.9	242	1	AGL6_ARATH 038676 arabidopsis
18	329	29.8	254	1	AGL5_SINLA 004067 sinapis alb
19	327.5	29.7	251	1	SEB1_ARATH 029382 arabidopsis
20	326.5	29.6	258	1	AGL3_ARATH 029383 arabidopsis
21	323.5	29.3	250	1	AGL8_SOLTU 042429 solanum tub
22	322	29.2	241	1	AGL8_SINLA 041274 sinapis alb
23	322	29.2	253	1	CAL_ARATH 039081 arabidopsis
24	320.5	29.1	248	1	AGL1_ARATH 029381 arabidopsis
25	319.5	29.0	246	1	AGL5_ARATH 029385 arabidopsis
26	319	28.9	252	1	AG_ARATH 017839 arabidopsis
27	318.5	28.9	241	1	AGL9_PETHY 003489 petunia hyb
28	318	28.8	254	1	AP1_SINLA 041266 sinapis alb
29	316	28.6	256	1	AP1_ARATH 035631 arabidopsis
30	316	28.6	240	1	SVP_ARATH 09fvc1 arabidopsis
31	314.5	28.5	250	1	AGL8_SOLCO 022328 solanum com
32	314	28.5	250	1	SEB2_ARATH 029384 arabidopsis
33	313	28.4	227	1	AGL8_LYCES 040170 lycopersico

34	311	28.2	233	1	CMB1_DIACA 039685 dianthus ca
35	311	28.2	252	1	AGL6_ARATH 029386 arabidopsis
36	308	27.9	252	1	AG_BRANA 001540 brassica na
37	305.5	27.7	224	1	AGL9_LYCES 042464 lycopersico
38	304	27.6	268	1	AGL5_ARATH 038847 arabidopsis
39	303	27.5	248	1	AG_TOBAC 043585 nicotiana t
40	301	27.3	242	1	AG_PANGI 040872 panax gins
41	300	27.2	230	1	AGL1_ARATH 038836 arabidopsis
42	300	27.2	250	1	AGL9_ARADE 038694 aranda debc
43	297.5	27.0	242	1	AG_PETHY 040885 petunia hyb
44	295	26.7	264	1	AGL5_BRANA 039295 brassica na
45	293	26.6	210	1	AP32_ASABU 0911a7 asarum euro

## ALIGNMENTS

RESULT 1	MAD2_PETHY	STANDARD;	PRT;	212 AA.
AC	007474:			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DE	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Floral homeotic protein PMADS 2.			
GN	PMADS2.			
OS	Petunia hybrida (Petunia).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiales; Solanales; Solanaceae; Petunia.			
OX	NCBI_TaxID=4102;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	Tissue=Petal;			
RX	MEDLINE=94105323; PubMed=8278527;			
RA	Kush A., Brumelle A., Shevell D., Chua N.-H.;			
RT	"The cDNA sequence of two MADs box proteins in Petunia.";			
RL	Plant Physiol. 102:1051-1052(1993).			
CC	-1- FUNCTION: Transcription factor involved in the genetic control of flower development.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- Tissue specificity: Predominantly expressed in petals and stamens.			
CC	-1- Tissue specificity: Predominantly expressed in petals and stamens.			
CC	-1- SIMILARITY: Contains 1 K-box dimerization domain.			
CC	-1- SIMILARITY: Contains 1 MADs-box domain.			
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CC	EMBL; X69947; CAA49568.1; -			
DR	PIR; S31707; S31707.			
DR	HSSP; P11746; 1MM.			
DR	TRANSFAC; T03134; -			
DR	InterPro; IPR002487; TF_Kbox.			
DR	InterPro; IPR002487; TF_MADSbox.			
DR	Pfam; PF01486; K-box; 1.			
DR	Pfam; PF00319; SRF-TF; 1.			
DR	PRINTS; PR00404; MADSDOMAIN.			
DR	SMART; SM00432; MADS; 1.			
DR	PROSITE; PS00350; MADS_BOX_1; 1.			
DR	PROSITE; PS50066; MADS_BOX_2; 1.			
KW	Transcription regulation; DNA-binding; Activator; Nuclear protein;			
KW	Developmental protein.			
FT	DOMAIN 3 58 MADS-box.			
FT	DOMAIN 93 165 K-BOX.			
FT	SEQUENCE 212 AA; 24785 MW; FCB10C16D52E4210 CRC64;			
Query Match	67.1%;	Score 740.5;	DB 1;	Length 212;

Best Local Similarity 67.4%; Pred. No. 46-40;  
Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGRKLEIKRINSSNRQVYTSRRNGIIKKAKETVLCDAYSLIIYSSGKMEYCSP 60  
D 1 MGRKLEIKRINSSNRQVYTSRRNGIIKKAKETVLCDAYSLIIYSSGKMEYCSP 60  
QY 61 STTLTILDKYHQSGLKMDAKHENTLSEVDRVKKNDMSQVLEHKLKGEDITSLNHYE 120  
D 61 STTLTILDKYHQSGLKMDAKHENTLSEVDRVKKNDMSQVLEHKLKGEDITSLNHYE 120  
QY 121 LMALEBALNGLTSLIDKQSKFVDMKRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
D 121 LMALEBALNGLTSLIDKQSKFVDMKRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
QY 181 NGYHORQLGNYNNQOQIPPAFRVQPIQPNLOER 215  
D 181 NGYHORQLGNYNNQOQIPPAFRVQPIQPNLOER 215  
QY 181 EYVHOR---DRDTETVQMPFALRVQMPQNPHERM 212  
D 181 EYVHOR---DRDTETVQMPFALRVQMPQNPHERM 212

RESULT 2

GLOB\_ANTMA STANDARD; PRT; 215 AA.  
ID GLOB\_ANTMA  
AC 003378;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Floral homeotic protein GLOBOSA.  
GN GLO.  
OS Antirrhinum majus (Garden snapdragon).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Antirrhinaceae; Antirrhineae; Antirrhinum.  
NCBI\_TaxID=4151;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9309842; PubMed=1361166;  
RA Trobner W., Ramirez L., Motte P., Hue I., Huiser P., Loeinig W.-E.,  
RA Saedler H., Sommer H., Schwartz-Sommer Z.;  
RT "GLOBOSA: a homeotic gene which interacts with DEFICIENS in the  
RT control of Antirrhinum floral organogenesis.";  
RL EMBO J. 11:4693-4704(1992).  
CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF  
CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- MISCELLANEOUS: NOTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS  
CC INTO SEPAL AND STAMINA INTO CARPELS.  
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
CC -1- SIMILARITY: Contains 1 MADS-box domain.  
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CC -----  
DR EMBL; X68831; CAA48725.1; -  
DR F1R; S28062; S28062.  
DR HSSP; P11746; IMNM.  
DR TRANSFAC; T01779; -  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1  
DR PRINTS; PF00319; SRF-TF; 1  
DR SMART; SM00432; MADS; 1.  
DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
DR PROSITE; PS00066; MADS\_BOX\_2; 1.  
DR Transcription regulation; DNA-binding; Activator; Nuclear protein;  
DR Developmental protein  
FT DOMAIN 3 57 MADS-box.

FT DOMAIN 93 165 K-BOX.  
SQ SEQUENCE 215 AA; 25363 MM; 0DE2A3E3781537E4 CRC64;  
Matches 135; Conservative 40; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGRKLEIKRINSSNRQVYTSRRNGIIKKAKETVLCDAYSLIIYSSGKMEYCSP 60  
D 1 MGRKLEIKRINSSNRQVYTSRRNGIIKKAKETVLCDAYSLIIYSSGKMEYCSP 60  
QY 61 STTLTILDKYHQSGLKMDAKHENTLSEVDRVKKNDMSQVLEHKLKGEDITSLNHYE 120  
D 61 STTLTILDKYHQSGLKMDAKHENTLSEVDRVKKNDMSQVLEHKLKGEDITSLNHYE 120  
QY 121 LMALEBALNGLTSLIDKQSKFVDMKRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
D 121 LMALEBALNGLTSLIDKQSKFVDMKRDNGKALEDENKRLTYELQKQEMKIKENVRNME 180  
QY 181 NGYHORQLGNYNNQOQIPPAFRVQPIQPNLOER 214  
D 181 NGYHORQLGNYNNQOQIPPAFRVQPIQPNLOER 214  
QY 181 AYVDHHHQNADYEAMQMPFAPRVQMPQNPLOER 214  
D 181 AYVDHHHQNADYEAMQMPFAPRVQMPQNPLOER 214

RESULT 3

GLOB\_TOBAC STANDARD; PRT; 209 AA.  
ID GLOB\_TOBAC  
AC 003416;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Floral homeotic protein GLOBOSA.  
GN GLO.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Nicotiana.  
NCBI\_TaxID=4097;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX STRAIN=cv. SRL; TISSUE=flower;  
RX MEDLINE=93288002; PubMed=8099711;  
RA Hansen G., Estruch J.J., Sommer H., Spena A.,  
RT "NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of  
RT Antirrhinum majus: cDNA sequence and expression pattern.";  
RL Mol. Gen. Genet. 239:310-312(1993).  
CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF  
CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN FLORAL ORGANS AND WITHIN  
CC THE FLOWER. EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.  
CC -1- MISCELLANEOUS: NOTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS  
CC INTO SEPAL AND STAMINA INTO CARPELS.  
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
CC -1- SIMILARITY: Contains 1 MADS-box domain.  
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CC -----  
DR EMBL; X67959; CAA48142.1; -  
DR F1R; S35226; S35226.  
DR HSSP; P11746; IMNM.  
DR TRANSFAC; T01779; -  
DR InterPro; IPR002487; TF\_Kbox.  
DR InterPro; IPR002100; TF\_MADSbox.  
DR Pfam; PF01486; K-box; 1  
DR PRINTS; PF00319; SRF-TF; 1  
DR PRINTS; PF00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX 1; 1.  
 DR PROSITE; PS00350; MADS\_BOX 2; 1.  
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;  
 KM Developmental protein.  
 FT DOMAIN 3 57 MADS-box.  
 FT 91 163 K-BOX.  
 SQ SEQUENCE 209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;

Query Match 64.1%; Score 707; DB 1; Length 209;  
 Best Local Similarity 63.6%; Pred. No. 5e-38; 31; Indels 6; Gaps 2;  
 Matches 136; Conservative 41; Mismatches 31;

QY 1 MGRKVEIKRIENSSNRQVYTSKRNGIILKKAKEITVLCDAKVSLLIYSSSGKWEYCSP 60  
 DB 1 MGRKVEIKRIENSSNRQVYTSKRNGIILKKAKEISVLCDAKVSIIIFASSGKWEH--S 58  
 QY 61 STLTLEILDKYHGGSGKKLMDAKHENTLSEVDYRKNDNSQVLRHLKGEDITSLNHVE 120  
 DB 59 STSLVDILDOYHKLTKGRRLMDAKHENTLSEVDYRKNDNSQVLRHLKGEDITSLNHRE 118  
 QY 121 LMALEALNGLTISIRKQSKFVDMWRDNGKALEDENKRLTYELQKQEKIKENVRNME 180  
 DB 119 LMLEDALNGLTISIRKQNDLLRMWRKKTQSGMEEDQDQNLQRLQLEIASNRRNGEIG 178  
 QY 181 NGYHQRQLGNVNNQOQIPPAFRVQPIQPNLOER 214  
 DB 179 EVFHQRE---NEYQTOMPEAFRVPQMPQPNLOER 208

## RESULT 4

FBP1\_PETHY STANDARD; PRT; 210 AA.

AC Q03488;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Floral homeotic protein FBP1 (Floral binding protein 1).  
 GN FBP1.  
 OS Petunia hybrida (petunia).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Petunia.  
 OC NCBI\_TaxID=4102;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93005737; PubMed=1365537;  
 RA Angenent G.C., Buschcher M., Franken J., Mol J.N.M., van Tunen A.J.;  
 RT "Differential expression of two MADS box genes in wild-type and  
 mutant petunia flowers";  
 RL Plant Cell 4:983-993(1992).  
 CC -!- FUNCTION: Probable transcription factor.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- TISSUE SPECIFICITY: PETAL.  
 CC -!- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -!- SIMILARITY: Contains 1 MADS-box domain.  
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 CC  
 DR EMBL; M91190; AAA33731.1; -.  
 DR F1R; JQ1689; JQ1689.  
 DR HSSP; P11746; 1MM.  
 DR TRANSFAC; T03092; -.  
 DR InterPro; IPR002487; TF\_KDOX.  
 DR InterPro; IPR002100; TF\_MADSBOX.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRP-TF; 1.

DR PRINTS; PF00404; MADSDOMAIN.

DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX 1; 1.  
 DR PROSITE; PS00350; MADS\_BOX 2; 1.  
 DR Transcription regulation; DNA-binding; Nuclear protein.  
 KM Developmental protein.  
 FT DOMAIN 3 57 MADS-box.  
 FT 91 163 K-BOX.  
 SQ SEQUENCE 210 AA; 24647 MW; B2D3718E6A157C8E CRC64;

Query Match 62.1%; Score 684.5; DB 1; Length 210;  
 Best Local Similarity 62.3%; Pred. No. 1.3e-36;  
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;

QY 1 MGRKVEIKRIENSSNRQVYTSKRNGIILKKAKEITVLCDAKVSLLIYSSSGKWEYCSP 60  
 DB 1 MGRKVEIKRIENSSNRQVYTSKRNGIILKKAKEISVLCDAKVSIIIFASSGKWEH--S 58  
 QY 61 STLTLEILDKYHGGSGKKLMDAKHENTLSEVDYRKNDNSQVLRHLKGEDITSLNHVE 120  
 DB 59 STSLVDILDOYHKLTKGRRLMDAKHENTLSEVDYRKNDNSQVLRHLKGEDITSLNHRE 118  
 QY 121 LMALEALNGLTISIRKQSKFVDMWRDNGKALEDENKRLTYELQKQEKIKENVRNME 180  
 DB 119 LMLEDALNGLTISIRKQNDLLRMWRKKTQSGMEEDQDQNLQRLQLEIASNRRNGEIG 178  
 QY 181 NGYHQRQLGNVNNQOQIPPAFRVQPIQPNLOER 215  
 DB 179 EVFHQREHNDYH--NMPAFRVPQMPQPNLOER 210

## RESULT 5

P1ST\_ABAATH STANDARD; PRT; 208 AA.

AC P48007; Q9SQ07; Q9SQ08; Q9SQ09; Q9SQ10; Q9SQ11; Q9SQ12; Q9SQ13;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Floral homeotic protein PISTILLATA (Transcription factor PI).  
 GN PI OR ARS20240 OR P5024.130.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eusteroideae; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=cv. Landsberg erecta;  
 RX MEDLINE=95047314; PubMed=7958839;  
 RA Goto K., Meyerowitz E.M.;  
 RT "Function and regulation of the Arabidopsis floral homeotic gene  
 PISTILLATA";  
 RL Genes Dev. 8:1548-1560(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=cv. Landsberg erecta;  
 RX MEDLINE=20233824; PubMed=10769227;  
 RA Honma T., Goto K.;  
 RT "The Arabidopsis floral homeotic gene PISTILLATA is regulated by  
 discrete cis-elements responsive to induction and maintenance  
 signals";  
 RL Development 127:2021-2030(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND VARIANTS.  
 RX STRAIN=cv. Bla-1, cv. Bretagne, cv. Bs-1, cv. Bu-0, cv. Bu-2,  
 cv. Chl-1, cv. Co-1, cv. Columbia, cv. Coracalla-1, cv. Cvi-0,  
 cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,  
 cv. Li-3, cv. Li-6, and cv. Lisee;  
 RX MEDLINE=99126449; PubMed=9927474;  
 RA Purganan M.D., Sudduth J.I.;  
 RT "Molecular population genetics of floral homeotic loci: departures  
 from the equilibrium-neutral model at the APTAL3 and PISTILLATA  
 genes of Arabidopsis thaliana";  
 RL Genetics 151:839-846(1999).

RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, Columbia;  
 RX MEDLINE=21016721; PubMed=1130714;  
 RA Tabata S., Kaneko T., Nakamura Y., Kozani H., Kato T., Asamizu E.,  
 RA Miyajima N., Sasanoto S., Kimura T., Hosouchi T., Kawashima K.,  
 RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,  
 RA Nakazaki N., Naito K., Okumura S., Shino S., Takeuchi C., Mada T.,  
 RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,  
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,  
 RA Haberman K., Murray J., Johnson D., Ronfing T., Nelson J.,  
 RA Stenking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,  
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Darte M.,  
 RA Du H., Edwards J., Fryman J., Hakensen B., Lamar E., Latreille P.,  
 RA Leonard S., Meyer R., Mulvaney E., Ozeraky P., Riley A., Strommatt C.,  
 RA Wagner-Watson C., Wollan A., Yeakum M., Bell M., Dedina N.,  
 RA Farnell L., Shah R., Rodriguez M., Hoon See L., Vi D., Baker J.,  
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,  
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,  
 RA Volckaert G., Wambut R., Duesterhoeft A., Stiekema W., Pohl T.,  
 RA Ertan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,  
 RA Langham S.A., McCullagh B., Robben J., Grynoprez B., Zimmermann W.,  
 RA Rampeger U., Wedler H., Balke K., Wedler E., Peters S.,  
 RA van Staveren M., Dirke G., Rose M., Hauf J., Bernerstor S., Hempel S.,  
 RA Weitzenecker T., Bothé G., Rose M., Hauf J., Bernerstor S., Hempel S.,  
 RA Feldpausch M., Lamberth S., Villarroel R., Giejen J., Ardiles W.,  
 RA Bents O., Lemcke K., Kolesov G., Mayer K.F., Rüd S., Schoof H.,  
 RA Schneller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.,  
 RA "Sequence and analysis of chromosome 5 of the plant Arabidopsis  
 chaliana."  
 RT Nature 408:823-826(2000).  
 RL [5]  
 RN FUNCTION.  
 RP MEDLINE=96152196; PubMed=8565821;  
 RX Krizek B.A., Meyerowitz E.M.,  
 RA "The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient  
 to provide the B class organ identity function."  
 RT Development 122:11-22(1996).  
 RL [6]  
 RN CHARACTERIZATION.  
 RP MEDLINE=96209811; PubMed=8643482;  
 RX Riechmann J.L., Krizek B.A., Meyerowitz E.M.,  
 RA "Dimerization specificity of Arabidopsis MADS domain homeotic proteins  
 APETALA1, APETALA3, PISTILLATA, and AGAMOUS."  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).  
 RL [7]  
 RN GENETIC REGULATION.  
 RP MEDLINE=21178805; PubMed=11283333;  
 RX Ng M., Yancovsky M.F.,  
 RA "Activation of the Arabidopsis B class homeotic genes by APETALA1."  
 RT Plant Cell 13:739-753(2001).  
 RL [8]  
 RN CHARACTERIZATION.  
 RP MEDLINE=21074934; PubMed=11206550;  
 RX Honma T., Goto K.,  
 RA "Complexes of MADS-box proteins are sufficient to convert leaves into  
 floral organs."  
 RT Nature 409:525-529(2001).  
 RL -1- FUNCTION: Probable transcription factor involved in the genetic  
 control of flower development. Is required for normal development  
 of petals and stamens in the wild-type flower. Forms an  
 heterodimer with APETALA3 that is required for autoregulation of  
 both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1  
 or SEPALLATA3 to form a ternary complex that could be responsible  
 for the regulation of the genes involved in the flower  
 development.  
 CC -1- SUBUNIT: Forms an heterodimer with APETALA3, capable of binding to  
 CAG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to form a  
 ternary complex.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- INDUCTION: Positively regulated by the meristem identity  
 proteins APETALA1 and LEAFY with the cooperation of UFO.  
 CC -1- MISCELLANEOUS: Mutations in PI cause transformation of petals into

CC sepals and stamens into carpels.  
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -1- SIMILARITY: Contains 1 MADS-box domain.  
 CC -----  
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 CC -----  
 DR EMBL; D30807; BA06465.1; -  
 DR EMBL; AB035137; BA087000.1; -  
 DR EMBL; AF115815; AAD51984.1; -  
 DR EMBL; AF115816; AAD51985.1; -  
 DR EMBL; AF115817; AAD51986.1; -  
 DR EMBL; AF115818; AAD51987.1; -  
 DR EMBL; AF115819; AAD51988.1; -  
 DR EMBL; AF115820; AAD51989.1; -  
 DR EMBL; AF115821; AAD51990.1; -  
 DR EMBL; AF115822; AAD51991.1; -  
 DR EMBL; AF115823; AAD51992.1; -  
 DR EMBL; AF115824; AAD51993.1; -  
 DR EMBL; AF115825; AAD51994.1; -  
 DR EMBL; AF115826; AAD51995.1; -  
 DR EMBL; AF115827; AAD51996.1; -  
 DR EMBL; AF115828; AAD51997.1; -  
 DR EMBL; AF115829; AAD51998.1; -  
 DR EMBL; AF115830; AAD51999.1; -  
 DR EMBL; AF296825; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A53839; A53839.  
 DR HSSP; P11746; 1MMN.  
 DR TRANSFAC; T03129; -  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRE-TF; 1.  
 DR PRINTS; PR00404; MADSOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS0066; MADS\_BOX\_2; 1.  
 KW Flowering; Transcription regulation; Activator; Developmental protein;  
 KW Nuclear protein; DNA-binding; Coiled coil; Polymorphism.  
 FT DOMAIN 3 57  
 FT DOMAIN 106 143  
 FT DOMAIN 75 117  
 FT DOMAIN 29 29  
 FT VARIANT 38 38  
 FT VARIANT 51 51  
 FT VARIANT 73 73  
 FT VARIANT 75 75  
 FT VARIANT 89 89  
 FT VARIANT 112 112  
 FT VARIANT 125 125  
 FT VARIANT 140 140  
 FT VARIANT 142 142  
 FT VARIANT 160 160  
 FT VARIANT 203 203  
 SQ SEQUENCE 208 AA; 24047 MW; 49728735AC883CCA CRC64;  
 Query Match 59.9%; Score 660.5; DB 1; Length 208;  
 Best Local Similarity 60.5%; Pred. No. 4,1e-35;  
 Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;  
 QY 1 MGRGKVEIKRIENSNROVTSKRNGIKKAKETIVCDARKVSLIYSSGKWEYCSP 60  
 1 MGRGKVEIKRIENSNRRVTSKRNGIKKAKETIVCDARKVSLIYSSGKWEYCSP 60  
 Db 1 MGRGKVEIKRIENSNRRVTSKRNGIKKAKETIVCDARKVSLIYSSGKWEYCSP 60  
 QY 61 STTLEILDKTHGSGGCKLMDAKHENSNEVDYKXNDNSQVLRHKGEDITSNAHE 120  
 61 SMDICAMLDQYKXSGKTLMDAKHENSNEVDYKXNDNSQVLRHKGEDITSNAHE 120  
 Db 61 SMDICAMLDQYKXSGKTLMDAKHENSNEVDYKXNDNSQVLRHKGEDITSNAHE 120

QY 121 LMALEALENGSLTIRDKOSKFPVDMRDNGKALEDENKRLTYELOKQEMKIKENRYNME 180  
 DB 121 LMAVEAHEGLKVDKVDHVEIILISKREKEMAEORQUTFOLQ-QQEWALASARGMM 179  
 QY 181 NGYHOSQOLGNVNNQOQIPFAFVQPIOPNLOERI 215  
 DB 180 MRDHDCQ-----FGYRVQPIQPTLQEKI 202  
 RESULT 6  
 M13\_GNEGN STANDARD; PRT; 237 AA.  
 ID M13\_GNEGN STANDARD; PRT; 237 AA.  
 AC Q9XGJ4;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE MADS box protein GGM13.  
 GN GGM13.  
 OS Gnetum gnemon (Bago).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Gnepophyta; Gnepopsida; Gnetales; Gnetales; Gnetum.  
 OX NCBI\_TaxID=3382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99307411; PubMed=10377416;  
 RA Winter K.-U., Becker A., Muenster T., Kim J.T., Saedler H.,  
 Theissen G.;  
 RT "MADS-box genes reveal that gnetophytes are more closely related to  
 RT confers than to flowering plants.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:7342-7347(1999).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=21851234; PubMed=11862488;  
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,  
 Saedler H., Theissen G.;  
 RT "A novel MADS-box gene subfamily with sistergroup relationship to  
 RT class B floral homeotic genes.";  
 RL Mol. Genet. Genomics 266:942-950(2002).  
 CC -1- FUNCTION: Probable transcription factor.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- TISSUE SPECIFICITY: Expression specific for female reproductive  
 CC structures: strong at the adaxial base of the cupules, where  
 CC cupules will later develop, then in the outermost cell layer of the  
 CC nucellus, in the inner envelope, and in the inner half of the  
 CC middle envelope at late stage of ovule development.  
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -1- SIMILARITY: Contains 1 MADS-box domain.  
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 CC  
 DR EMBL: AJ132219; CAB44459.1; -.  
 DR HSPF: F11746; 1MMN.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR PRINTS: PR00404; MADSBOX.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_2; 1.  
 DR TRANSCRIPTION regulation; DNA-binding; Nuclear protein.  
 FT DOMAIN 1 61 MADS-box.  
 KM DOMAIN 1 61 MADS-box.  
 SO SEQUENCE 237 AA; 26943 MW; 5C65191A5ID08691 CRC64;  
 Query Match 38.2%; Score 421; DB 1; Length 237;  
 Best Local Similarity 37.7%; Pred. No. 5; 2e-20;

Matches 90; Conservative 52; Mismatches 57; Indels 40; Gaps 4;  
 QY 1 MGRGVEIKRIENSSNROVYTSKRRNGIKKAKITVLCDAKVALIYSSSGKAVRYCSP 60  
 DB 1 MGRGVEIKRIENSSNROVYTSKRRNGIKKAKITVLCDAKVALIYSSSGKAVRYCSP 60  
 QY 61 STTELEIDKYGOSGKKLMDAKENLSNEVDYRVKQNDQVQVRLHKGSDITSLNHYE 120  
 DB 61 SSMKATIERKQYKSGARITFYDQHLXCETTRAKNENKIQTNIRRMGGDLTSLNHYE 120  
 QY 121 LMALEALENGSLTIRDKOSKFPVDMRDNGKALEDENKRLTYELOKQ----- 168  
 DB 121 LHLHGOQLSASASRYRSRKNQIMQOLENLRKERILEDQSHLCRLAEQQAAVEGQOE 180  
 QY 169 -----EMKIKENVRMNGYHQROLGANNNNQOQIPFAFVQPIOPNLOE 213  
 DB 181 PLLEGVCFPPDNKRTAAANAGPLHGH-----LP-AFRLQPTOPNLOE 225  
 RESULT 7  
 M17\_MAIZE STANDARD; PRT; 259 AA.  
 ID M17\_MAIZE STANDARD; PRT; 259 AA.  
 AC Q8VWMS;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE MADS box protein ZMM17.  
 GN M17.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=CY 7232; TISSUE=flower;  
 RX MEDLINE=21851234; PubMed=11862488;  
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,  
 Saedler H., Theissen G.;  
 RT "A novel MADS-box gene subfamily with sistergroup relationship to  
 RT class B floral homeotic genes.";  
 RL Mol. Genet. Genomics 266:942-950(2002).  
 CC -1- FUNCTION: Probable transcription factor.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- TISSUE SPECIFICITY: Strong expression in female inflorescences  
 CC (ears), but also weak expression in male inflorescences (tassels).  
 CC At early stages of the development of the female spikelet,  
 CC and the developing silk. At very late stages of development,  
 CC expression becomes restricted to parts of the silk.  
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -1- SIMILARITY: Contains 1 MADS-box domain.  
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 CC  
 DR EMBL: AJ271208; CAC91053.1; -.  
 DR InterPro: IPR002487; TF\_Kbox.  
 DR InterPro: IPR002100; TF\_MADSbox.  
 DR Pfam: PF01486; K-box; 1.  
 DR Pfam: PF00319; SRF-TF; 1.  
 DR PRINTS: PR00404; MADSBOX.  
 DR SMART: SM00432; MADS; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE: PS00350; MADS\_BOX\_2; 1.  
 DR TRANSCRIPTION regulation; DNA-binding; Nuclear protein.  
 FT DOMAIN 1 61 MADS-box.  
 KM DOMAIN 1 61 MADS-box.  
 SO SEQUENCE 259 AA; 26943 MW; 5C65191A5ID08691 CRC64;





DR InterPro; IPR002487; TF\_Kbox.

RN [3]-  
RP SEQUENCE FROM N.A., AND VARIANTS.  
RC STRAIN=cv. Bla-1, cv. Bretagne, cv. Bs-1, cv. Bu-0, cv. Bu-2

RN [3]-  
RP SEQUENCE FROM N.A., AND VARIANTS.  
RC STRAIN=cv. Bla-1, cv. Bretagne, cv. Bs-1, cv. Bu-0, cv. Bu-2

RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,  
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,  
RC cv. Li-3, cv. Li-8, and cv. Lisse;  
RX MEDLINE=99126449; PubMed=9927474;  
RT Purganan M.D., Suddith J.I.;  
RT "Molecular population genetics of floral homeotic loci: departures  
RT from the equilibrium-neutral model at the *APETALA3* and *PISTILLATA*  
RT genes of *Arabidopsis thaliana*.";  
RL Genetics 151:839-848(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016720; PubMed=1130713;  
RA Farnoudat M., Lemcke K., Rieger H., Peter-Alonso M., Oberwasser B.,  
RA Saranbat M., Valle G., Bloeker H., Peter-Alonso M., Oberwasser B.,  
RA Delenly M., Boutry M., Griwell L.A., Maché R., Purgosench P.,  
RA De Simone V., Choisme N., Artiguenave F., Robert C., Broillet P.,  
RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Queller F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wurmach E., Drzonek H., Erle H., Jordan N., Banger S.,  
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nvakatura G.,  
RA Verzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,  
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,  
RA Reichelt J., Scharte M., Schoen O., Barques M., Terol J., Clement J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,  
RA Cooke R., Laurie M., Berger-Liauro C., Purnelle B., Masny D.,  
RA de Haan M., Maeres A.C., Alcaraz J.-P., Cortet A., Gascubeta E.,  
RA Montaubert A., Aguirou A., Flores R., Liguori R., Vitale D.,  
RA Manhardt G., Haese D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujil C.Y., Shea T.P.,  
RA Cressy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,  
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlym T.V.,  
RA Prens D., Lin X., Nieman W.C., Salberg S.L., White O., Venter J.C.,  
RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida A.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
RA Nakayama A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis thaliana*.";  
RL Nature 408:820-823(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldman K.A.;  
RT "Full-length cDNA from *Arabidopsis thaliana*.";  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=23954850; PubMed=14593172;  
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
RA Karlin-Nemman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
RA Arakawa T., Bah J., Banno F., Bowser L., Brooks S.Y., Carrinci P.,  
RA Chao Q., Choy N., Enyu A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.M., Iida K., Karnes M.,  
RA Khan S., Koeseema E., Ishida J., Yang P.X., Jones T., Kawai J.,  
RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Empirical analysis of transcriptional activity in the *Arabidopsis*  
RT genome.";  
RL Science 302:842-846(2003).  
RN [7]  
RP SEQUENCE OF 36-128 FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=9911297; PubMed=10382288;  
RA Brunel D., Proger N., Pelletier G.;  
RT "Development of amplified consensus genetic markers (ACGM) in *Brassica*

RT napus from *Arabidopsis thaliana* sequences of known biological  
RT function.";  
RL Genome 42:387-402(1999).  
RN [8]  
RP FUNCTION.  
RX MEDLINE=96152196; PubMed=8565821;  
RA Krizek B.A., Meyerowitz E.M.;  
RT "The *Arabidopsis* homeotic genes *APETALA3* and *PISTILLATA* are sufficient  
RT to provide the B class organ identity function.";  
RL Development 122:11-22(1996).  
RN [9]  
RP CHARACTERIZATION.  
RX MEDLINE=96209811; PubMed=8643482;  
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;  
RT "Dimerization specificity of *Arabidopsis* MADS domain homeotic proteins  
RT *APETALA1*, *APETALA3*, *PISTILLATA*, and *AGAMOUS*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).  
RN [10]  
RP GENETIC REGULATION.  
RX MEDLINE=21178805; PubMed=11283333;  
RA Ng M., Yanofsky M.F.;  
RT "Activation of the *Arabidopsis* B class homeotic genes by *APETALA1*,"  
RL Plant Cell 13:739-753(2001).  
RN [11]  
RP CHARACTERIZATION.  
RX MEDLINE=21074934; PubMed=11206550;  
RA Honma T., Goto K.;  
RT "Complexes of MADS-box proteins are sufficient to convert leaves into  
RT floral organs.";  
RL Nature 409:525-529(2001).  
RN [12]  
RP FUNCTION: Probable transcription factor involved in the genetic  
CC control of flower development. Is required for normal development  
CC of petals and stamens in the wild-type flower. Forms an  
CC heterodimer with *PISTILLATA* that is required for autoregulation of  
CC both *AP3* and *PI* genes. *AP3/PI* heterodimer interacts with *APETALA1*  
CC or *SEPALLATA3* to form a ternary complex that could be responsible  
CC for the regulation of the genes involved in the flower  
CC development.  
CC -1- SUBUNIT: Forms an heterodimer with *PISTILLATA*, capable of binding  
CC to CARG-box sequences. *AP3/PI* heterodimer binds *AP1* or *SEP3* to  
CC form complexes.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: Expressed in petals and stamens.  
CC -1- INDUCTION: Positively regulated by the meristem identity proteins  
CC *APETALA1* and *LEAFY* with the cooperation of UFO.  
CC -1- MISCELLANEOUS: Mutations in *AP3* cause transformation of petals  
CC into sepals and stamens into carpels.  
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
CC -1- SIMILARITY: Contains 1 MADS-box domain.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: M66357; AAA32740.1; -  
DR EMBL: D21125; BAB04665.1; -  
DR EMBL: AF115798; AAD51887.1; -  
DR EMBL: AF115799; AAD51888.1; -  
DR EMBL: AF115800; AAD51889.1; -  
DR EMBL: AF115801; AAD51890.1; -  
DR EMBL: AF115802; AAD51891.1; -  
DR EMBL: AF115803; AAD51892.1; -  
DR EMBL: AF115804; AAD51893.1; -  
DR EMBL: AF115805; AAD51894.1; -  
DR EMBL: AF115806; AAD51895.1; -  
DR EMBL: AF115807; AAD51896.1; -  
DR EMBL: AF115808; AAD51897.1; -  
DR EMBL: AF115809; AAD51898.1; -  
DR EMBL: AF115810; AAD51899.1; -

DR EMBL/ AF115811; AAD51900.1; -  
 DR EMBL/ AF115812; AAD51901.1; -  
 DR EMBL/ AF115813; AAD51902.1; -  
 DR EMBL/ AF115814; AAD51903.1; -  
 DR EMBL/ AL132971; CAB81799.1; -  
 DR EMBL/ AY087369; AAL64919.1; -  
 DR EMBL/ AY070397; AAL49893.1; -  
 DR EMBL/ AY142590; AAN13159.1; -  
 DR EMBL/ AF056541; AAD41557.1; -  
 DR PIR/ A42095; A42095.  
 DR HSSP/ P11746; 1NMN.  
 DR TRANSFAC; T01008.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRF-TF; 1.  
 DR PRINTS; PR00404; MADSDOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
 DR Flowering; Transcription regulation; Activator; Developmental protein;  
 KW  
 Query Match 32.3%; Score 356.5; DB 1; Length 232;  
 Best Local Similarity 35.1%; Pred. No. 5,7e-16;  
 Matches 79; Conservative 46; Mismatches 73; Indels 27; Gaps 3;  
 QY 1 MGRKVEIKRIENSSNRQVYTSKRNGIIRKAEITVLCDAKVSLLIYSSSGKVCYCSF 60  
 DB 1 MARGKIQIKRIENQTRQVYTSKRNGIFKKAHEITVLCDAKVSIIIMFSSNKLHEIYISF 60  
 QY 61 STLTLELDKYGSGGKKLMDAKHENTLSNEVDYVKKDNDSMQVLEHLKGEDITSLNHVE 120  
 DB 61 NTTKKQLVDYQKXAVGVDMLSHVEKQEHKLNENVRNLRRIQRMGESLNDLGYEQ 120  
 QY 121 LMALEBALENGLTSTIRKOSKSFVDMMDNGKALEDENKELTYELOKQOEKIKENV 176  
 DB 121 LRLEDEMENTFTLVAREKFKSLGNQIEETTKKNGKQOQIQLKLNHELELRAE---DPHY 177  
 QY 177 RMNENG-----YHQQLGNVNNNQOQIPFA 201  
 DB 178 GLVNDGQDYDVLGYQIEGSRAYALRFHONHHYHNGHLMAPSA 222  
 RESULT 12  
 DEF1 ANTMA STANDARD; PRT; 227 AA.  
 AC P23706;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Floral homeotic protein deficiencies.  
 GN DEFA  
 OS Antirrhinum majus (Garden snapdragon).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Antirrhinales; Antirrhinaeae; Antirrhinae; Antirrhinum.  
 OX NCBI\_TaxID=4151;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=90183955; PubMed=1968830;  
 RA Sommer H., Beltran J.-P., Hulsner P., Pape H., Loennig W.-E.,  
 Saedler H., Schwarz-Sommer Z.;  
 RT "Deficiens, a homeotic gene involved in the control of flower  
 morphogenesis in Antirrhinum majus: the protein shows homology to  
 transcription factors";  
 RL EMBO J. 9:605-613(1990).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Sipe 50;  
 RC MEDLINE=92155166; PubMed=1346760;  
 RA Schwarz-Sommer Z., Hue I., Hulsner P., Flor P.J., Hansen R.,  
 Teters F., Loennig W.-E., Saedler H., Sommer H.;  
 RT "Characterization of the Antirrhinum floral homeotic MADS-box gene

RT deficiencies: evidence for DNA binding and autoregulation of its  
 RT persistent expression throughout flower development.";   
 RL EMBO J. 11:251-263(1992).  
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF  
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH GLOBOSA (GLO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- MISCELLANEOUS: MUTATIONS IN DEFA CAUSE TRANSFORMATION OF PETALS  
 CC INTO SEPALs AND STAMINA INTO CARPELS.  
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -1- SIMILARITY: Contains 1 MADS-box domain.  
 CC  
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 CC  
 DR EMBL/ X52023; CAA36268.1; -  
 DR EMBL/ X62810; CAA44629.1; -  
 DR PIR/ S12378; S12378.  
 DR HSSP/ P11746; 1NMN.  
 DR TRANSFAC; T01008.  
 DR InterPro; IPR002487; TF\_Kbox.  
 DR InterPro; IPR002100; TF\_MADSbox.  
 DR Pfam; PF01486; K-box; 1.  
 DR Pfam; PF00319; SRF-TF; 1.  
 DR PRINTS; PR00404; MADSDOMAIN.  
 DR SMART; SM00432; MADS; 1.  
 DR PROSITE; PS00350; MADS\_BOX\_1; 1.  
 DR PROSITE; PS50066; MADS\_BOX\_2; 1.  
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein;  
 KW Developmental protein.  
 FT DOMAIN 3 57 MADS-box.  
 FT DOMAIN 93 165 K-BOX.  
 SQ SEQUENCE 227 AA; 26279 MW; 95B3FF60924FDEB0 CRC64;  
 Query Match 31.6%; Score 349; DB 1; Length 227;  
 Best Local Similarity 39.3%; Pred. No. 1.6e-15;  
 Matches 68; Conservative 42; Mismatches 59; Indels 4; Gaps 1;  
 QY 1 MGRKVEIKRIENSSNRQVYTSKRNGIIRKAEITVLCDAKVSLLIYSSSGKVCYCSF 60  
 DB 1 MARGKIQIKRIENQTRQVYTSKRNGIFKKAHEITVLCDAKVSIIIMFSSNKLHEIYISF 60  
 QY 61 STLTLELDKYGSGGKKLMDAKHENTLSNEVDYVKKDNDSMQVLEHLKGEDITSLNHVE 120  
 DB 61 TTATKQLVDYQKXAVGVDMLSHVEKQEHKLNENVRNLRRIQRMGESLNDLGYEQ 120  
 QY 121 LMALEBALENGLTSTIRKOSKSFVDMMDNGKALEDENKELTYELOKQOEKIKENV 169  
 DB 121 IVNLEIDMNSLKLIIRKRVKVISNQIDTSKKXVRNVEIHRNLVLEFARRE 173  
 RESULT 13  
 TT16 ARATH STANDARD; PRT; 252 AA.  
 AC Q8R1D9; Q8R1D9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE TRANSPARENT TESTA 16 protein (Arabidopsis BSISTER MADS box protein).  
 GN TT16 OR ABS OR AT5G23260 OR MCD15.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=cv. Columbia; TISSUE=Green siliques;  
 RC MEDLINE=21851234; PubMed=11862488;  
 RX

RA Becker A., Kaufmann K., Fretaldenhoven A., Vincent C., Li M.-A.,  
 RA Saedler H., Theissen G.,  
 RT "A novel MADS-box gene subfamily with sistergroup relationship to  
 RT class B floral homeotic genes.",  
 RL Mol. Genet. Genomics 266:942-950 (2002).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98162728; PubMed=9501997;  
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,  
 RA Tabata S.,  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.  
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen  
 RT physically assigned P1 clones.",  
 RL DNA Res. 4:401-414 (1997).  
 RN [3].  
 RP CHARACTERIZATION, AND ALTERNATIVE SPLICING.  
 RX MEDLINE=2256155; PubMed=12368498;  
 RA Nest N., Debeaujon I., Jond C., Stewart A.J., Jenkins G.I.,  
 RA Caboche M., Lepoint L.,  
 RT "The TRANSPARENT TESTA16 locus encodes the ARABIDOPSIS BISTER MADS  
 RT domain protein and is required for proper development and  
 RT pigmentation of the seed coat.",  
 RL Plant Cell 14:2463-2479 (2002).  
 CC -1- FUNCTION: Transcription factor involved in the developmental  
 CC regulation of the endothelium and in the accumulation of  
 CC proanthocyanidins (PAs) or condensed tannins which give the seed  
 CC its brown pigmentation after oxidation. Necessary for the normal  
 CC activation of the BANYUS promoter in the endothelium body.  
 CC -1- PATHWAY: Flavonoid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q8RYD9-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q8RYD9-2; Sequence=VSP\_006257;  
 CC -1- TISSUE SPECIFICITY: Expressed in buds, flowers and immature seeds,  
 CC but not in roots, stems, leaves, seedlings or siliques valves.  
 CC Expression in seed coat is confined to the endothelium layer.  
 CC DEVELOPMENTAL STAGE: Expressed during seed development.  
 CC -1- MISCELLANEOUS: The two isoforms were always coexpressed in the  
 CC tissues investigated. The pigmentation of the chalazal-micropyle  
 CC region is not under the control of ABS, as opposed to the  
 CC pigmentation of the seed body.  
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
 CC -1- SIMILARITY: Contains 1 MADS-box domain.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -----  
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 CC -----  
 CC EMBL: AJ318098; CAC85664.1; -  
 CC EMBL: AB007648; BAB1181.1; ALT\_SEQ.  
 CC InterPro: IPR002487; TF\_Kbox.  
 CC InterPro: IPR002100; TF\_MADSbox.  
 CC Pfam: PF01486; K-box\_1.  
 CC Pfam: PF0319; SR-TF\_1.  
 CC PRINTS: PR00404; MADSDOMAIN.  
 CC SMART: SM00432; MADS\_1.  
 CC PROSITE: PS00350; MADS\_BOX\_1; 1.  
 CC PROSITE: PS00066; MADS\_BOX\_2; 1.  
 CC Flavonoid biosynthesis; Transcription; Transcription regulation;  
 CC DNA-binding; Alternative splicing; Nuclear protein; Coiled coil.  
 FT DOMAIN 1 61  
 FT DOMAIN 73 172  
 FT DOMAIN 121 174 COILED COIL (POTENTIAL).

FT DOMAIN 180 222 GIN-RICH.  
 FT VARSPLIC 142 146 Missing (in isoform 2).  
 FT FTID=VSP\_006257.  
 SQ SEQUENCE 252 AA; 29697 MW; 2C4CB9D9C1DEA8 CRC64;  
 Query Match 31.0%; Score 342; DB 1; Length 252;  
 Best local Similarity 32.0%; Pred. No. 5; le-15;  
 Matches 78; Conservative 62; Mismatches 72; Indels 32; Gaps 7;  
 QY 1 MGRGKVEIKRIENSNRQVYTSKRNGIITKKAKETVLCDAVSLITSSGKMEYCSF 60  
 DB 1 MGRGKVEIKRIENSNRQVYTSKRNGIITKKAKETVLCDAVSLITSSGKMEYCSF 60  
 QY 61 STLTLEILPKYGGQSGKLMW--AKHENSNEVDYKQNDNOVELRLTKGEDITSLNH 118  
 DB 61 QNRKPOLIDRYLHTNGLRPDHDHDEQLHHEMLLRCTCLRLRFRGHDLASIFP 120  
 QY 119 VELMALEALENGSLTIRDSKQFVMDN---GKALEDNKLLTYELQOQ-EMKIK 173  
 DB 121 NEIDGLEQLQELSHVLKYRKRKHELMQOOLENLSRKRMLEEDNNMYRWLHEHRAAMEFO 180  
 QY 174 ENVRNMENGVHOR---CL-----GNYN---NNQOQIPFA-----FVVOPIQ 208  
 DB 181 QAGIDTPGPGHYOQFTLQCCYRGGYQGLFEGQQQCPNSVLQALPLPSRIDPTYNLQLAQ 240  
 QY 209 PNLQ 212  
 DB 241 PNLQ 244  
 RESULT 14  
 SEPI\_ARATH STANDARD; PRT; 251 AA.  
 ID SEPI\_ARATH O8GWQ4; O8LPR5;  
 AC 022456; O8GWQ4; O8LPR5;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DS Developmental protein SEPIALAT3 (Agamous-like MADS box protein AGL3).  
 GN SEPI OR AGL3 OR AT1G24260 OR F316.19.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN=cv. Landsberg erecta;  
 RA Mandel M.A., Yanofsky M.F.;  
 RT "The Arabidopsis AGL3 MADS box gene is expressed in young flower  
 RT primordia".  
 RL Sex. Plant Reprod. 11:22-28 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=1130712;  
 RA Theologis A., Ecker J.R., Palm C.J.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,  
 RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gall J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenskaia I., Kutz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Maritali A.,  
 RA Miltiescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utterback T., Van Aken S., Vayberg M., Vysotskaja V.S., Walker M.,  
 RA Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.,  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana.";

RL Nature 408:816-820(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,  
RA Feldmann K.A.,  
RT "Full-length cDNA from Arabidopsis thaliana,"  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 114-251 FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=22954850; PubMed=14593172;  
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
RA Arakawa T., Banch J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
RA Chao Q., Choy N., Ebnji A., Goldsmith A.D., Gurfil M., Hansen N.F.,  
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
RA Khan S., Kossema E., Ishida Y., Jiang P.X., Jones T., Kawai J.,  
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinozaki K., Davis R.M., Thollogis A., Ecker J.R.,  
RT "Empirical analysis of transcriptional activity in the Arabidopsis  
genome,"  
RL Science 302:842-846(2003).  
RN [5]  
RP CHARACTERIZATION.  
RX MEDLINE=98079237; PubMed=9418042;  
RA Fan H.-Y., Hu Y., Tudor M., Ma H.,  
RT "Specific interactions between the K domains of AG and AGHs, members  
of the MADS domain family of DNA binding proteins,"  
RL Plant J. 12:999-1010(1997).  
RN [6]  
RP CHARACTERIZATION.  
RX MEDLINE=20279298; PubMed=10821278;  
RA Pelaz S., Ditta G.S., Baumann E., Wisman E., Yanofsky M.F.,  
RT "B and C floral organ identity functions require SEPALLATA MADS-box  
genes,"  
RL Nature 405:200-203(2000).  
RN [7]  
RP CHARACTERIZATION.  
RX MEDLINE=21074934; PubMed=11206550;  
RA Honma T., Goto K.,  
RT "Complexes of MADS-box proteins are sufficient to convert leaves into  
floral organs,"  
RL Nature 409:525-529(2001).  
RN [8]  
RP FUNCTION: Probable transcription factor active in inflorescence  
development and floral organogenesis. Functions with  
SEPALLATA1/AGL2 and SEPALLATA2/AGL4 to ensure proper development  
of petals, stamens and carpels and to prevent the indeterminate  
growth of the flower meristem. Interacts with APERATA1, AGAMOUS or  
APERTAL3/PISTILLATA to form complexes, that could be involved in  
genes regulation during floral meristem development.  
RN [9]  
RP SUBUNIT: Heterodimer with API or AG capable of binding to CARG-box  
sequences. Binds AP3/PI to form a ternary complex.  
RN [10]  
RP SUBCELLULAR LOCATION: Nuclear (By similarity).  
RN [11]  
RP ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=O22456-1; Sequence=displayed;  
CC Name=2;  
CC IsoId=O22456-2; Sequence=VSP\_008893;  
CC Note=May be due to a competing acceptor splice site. No  
CC experimental confirmation available;  
CC DEVELOPMENTAL STAGE: Expressed early during flower development  
CC within petals, stamens, and carpels.  
CC MISCELLANEOUS: Triple mutations in the SEPI, SEP2 and SEP3 genes  
CC result in the replacement of the stamens and petals by sepals and  
CC of the carpels by a new mutant flower with sepaloid organs.  
CC -1- SIMILARITY: Contains 1 K-box dimerization domain.  
CC -1- SIMILARITY: Contains 1 MADS-box domain.

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CC -----  
CC EMBL; AF015552; AAB67832.1; -  
CC EMBL; AC002396; AAC00586.1; -  
CC EMBL; AY088272; AAM65812.1; -  
CC EMBL; AK118696; BAC43290.1; ALT\_INIT.  
CC PIR; T00656; T00656.  
CC HSSP; P11746; IMMW.  
CC TRANSFAC; T03032; -  
CC InterPro; IPR002487; TP\_KDOX.  
CC InterPro; IPR002100; TF\_MADSbox.  
CC Pfam; PF01486; K-box; 1.  
CC Pfam; PF00319; SRP-TRF; 1.  
CC PRINTS; PR00404; MADSDOMAIN.  
CC SMART; SM00432; MADS; 1.  
CC PROSITE; PS00350; MADS\_BOX\_1; 1.  
CC PROSITE; PS50066; MADS\_BOX\_2; 1.  
CC FLOWERING: Transcription regulation; Activator; Developmental protein;  
CC Nuclear protein; DNA-binding; Coiled coil; Alternative splicing.  
CC DOMAIN 3 57 MADS-box.  
CC FT DOMAIN 100 172 K-BOX.  
CC FT DOMAIN 94 177 COILED COIL (POTENTIAL).  
CC FT VARSPLC 90 Missing (in isoform 2).  
CC FT FTD VSP\_008893.  
CC SQ SEQUENCE 251 AA; 29066 MW; 0057CABD3F1AFC4 CRC64;  
Query Match 30.4%; Score 335; DB 1; Length 251;  
Best Local Similarity 37.4%; Pred. No. 1,4e-14;  
Matches 86; Conservative 49; Mismatches 67; Indels 28; Gaps 8;  
QY 1 MGRGVEIKRIENSNQVYTSKRRNGIKKAEITVLCDAKVALIIYSSGKXVEYCSF 60  
DB 1 MGRGVEIKRIENSNQVYTSKRRNGIKKAEITVLCDAKVALIIYSSGKXVEYCSF 60  
QY 61 STLTETIDKTHGSGGKKLMDAKHENT-----SNEVDVKKDNDSDQVEIRHL 108  
DB 60 SSSMIRTLERYO---KKNYGAPEPNVPSREALAVELSSQGEYDKLXERYPDALORTORNL 115  
QY 109 KGEIDTSLNHVELMALEPALENGLTSLRDKOSKF-VDMNRD---NGALEDEKRLTYEL 164  
DB 116 LGEIDGPISTELSLERQDLSLKQIRALRTQVMDQNDLQSKERMLTETKTLRL 175  
QY 165 QKQEMKIKENYNNMENGTHQROLGNTNNNOQIIPFAFVQPI--QPNLQ 212  
DB 176 ADGQMPQLNPNQOEVDVY---GRHHHQOQCSQAF-FQPLCEPILQ 220  
RESULT 15  
JOIN\_LYCES  
ID JOIN\_LYCES STANDARD; PRT; 265 AA.  
AC Q9FYU6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE MADS-box JOINTLESS protein (LEMADS).  
GN J.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RP STRAIN=cv. Heinz 1706;  
RX MEDLINE=20426111; PubMed=10972295;  
RA Mao L., Begum D., Chuang H.W., Sudman M.A., Szymkowiak E.J.,  
RA Irish E.E., Wing R.A.,







QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215  
 DB 178 NGFDQ-SVRDYNH--MPFAFRVQPMQPNLOERI 208

## RESULT 2

US-10-425-114-40799  
 ; Sequence 40799, Application US/10425114  
 ; Publication No. US20040034889A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(51313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 40799  
 ; LENGTH: 209  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: L1B3030-006-D8\_FLI.pep  
 US-10-425-114-40799

Query Match 64.8%; Score 714.5; DB 12; Length 209;  
 Best Local Similarity 64.7%; Pred. No. 1.4e-54;  
 Matches 139; Conservative 38; Mismatches 31; Indels 7; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIITVLCDAKVSLLIYSSSGKWEYCSP 60  
 DB 2 MGRGKIEIKRIENSSNRQVTSKRNGIITVLCDAKVSLLIYSSSGKWEYCSP 61  
 QY 61 STTLEILDKYHGGSGKGLMDAKHENTLSNEVDVKKDMSQVLEIRHLKGEDITSLNHVE 120  
 DB 62 STTLEILDKYHGGSGKGLMDAKHENTLSNEVDVKKDMSQVLEIRHLKGEDITSLNHVE 121  
 QY 121 LMALEBALENGITSTIRKOSKRVDMWRDNGKALEDENKRLTYELQKQEMKIKENYRME 180  
 DB 122 LMALEBALENGITSTIRKOSKRVDMWRDNGKALEDENKRLTYELQKQEMKIKENYRME 181  
 QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215  
 DB 179 NGFDQ-SVRDYNH--MPFAFRVQPMQPNLOERI 208

## RESULT 3

US-10-412-699B-56  
 ; Sequence 56, Application US/10412699B  
 ; Publication No. US20040045049A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mendel Biotechnology, Inc.  
 ; APPLICANT: Zhang, James  
 ; APPLICANT: Fromm, Michael E.  
 ; APPLICANT: Heard, Jacqueline E.  
 ; APPLICANT: Riechmann, Jose Luis  
 ; APPLICANT: Adam, Luc J.  
 ; APPLICANT: Brown, Pierre E.  
 ; APPLICANT: Pineta, Omaira  
 ; APPLICANT: Reuber, T. Lynne  
 ; APPLICANT: Keddie, James S.  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Jiang, Cai-Zhong  
 ; APPLICANT: Samaha, Raymond R.  
 ; APPLICANT: Pilgrim, Marsha L.  
 ; APPLICANT: Creelman, Robert A.  
 ; APPLICANT: Dubell, Arnold N.

APPLICANT: Ratcliffe, Oliver  
 APPLICANT: Kumimoto, Rogerick  
 APPLICANT: Sherman, Bradley K.  
 TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
 FILE REFERENCE: MBI-0048CIP  
 CURRENT APPLICATION NUMBER: US/10/412,699B  
 CURRENT FILING DATE: 2003-04-10  
 PRIOR APPLICATION NUMBER: 09/394,519  
 PRIOR FILING DATE: 1999-09-13  
 PRIOR APPLICATION NUMBER: 09/489,376  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: 09/506,720  
 PRIOR FILING DATE: 2000-02-17  
 PRIOR APPLICATION NUMBER: 09/533,030  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,392  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,029  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/532,591  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/533,648  
 PRIOR FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: 09/713,994  
 PRIOR FILING DATE: 2000-11-16  
 PRIOR APPLICATION NUMBER: 09/819,142  
 PRIOR FILING DATE: 2001-03-27  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 2011  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 56  
 LENGTH: 208  
 TYPE: PRT  
 ORGANISM: Arabidopsis thaliana  
 FEATURE:  
 OTHER INFORMATION: G134  
 US-10-412-699B-56

Query Match 59.9%; Score 660.5; DB 12; Length 208;  
 Best Local Similarity 60.5%; Pred. No. 7.4e-50;  
 Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIITVLCDAKVSLLIYSSSGKWEYCSP 60  
 DB 1 MGRGKIEIKRIENSSNRQVTSKRNGIITVLCDAKVSLLIYSSSGKWEYCSP 60  
 QY 61 STTLEILDKYHGGSGKGLMDAKHENTLSNEVDVKKDMSQVLEIRHLKGEDITSLNHVE 120  
 DB 61 SMDLGMDQYQKLSGKGLMDAKHENTLSNEVDVKKDMSQVLEIRHLKGEDITSLNHVE 120  
 QY 121 LMALEBALENGITSTIRKOSKRVDMWRDNGKALEDENKRLTYELQKQEMKIKENYRME 180  
 DB 122 LMALEBALENGITSTIRKOSKRVDMWRDNGKALEDENKRLTYELQKQEMKIKENYRME 179  
 QY 181 NGYHQRGLGNVNNNOQOIPFAFRVQPIQPNLOERI 215  
 DB 180 MEDHDQ-----FGYRVQPIQPNLOERI 202

## RESULT 4

US-10-424-599-175060  
 ; Sequence 175060, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(51323)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 175060  
LENGTH: 207  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1) (207)  
OTHER INFORMATION: unsure at all Xaa locations  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129098C.1.pcp  
US-10-424-599-175060

Query Match 59.7%; Score 659; DB 12; Length 207;  
Best Local Similarity 62.0%; Pred. No. 1e-49;  
Matches 134; Conservative 35; Mismatches 37; Indels 10; Gaps 4;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 60  
DB 1 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 60  
QY 61 STTLEILDYKYGSGKGLMDAKHENTLSNEVDVKKNDSDMOVELRHUKGEDITSINAVE 120  
DB 61 STTLEILDYKYGSGKGLMDAKHENTLSNEVDVKKNDSDMOVELRHUKGEDITSINAVE 120  
QY 121 LMALEBALENGSLIRDKOSKRFVDMRDGKALEDEENKRLITVELQKQEMKIKENVRN-M 179  
DB 121 LMALEBALENGSLIRDKOSKRFVDMRDGKALEDEENKRLITVELQKQEMKIKENVRN-M 179  
QY 180 ENGKHOROLGNYNNOQOIFPAFRVQPIQPNLQEBRI 215  
DB 178 DNGFVN--EIKRVFNHMQRAASLK---QPNLKERI 207

RESULT 5  
US-10-425-114-66169  
Sequence 66169, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 66169  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB4606-002-H7\_FLI.pcp  
US-10-425-114-66169

Query Match 58.3%; Score 642.5; DB 12; Length 228;  
Best Local Similarity 58.2%; Pred. No. 3.2e-48;  
Matches 144; Conservative 40; Mismatches 46; Indels 3; Gaps 2;  
QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 60  
DB 17 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 76  
QY 61 STTLEILDYKYGSGKGLMDAKHENTLSNEVDVKKNDSDMOVELRHUKGEDITSINAVE 120  
DB 77 RUSLSILIRKIQNSKILMGEKRLSLAIDRVKKNENNMQIQRHLGSEDLNLPRE 136  
QY 121 LMALEBALENGSLIRDKOSKRFVDMRDGKALEDEENKRLITVELQKQEMKIKENVRN-M 180

DB 137 LIALEBLONGQINMEKQMDYWRMKTNGKMLEDEHKILITFRMH-QQAVDSGKRELE 195  
QY 181 NGYHOROGLGNYNNOQOIFPAFRVQPIQPNLQEBRI 213  
DB 196 TGYHQVQ--HBRDFISQMPFTFRVQPNHPRLOE 226

RESULT 6  
US-10-425-114-39944  
Sequence 39944, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 39944  
LENGTH: 205  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: 700903463\_FLI.pcp  
US-10-425-114-39944

Query Match 57.2%; Score 630.5; DB 12; Length 205;  
Best Local Similarity 68.7%; Pred. No. 3.1e-47;  
Matches 123; Conservative 26; Mismatches 27; Indels 3; Gaps 1;

QY 1 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 60  
DB 25 MGRGKVEIKRIENSSNRQVYTSKRNGIIRKAKETIVLCDAYSLIIYSSGKWEYCSP 84  
QY 61 STTLEILDYKYGSGKGLMDAKHENTLSNEVDVKKNDSDMOVELRHUKGEDITSINAVE 120  
DB 85 STTLEILDYKYGSGKGLMDAKHENTLSNEVDVKKNDSDMOVELRHUKGEDITSINAVE 144  
QY 121 LMALEBALENGSLIRDKOSKRFVDMRDGKALEDEENKRLITVELQKQEMKIKENVRN-M 179  
DB 145 LMALEBALENGSLIRDKOSKRFVDMRDGKALEDEENKRLITVELQKQEMKIKENVRN-M 200

RESULT 7  
US-10-425-114-39581  
Sequence 39581, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 39581  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: 700382572\_FLI.pcp  
US-10-425-114-39581

Query Match 51.0%; Score 563; DB 12; Length 190;  
Best Local Similarity 61.7%; Pred. No. 2.3e-41;  
Matches 103; Conservative 35; Mismatches 29; Indels 0; Gaps 0;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCAKAVSLIIYSSSGKWEYCSP 60  
DB 17 MGRGKIKIKRIENSTNRQVTSKRAGLVKAREIGVLCDAVGVVIFSSGSKLYDCSP 76

QY 61 STTLEILDKYHGQSGKULMDAKHENSNEVDYKKNDSQVLELRLKGEDITSLNHVE 120  
DB 77 RLSLRIILEKYQTSNGKILWGEKKNLSAEIDRYKKNENNOIQLRLHKGEDLSLQHRE 136

QY 121 LMALEALENGLTISRDKOSKFVDMWRDNGKALDENRRLTYELOKQ 167  
DB 137 LIAIEEGQNGQTNREKQMDYMRHKNKNGMLDEDEHKLILFRHHQO 183

RESULT 8  
US-10-425-114-40296  
; Sequence 40296, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5321)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 40296  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701160751\_FLI.pep  
US-10-425-114-40296

Query Match 50.9%; Score 561; DB 12; Length 190;  
Best Local Similarity 61.1%; Pred. No. 3.5e-41;  
Matches 102; Conservative 35; Mismatches 30; Indels 0; Gaps 0;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCAKAVSLIIYSSSGKWEYCSP 60  
DB 17 MGRGKIKIKRIENSTNRQVTSKRRTGLVKAREIGVLCDEVGVIFFSSGSKLYDCSP 76

QY 61 STTLEILDKYHGQSGKULMDAKHENSNEVDYKKNDSQVLELRLKGEDITSLNHVE 120  
DB 77 RLSLRIILEKYQTSNGKILWGEKKNLSAEIDRYKKNENNOIQLRLHKGEDLSLQHRE 136

QY 121 LMALEALENGLTISRDKOSKFVDMWRDNGKALDENRRLTYELOKQ 167  
DB 137 LIAIEEGQNGQTNREKQMDYMRHKNKNGMLDEDEHKLILFRHHQO 183

RESULT 9  
US-10-424-599-263636  
; Sequence 263636, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 263636  
; LENGTH: 227  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_80083C.1.pep  
US-10-424-599-263636

Query Match 34.5%; Score 380; DB 12; Length 227;  
Best Local Similarity 37.0%; Pred. No. 3.2e-25;  
Matches 80; Conservative 50; Mismatches 78; Indels 8; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCAKAVSLIIYSSSGKWEYCSP 60  
DB 1 MGRGKIKRIENSTNRQVTSKRNGIFKANEITVLCDAKVSITMSTCKLHEIYISP 60

QY 61 STTLEILDKYHGQSGKULMDAKHENSNEVDYKKNDSQVLELRLKGEDITSLNHVE 120  
DB 61 STSKQFPQYQMTLGVLDLMSHYENMOENLKKLVAVRNLRLKEIRQEWGCDLNDLGMED 120

QY 121 LMALEALENGLTISRDKOSKFVDMWRDNGKALDENRRLTYELOKQEMKIKENY 176  
DB 121 LKLEBEMDKAAKVVRERKXVITVNOIDQKXKFNEXAVNRLHLDLDAKAE--DPRF 177

QY 177 RMNENGYHORQLGNVNNNOQIIPFAFRVQPIQPNLQ 212  
DB 178 ALINDGEYEVSVIGFSNLGPRM-FALSLQPSHPSAQ 212

RESULT 10  
US-10-437-963-113197  
; Sequence 113197, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbasuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 113197  
; LENGTH: 260  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_17007C.1.pep  
US-10-437-963-113197

Query Match 33.3%; Score 367.5; DB 16; Length 260;  
Best Local Similarity 31.4%; Pred. No. 4.8e-24;  
Matches 80; Conservative 49; Mismatches 69; Indels 57; Gaps 5;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCAKAVSLIIYSSSGKWEYCSP 60  
DB 1 MGRGKIKRIENSTNRQVTSKRNGILKKANLAVLCAKAVGVVIFSSGKWEYCSP 60

QY 61 STTLEILDKYHGQSGKULMDAKHENSNEVDYKKNDSQVLELRLKGEDITSLNHVE 119  
DB 61 TCSLLEILHRYQVNTNTHFEELNHQOIFVETWTRVNRNMEKLDGIRFRTDDBDLSNLTLA 120

QY 120 EMLALEALENGLTISRDKOSKFVDMWRDNGK--ALEDENRRLTYELOKQEWKIKEN 175  
DB 121 DINDLEQQLSFVTVRARKQLNLNOQLDNLARKHILDEQNSFL----- 165

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QY 176 VNNMNGYHQRQLGN-----YNNNQOQ:PF----- 200
DB 166 CEMINENHQAAGVGGDVXAVWEMAPVLSMLTAPAYGEBSSSTALQUTPLHVAADAA 225
QY 201 --AFRVQPIQPNLQ 213
DB 226 AAGFRLQPTQPNLQD 240

RESULT 11
US-10-424-599-263637
; Sequence 263637, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 265684
; SEQ ID NO 263637
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pep
US-10-424-599-263637

Query Match 33.0%; Score 364.5; DB 12; Length 234;
Best Local Similarity 33.9%; Pred. No. 7.7e-24;
Matches 78; Conservative 51; Mismatches 72; Indels 29; Gaps 4;

QY 1 MARGKEIKRIENSNROVYTSKRNGIIRKAKEITVLCDAKVSLLIYSSGKXVEYCSPTTL 60
DB 1 MARGKIQIKRIENTNRQVTSKRNGLFKCANELTVLCDAKVSLLIYSSGKXHEIYSP 60
QY 61 STTLTEILDYKHGSGSKLMDAKHENLSEVDYKXNDQSMQVELRHLKGEDITSLNHYE 120
DB 61 STSKQFPOQYQMTLGVLDLMSHYEMQENLKKLKDVRNRLRKEIRQKRGDCIANDLGMD 120
QY 121 LMALEALENGSLTRDKSKFVDMKRDNGKALDEENKRLTYELQKQ-QEMKIKENYAN- 178
DB 121 LKLEBEMDKAAKVVAERSC-----MTWRKQKQVTHRIYVTRKKFNNEKEVHNR 170
QY 179 -----MNGYHQRQLGNYNNNQOQIPFAFRVQPIQPNLQ 212
DB 171 LURDLARADPRFALIDNGEYESVIGPSNLGPRM-FALSLQPSHPSAQ 219

RESULT 12
US-10-767-701-39443
; Sequence 39443, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39443
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
```

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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1852_1.pep
US-10-767-701-39443

Query Match 32.6%; Score 360; DB 16; Length 149;
Best Local Similarity 49.0%; Pred. No. 1e-23;
Matches 73; Conservative 29; Mismatches 39; Indels 8; Gaps 3;

QY 66 EILDYKHGSGSKLMDAKHENLSEVDYKXNDQSMQVELRHLKGEDITSLNHYEMLALE 125
DB 6 KLEKYQTSNGSKILMBEKKSLSAIDRIKENDTQIEIRHLKGEDLNSLQCPDLTIMIE 65
QY 126 EALENGLSTRDKSKFVDMKRDNGKALDEENKRLTYELQKQEMKIKENYANMNGYH- 184
DB 66 EALDNGLTNQNEKLMDEKERRVANNKXMEDEKTLAFKJH-QQDIALSGSMRELEJGTHP 124
QY 185 QROLGNNNNQOQIPFAFRVQPIQPNLQ 213
DB 125 DRDLA-----AQMPITFRVQPSHPNLQD 147

RESULT 13
US-10-425-114-42492
; Sequence 42492, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K.
; APPLICANT: Screen Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42492
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700958586_FLI.pep
US-10-425-114-42492

Query Match 32.6%; Score 360; DB 12; Length 223;
Best Local Similarity 36.3%; Pred. No. 1.8e-23;
Matches 77; Conservative 49; Mismatches 78; Indels 8; Gaps 3;

QY 5 KVEIKRIENSNROVYTSKRNGIIRKAKEITVLCDAKVSLLIYSSGKXVEYCSPTTL 64
DB 1 KIQIKRIENTNRQVTSKRNGLFKCANELTVLCDAKVSLLIYSSGKXHEIYSPST 60
QY 65 TELDKYKHGSGSKLMDAKHENLSEVDYKXNDQSMQVELRHLKGEDITSLNHYEMLAL 124
DB 61 KQFPOQYQMTLGVLDLMSHYEMQENLKKLKDVRNRLRKEIRQKRGDCIANDLGMDIKL 120
QY 125 EALENGLSTRDKSKF-----VDMKRDNGKALDEENKRLTYELQKQEMKIKENYANME 180
DB 121 EEMDKAAKVVAERKQVITINQIDTQKCKKFNNEKEVANNRLRLDLDAAE--DPRFALID 177
QY 181 NGYHQRQLGNYNNNQOQIPFAFRVQPIQPNLQ 212
DB 178 NGEYESVIGPSNLGPRM-FALSLQPSHPSAQ 208

RESULT 14
US-10-104-580-4
; Sequence 4, Application US/10104580
; Publication No. US2003003628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
```

; ORGANISM: *Oryza sativa*  
US-10-259-165-46

```

Search completed: September 21, 2004, 09:44:49
Job time : 85.2103 secs

```

```
Search completed: September 27, 2004, 09:44:45
Job time : 85.2103 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 09:19:49 / Search time 24.0492 Seconds  
(without alignments)  
859,952 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGVEIKRIENSSNRQVT.....QQIPFAFVQPIQPLQERI 215

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR 78:\*\*\*  
2: PIR:\*\*\*  
3: PIR:\*\*\*  
4: PIR:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740.5	67.1	212	2 S31707	floral homeotic pr
2	739.5	67.0	212	2 S60288	FBP3 protein gar
3	713	64.6	215	2 S28062	homeotic protein g
4	707	64.1	209	2 S35226	homeotic protein g
5	684.5	62.1	210	2 JQ1689	floral binding pro
6	660.5	59.9	208	2 A53839	B function floral
7	620.5	56.3	210	2 T03902	MADS4 box protein
8	617	55.9	209	2 T03894	MADS box protein
9	411	37.3	222	2 S23731	MADS box protein T
10	377.5	34.5	229	2 T09335	MADS-box protein N
11	377.5	34.2	231	2 S31693	MADS box protein g
12	367.5	33.3	224	2 T14474	MADS box protein 2
13	360	32.6	228	2 T07066	MADS-box protein h
14	359	32.5	228	2 T07410	MADS box protein h
15	356.5	32.3	232	2 A42095	floral homeotic pr
16	349	31.6	227	2 S12378	MADS box protein d
17	346	31.4	273	2 T03470	MADS box protein -
18	343.5	31.1	224	2 T14474	MADS box protein a
19	335	30.4	251	2 T00656	MADS box protein A
20	334.5	30.3	243	2 S71756	MADS box protein D
21	334	30.3	248	2 B39534	MADS box protein A
22	332	30.1	214	2 T10715	MADS-box protein C
23	332	30.1	247	2 T06843	MADS-box protein -
24	331	30.0	261	2 T09603	MADS-box protein 3
25	330	29.9	242	2 S71208	MADS box protein A
26	329	29.8	242	2 T10467	MADS box protein D
27	327.5	29.7	245	2 T09569	MADS box protein M
28	327.5	29.7	252	2 T51409	MADS box protein A
29	326.5	29.6	258	2 S57393	MADS box protein A

30	326	29.6	261	2 S51935	probable MADS-box
31	325	29.5	228	2 T14737	MADS box protein -
32	324	29.4	242	2 T10486	MADS box protein M
33	324	29.4	242	2 T09571	MADS box protein l
34	323.5	29.3	220	2 T51827	MADS-box protein l
35	323.5	29.3	220	2 T05580	MADS-box protein A
36	323.5	29.3	250	2 T07100	MADS box protein h
37	321.5	29.1	246	2 T17023	MADS box protein 1
38	320.5	29.1	248	2 A39534	floral homeotic pr
39	319.5	29.0	246	2 E39534	floral homeotic pr
40	319.5	29.0	258	2 G84858	floral homeodomain
41	319	28.9	284	2 T05033	floral homeotic pr
42	319	28.9	284	2 A85214	floral homeotic pr
43	318.5	28.9	247	2 S78015	MADS box protein D
44	318	28.8	253	2 S7386	MADS box protein A
45	318	28.8	254	2 S52236	MADS box protein a

## ALIGNMENTS

RESULT 1  
S31707  
floral homeotic protein pmas2 - garden petunia  
N/Alternate names: MADS box-containing protein; transcription factor pmas2  
C/Species: Petunia x hybrida (garden petunia)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 03-Dec-1999  
C/Accession: S31707  
R/Kush, A.; Brunelle, A.; Shevell, D.; Chua, N.H.  
submitted to the EMBL Data Library, November 1992  
A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box  
A/Reference number: S31693  
A/Accession: S31707  
A/Molecule type: mRNA  
A/Residues: 1-212 (KUS)  
A/Cross-references: EMBL X69947, NID:G22666, PID:G22667  
C/Species: Petunia x hybrida (garden petunia)  
C/Suprafamily: transcription factor squa; serum response factor DNA-binding domain homo;  
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 67.1%; Score 740.5; DB 2; Length 212;  
Best Local Similarity 67.4%; Pred. No. 8.3e-41;  
Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGRGVEIKRIENSSNRQVTYSKRNGLIKKAKETIVCDKAVSLIYSSGKWEYCSP 60  
DB 1 MGRGVEIKRIENSSNRQVTYSKRNGLIKKAKETIVCDKAVSLIYSSGKWEYCSP 60  
QY 61 STTLEIIDKTHGSGGKCLMDAKHENSNEVDYVKNDMSQVBLRHKGEDITSINAVE 120  
DB 61 STTLEIIDKTHGSGGKCLMDAKHENSNEVDYVKNDMSQVBLRHKGEDITSINAVE 120  
QY 121 LMALFEALENGTLSTIRDSKSKFVDMWRDNGKALJEDENRILTYELOQOEMIKENVRNME 180  
DB 121 LMALFEALENGTLSTIRDSKSKFVDMWRDNGKALJEDENRILTYELOQOEMIKENVRNME 180  
QY 181 NGYHQRQICANNNOQIIPFAFVQPIQPLQERI 215  
DB 181 NGYHQRQICANNNOQIIPFAFVQPIQPLQERI 215  
QY 181 EYVHOR---DRDYEQWPFALRVQPMQPNLHERM 212  
DB 181 EYVHOR---DRDYEQWPFALRVQPMQPNLHERM 212

## RESULT 2

S60288  
FBP3 protein - garden petunia  
C/Species: Petunia x hybrida (garden petunia)  
C/Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jul-2000  
C/Accession: S60288  
R/Range: G.C.; Franken, J.; Busscher, M.; Weiss, D.; van Tunen, A.J.  
Plant J. 5, 33-44, 1994  
A/Title: Co-suppression of the petunia homeotic gene fbp3 affects the identity of the g  
A/Reference number: S60288; MUID:94177174; PMID:7907515  
A/Accession: S60288  
A/Status: preliminary



A:Molecule type: mRNA  
 A:Residues: 1-212 <ANG>  
 A:Cross-references: EMBL:X71417; NID:9454264; PIDN:CAA50549.1; PID:9454265  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 67.0%; Score 739.5; DB 2; Length 212;  
 Best Local Similarity 67.4%; Pred. No. 9.6e-41;  
 Matches 145; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 DB 1 MGRGKEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 QY 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 DB 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 QY 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 DB 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPICPNIQER 215  
 DB 181 EVYHQR---DRDYEQMPFALRVQPMQENLHERM 212

## RESULT 3

S28062  
 homeotic protein globosa - garden snapdragon  
 C:Species: Antirrhinum majus (garden snapdragon)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jul-2000  
 C:Accession: S28062  
 R:Prodbner, W.; Ramirez, L.; Morte, P.; Hue, I.; Hultjser, P.; Loemig, W.F.; Saedler, H.  
 EXMO J. 11, 4693-4704, 1992  
 A:Title: GLOBOSA: a homeotic gene which interacts with DEFICIENS in the control of Antirrhinum majus flower development  
 A:Reference number: S28062; MUID:9309942; PMID:1361166  
 A:Accession: S28062  
 A:Molecule type: DNA  
 A:Residues: 1-215 <TRO>  
 A:Cross-references: EMBL:X68831; NID:g16023; PIDN:CAA48725.1; PID:g16024  
 C:Genetics:  
 A:Gene: glo  
 A:Introns: 63/2; 85/3; 106/2; 139/3; 149/3; 164/3  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 C:Keywords: DNA binding; nucleus; transcription regulation  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 64.6%; Score 713; DB 2; Length 215;  
 Best Local Similarity 63.1%; Pred. No. 4.9e-39;  
 Matches 135; Conservative 40; Mismatches 39; Indels 0; Gaps 0;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 DB 1 MGRGKEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 QY 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 DB 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 QY 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 DB 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPICPNIQER 214  
 DB 181 AVYDHHHONTADYEAGPFAFRVOPICPNIQER 214

## RESULT 4

S35226  
 homeotic protein globosa homolog - common tobacco  
 C:Species: Nicotiana tabacum (common tobacco)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 21-Jul-2000  
 C:Accession: S35226; S31360  
 R:Hasen, G.; Estruch, J.J.; Sommer, H.; Spena, A.  
 Mol. Gen. Genet. 239, 310-312, 1993  
 A:Title: WGLD: a tobacco homologue of the GLOBOSA floral homeotic gene of Antirrhinum m  
 A:Reference number: S35226; MUID:93288002; PMID:8099711  
 A:Accession: S35226  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <HAN>  
 A:Cross-references: EMBL:X67959; NID:g19870; PIDN:CAA48142.1; PID:g19871  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 C:Keywords: DNA binding; nucleus; transcription regulation  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 64.1%; Score 707; DB 2; Length 209;  
 Best Local Similarity 63.6%; Pred. No. 1.2e-38;  
 Matches 136; Conservative 41; Mismatches 31; Indels 6; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 DB 1 MGRGKEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 QY 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 DB 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 QY 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 DB 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPICPNIQER 214  
 DB 179 EVYHQR---NEYOTMPFAFRVOPICPNIQER 208

## RESULT 5

J01689  
 floral binding protein 1 - garden petunia  
 C:Species: Petunia x hybrida (garden petunia)  
 C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 21-Jul-2000  
 C:Accession: J01689  
 R:Aggenent, G.C.; Busscher, M.; Franken, J.; Mol, J.N.M.; van Tunen, A.J.  
 Plant Cell 4, 983-993, 1992  
 A:Title: Differential expression of two MADS box genes in wild-type and mutant Petunia fl  
 A:Reference number: J01689; MUID:9300537; PMID:1356537  
 A:Accession: J01689  
 A:Molecule type: mRNA  
 A:Residues: 1-210 <ANG>  
 A:Cross-references: GB:M91190; NID:g169253; PIDN:AAA3731.1; PID:g169254  
 A:Experimental source: flower  
 C:Genetics:  
 A:Gene: fbpl  
 A:Introns: 61/3; 83/3; 104/3; 137/3; 147/1; 162/3  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 C:Keywords: DNA binding; nucleus; transcription regulation  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 62.1%; Score 684.5; DB 2; Length 210;  
 Best Local Similarity 62.3%; Pred. No. 3.2e-37;  
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;

QY 1 MGRGVEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 DB 1 MGRGKEIKRIENSSNRQVTVSKRRNGIIRKAKEITVLCDAKVSLLIYSSSGKRVYCSF 60  
 QY 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 DB 61 STLTLEIDKYHGQSGKGLMDAKHENTLSNEVDKVKNDSDMOVELRHLKGGEDITSLNHVE 120  
 QY 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 DB 121 LMALEBALENGTLTSIRDSKSFVDMKRDNGKALDENKRLTYELQKQGEKIKENYRAME 180  
 QY 181 NGYHOROLGNVNNQOQIPFAFRVOPICPNIQER 214  
 DB 181 AVYDHHHONTADYEAGPFAFRVOPICPNIQER 214

QY 181 NGYHQRQLGNNYNNQOQIPFAFRVQPIQPNLOE 215  
 DB 179 EVFQOQRHNDYXNH---MFAFRVQPMQPNLOE 210

## RESULT 6

AE3836  
 B function floral homeotic protein PI - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jul-2000  
 C:Accession: A53839  
 R:Goto, K.; Meyerowitz, E.M.  
 Genes Dev. 8, 1548-1560, 1994  
 A>Title: Function and regulation of the Arabidopsis floral homeotic gene PISTILLATA.  
 A:Reference number: A53839; MUID:95047314; PMID:7958839  
 A:Accession: A53839  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-208 <GOT>  
 A:Cross-references: GB:DJ0807; NID:9642128; PIDN:BA06465.1; PID:9493620  
 C:Genetics:  
 A:Gene: PI  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 C:Keywords: homeobox  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 59.9%; Score 660.5; DB 2; Length 208;  
 Best Local Similarity 60.5%; Pred. No. 1.1e-35; Indels 13; Gaps 2;  
 Matches 10; Conservative 33; Mismatches 39;

QY 1 MGRGKVEIKRIENSNNQVTSKRRNGIIRKAKETVLCDAKVSLLIYSSSGKMYEYCS 60  
 DB 1 MGRGKVEIKRIENANNRVVTFSKRRNGIIRKAKETVLCDAKVALIFASNGMIDYCCP 60  
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKQNDNSQVLEPHLKGEDITSLNHYE 120  
 DB 61 SMDLGMLDQYQKLSKSKLMDAKHENTLSNEIDRIKENSTLOELHKLGEIDISLNLKN 120  
 QY 121 LMALEALENGLTSIRDKOSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENYANNE 180  
 DB 121 LMAVEALEHGLDKVNDHGMELISKRREKMAEQRQRLTQLQ-QQSMALASNAKGM 179  
 QY 181 NGYHQRQLGNNYNNQOQIPFAFRVQPIQPNLOE 215  
 DB 180 MRDHDGQ-----FGYRVQPIQPNLOE 202

## RESULT 7

T03902  
 MADS4 box protein - rice  
 C:Species: Oryza sativa (rice)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 03-Dec-1999  
 C:Accession: T03902  
 R:Chung, Y.Y.; Kim, S.R.; Kang, H.G.; Noh, Y.S.; Park, M.C.; Finkel, D.; An, G.  
 Plant Sci. 109, 45-56, 1995  
 A>Title: Characterization of two rice MADS box genes homologous to GLOBOSA.  
 A:Reference number: Z15129  
 A:Accession: T03902  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-210 <CHU>  
 A:Cross-references: EMBL:L37527; NID:92961436; PIDN:AAC05723.1; PID:92961437  
 A:Experimental source: flower  
 C:Genetics:  
 A:Gene: MADS4  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 56.3%; Score 620.5; DB 2; Length 210;  
 Best Local Similarity 55.9%; Pred. No. 4.1e-33; Indels 5; Gaps 2;  
 Matches 119; Conservative 41; Mismatches 48;

QY 1 MGRGKVEIKRIENSNNQVTSKRRNGIIRKAKETVLCDAKVSLLIYSSSGKMYEYCS 60

DB 1 MGRGKVEIKRIENSTNRQVTFSSKRRGILKAKETVLCDAKREVGAVIFSSAGLSDYCTP 60  
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKQNDNSQVLEPHLKGEDITSLNHYE 120  
 DB 61 KTLISRLIEKYQTSNGKILWDEKHSLSAIDRVKENDWQTELRHMKGEDINLSQPK 120  
 QY 121 LMALEALENGLTSIRDKOSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENYANNE 180  
 DB 121 LMALEALNDGIVANNNDLMDHMERHVRTDKALEDENKRLFAFKH-QQDIALSSMYDLE 179  
 QY 181 NGYHQRQLGNNYNNQOQIPFAFRVQPIQPNLOE 213  
 DB 180 LGYHNR---DDRDAASMPFTFRVQPSHPNLOE 208

## RESULT 8

T03894  
 MADS box protein - rice  
 C:Species: Oryza sativa (rice)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 03-Dec-1999  
 C:Accession: T03894  
 R:Chung, Y.Y.; Kim, S.R.; Kang, H.G.; Noh, Y.S.; Park, M.C.; Finkel, D.; An, G.  
 Plant Sci. 109, 45-56, 1995  
 A>Title: Characterization of two rice MADS box genes homologous to GLOBOSA.  
 A:Reference number: Z15129  
 A:Accession: T03894  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-209 <CHU>  
 A:Cross-references: EMBL:L37526; NID:9686400; PIDN:AA52709.1; PID:9686401  
 A:Experimental source: flower  
 C:Genetics:  
 A:Gene: MADS2  
 C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol  
 F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 55.9%; Score 617; DB 2; Length 209;  
 Best Local Similarity 55.4%; Pred. No. 6.9e-33; Indels 6; Gaps 2;  
 Matches 118; Conservative 44; Mismatches 45;

QY 1 MGRGKVEIKRIENSNNQVTSKRRNGIIRKAKETVLCDAKVSLLIYSSSGKMYEYCS 60  
 DB 1 MGRGKVEIKRIENSTNRQVTFSSKRRGILKAKETVLCDAKREVGAVIFSSAGLSDYCTP 60  
 QY 61 STLTLEILDKYHGSGSKLMDAKHENTLSNEVDYKQNDNSQVLEPHLKGEDITSLNHYE 120  
 DB 61 KTLISRLIEKYQTSNGKILWDEKHSLSAIDRVKENDWQTELRHMKGEDINLSQPK 120  
 QY 121 LMALEALENGLTSIRDKOSKFVDMRDNGKALEDENKRLTYELQKQEMKIKENYANNE 180  
 DB 121 LMALEALNDGIVANNNDLMDHMERHVRTDKALEDENKRLFAFKH-QQDIALSSMYDLE 179  
 QY 181 NGYHQRQLGNNYNNQOQIPFAFRVQPIQPNLOE 213  
 DB 180 LGYHNR---DDRDAASMPFTFRVQPSHPNLOE 207

## RESULT 9

S23731  
 MADS box protein TDR6 - tomato (fragment)  
 N:Alternate names: floral homeotic protein TW6  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 27-May-1994 #sequence\_revision 26-May-1995 #text\_change 26-Aug-1999  
 C:Accession: S23731; S38778  
 R:Pnueli, L.; Abu-Abed, W.; Zamir, D.; Macken, W.; Schwarz-Sommer, Z.; Lifschitz, E.  
 Plant J. 1, 255-266, 1991  
 A>Title: The MADS box gene family in tomato: temporal expression during floral developm  
 A:Reference number: S23728; MUID:93251098; PMID:1688249  
 A:Accession: S23731  
 A:Molecule type: mRNA  
 A:Residues: 1-222 <PNU>  
 A:Cross-references: EMBL:X60759

R.Pruelli, L.  
submitted to the EMBL Data Library, July 1991

A/Reference number: S38778

A/Accession: S38778

A/Molecule type: mRNA

A/Residues: 1-159, 'T', 161-222 <PNF>

A/Cross-references: EMBL:X60759; NID:g19385; PID:g19386

C/Genetics:

A/Map position: 2

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>

Query Match 37.3%; Score 411; DB 2; Length 222;  
Best Local Similarity 41.3%; Pred. No. 1.2e-19;

Matches 88; Conservative 43; Mismatches 74; Indels 8; Gaps 4;

QY 4 GATGATKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSPET 63

DB 1 GKIEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSPET 60

QY 64 LTELIDKRYHGSQSKLMDAKHENLSNEVDYVKDMSQVLEHRLHKGEDITSLNHVELMA 123

DB 61 TKKMDIYOSALGVDMISIHFKMOENLTKLKEINNKLRERQRTGDSGLMDQLCH 120

QY 124 LEALENGITSIIRDKOSKRV---DMRDNGKALDENKRLTYELQKQEMKIKENVRNM 179

DB 121 LOENTITESVAEIRERKHYIKQDTCKKAKANLEQKGNVLDLAKCE-DPKYGVEN 179

QY 180 ENGYNOROLGNVNNQOIPFAFRVOPIQPNQ 212

DB 180 EGHYSAVA--FANGVHNL-YAFRLQPLHPNQ 209

#### RESULT 10

T09335

MADS-box protein NMH 7 - alfalfa

C/Species: Medicago sativa (alfalfa)

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 03-Dec-1999

C/Accession: T09335

R/Kirby, C.; Heard, J.; Carroll, S.; Lesher, J.; Ganter, G.; Dunn, K.

submitted to the EMBL Data Library, January 1998

A/Reference number: Z16647

A/Accession: T09335

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-229 <KIR>

A/Cross-references: EMBL:AF042068; NID:g2827299; PID:g2827300

A/Experimental source: strain Iroquois; root nodules

C/Genetics:

A/Gene: nmh 7

A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 34.5%; Score 381; DB 2; Length 229;  
Best Local Similarity 37.9%; Pred. No. 1.1e-17;

Matches 81; Conservative 47; Mismatches 78; Indels 8; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSP 60

DB 1 MARGKIQRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSP 60

QY 61 STTLEIDKRYHGSQSKLMDAKHENLSNEVDYVKDMSQVLEHRLHKGEDITSLNHVE 120

DB 61 SASTKQFPDQYQVTVGIDLVNSHYENQENLTKLKDVRNLKREIRQMGESCLNDLSMEY 120

QY 121 LMALEALENGITSIIRDKOSKRV---VDMRDNGKALEDENKRLTYELQKQEMKIKENY 176

DB 121 LRLLEEDMDKAAKXIRERKHYIKQDTCKKAKANLEQKGNVLDLAKCE---DPK 177

QY 177 RNENGYNOROLGNVNNQOIPFAFRVOPIQPN 210

DB 178 EMARDNGGEYESVIGFISNLGPRM-FALSLOETHPN 210

#### RESULT 11

S31693

MADS box protein gp - garden petunia

N/Alternate names: floral homeotic protein gp; transcription factor gp

C/Species: Petunia x hybrida (garden petunia)

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 29-Sep-1999

C/Accession: S31693

R/Kush, A.; Brunelle, A.; Shevell, D.; Chu, N.H.

submitted to the EMBL Data Library, November 1992

A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box

A/Reference number: S31693

A/Accession: S31693

A/Molecule type: mRNA

A/Residues: 1-231 <KUS>

A/Cross-references: EMBL:X69946; NID:g22664; PID:g22665

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 34.2%; Score 377.5; DB 2; Length 231;  
Best Local Similarity 38.5%; Pred. No. 1.8e-17;

Matches 84; Conservative 47; Mismatches 72; Indels 15; Gaps 4;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSP 60

DB 1 MARGKIQRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSP 60

QY 61 STTLEIDKRYHGSQSKLMDAKHENLSNEVDYVKDMSQVLEHRLHKGEDITSLNHVE 120

DB 61 SITTKQLPDQYQVTVGIDLVNSHYENQENLTKLKEINNKLRERQRTGDSGLMDQLCH 120

QY 121 LMALEALENGITSIIRDKOSKRV---VDMRDNGKALEDENKRLTYELQKQEMKIKENY 180

DB 121 LERLMENVDNSKLIRERKHYIKQDTCKKAKANLEQKGNVLDLAKCE---DPK 174

QY 181 NGYHQROLGNVNNQOIPFAFRVOP--IQPN 210

DB 175 PGLVDSQBDVNSVGLFPGHGRI-LALRLQGNHHPN 211

#### RESULT 12

T14473

MADS box protein 2AP3 - broccoli

N/Alternate names: homeotic protein 2AP3

C/Species: Brassica oleracea var. botrytis (broccoli)

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 11-May-2000

C/Accession: T14473

R/Carr, S.M.; Irish, V.F.

Planta 201, 179-188, 1997

A/Title: Floral homeotic gene expression defines developmental arrest stages in Brassica

A/Reference number: Z18110; MUID:97237761; PMID:9084216

A/Accession: T14473

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-224 <CAR>

A/Cross-references: EMBL:U67455; NID:g1561785; PID:g1561786

A/Experimental source: variety Italica; flower

C/Genetics:

A/Gene: 2AP3

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 33.3%; Score 367.5; DB 2; Length 224;  
Best Local Similarity 37.1%; Pred. No. 7.6e-17;

Matches 78; Conservative 47; Mismatches 66; Indels 19; Gaps 3;

QY 1 MGRGVEIKRIENSSNRQVTSKRNGIIRKAKETIVLCDAKVSLLIYSSGKRWYECSP 60

Db 1 MARGKIQIKRIENQTNQVYTSKRANGLFKKAHELTVLCDARVSIIMSSSNKLHEFISP 60  
 QY 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 Db 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 QY 121 LMALFEALENGSLTIRDKQSKF---VDMWRDNGKALEDENKRLTYELQKQEKIKENV 176  
 Db 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKNGSQODIQNLHLELBAE---DPHY 177  
 QY 177 RMWENG-----YHQRLGNYN 194  
 Db 178 GLVNDGQDYSLVGYQLRPHQNHHPY 207

## RESULT 13

T07066  
 MADS-box protein homolog DEF4 - potato  
 N/Alternate names: deficient analog  
 C/Species: Solanum tuberosum (potato)  
 C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
 C/Accession: T07066  
 R/Garcia-Maroto, F.; Salami, F.; Rohde, W.  
 Plant J. 4, 771-780, 1993  
 A/Title: Molecular cloning and expression patterns of three alleles of the Deficiens-hom  
 A/Reference number: Z15896; MUID:94100991; PMID:7903890  
 A/Accession: T07066  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-228 <GAR>  
 A/Cross-references: EMBL:X67511; NID:9431225; PIDN:CAA47846.1; PID:9431226  
 A/Experimental source: cv. Granola; leaf  
 A/Genetics:  
 A/Note: def4  
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C/Accession: A42095; S52633; T47593  
 R/Jack, T.; Brockman, L.L.; Meyerowitz, E.M.  
 Cell 68, 683-697, 1992  
 A/Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is ex  
 A/Reference number: A42095; MUID:92154682; PMID:1346756  
 A/Accession: A42095  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-232 <JAC>  
 A/Cross-references: GB:M66357; NID:9166607; PIDN:AAA32740.1; PID:9166608  
 A/Experimental source: petals, stems  
 A/Note: Sequence extracted from NCBI Backbone (NCBI:82520, NCBI:82521)  
 R/Okamoto, H.; Yano, A.; Shirasahi, H.; Okada, K.; Shimura, Y.  
 Plant Mol. Biol. 26, 465-472, 1994  
 A/Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid  
 A/Reference number: S52633; MUID:95036018; PMID:7948893  
 A/Accession: S52633  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-63 <OKA>  
 A/Cross-references: GB:D21125  
 R/Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queller, F.; Salanoubat M.Mewes,  
 submitted to the Protein Sequence Database, March 2000  
 A/Reference number: 22469  
 A/Accession: T47593  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-232 <BLO>  
 A/Cross-references: EMBL:AL132971  
 A/Experimental source: cultivar Columbia; BAC clone T12E18  
 C/Genetics:  
 A/Map position: 3  
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
 A/Note: T12E18.30  
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo  
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 32.6%; Score 360; DB 2; Length 228;  
 Best Local Similarity 37.5%; Pred. No. 2.4e-16;  
 Matches 78; Conservative 44; Mismatches 72; Indels 14; Gaps 3;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKKEITVLCDAKVSLIYSSSGMVEYCSF 60  
 Db 1 MARGKIQIKRIENQTNQVYTSKRANGLFKKAHELTVLCDARVSIIMSSSNKLHEFISP 60  
 QY 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 Db 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 QY 121 LMALFEALENGSLTIRDKQSKF---VDMWRDNGKALEDENKRLTYELQKQEKIKENV 176  
 Db 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKNGSQODIQNLHLELBAE---DPHY 177  
 QY 177 RMWENG-----YHQRLGNYN 194  
 Db 178 GLVNDGQDYSLVGYQLRPHQNHHPY 207

## RESULT 14

T07410  
 MADS box protein homolog DEF2 - potato  
 N/Alternate names: deficient analog  
 C/Species: Solanum tuberosum (potato)  
 C/Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 03-Dec-1999  
 C/Accession: T07410  
 R/Garcia-Maroto, F.  
 submitted to the EMBL Data Library, August 1992  
 A/Reference number: Z16019  
 A/Accession: T07410  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA

A/Residues: 1-228 <GAR>  
 A/Cross-references: EMBL:X67508; NID:9511064; PIDN:CAA47845.1; PID:9511065  
 A/Experimental source: cv. H81.1506/60; dev. stage vegetative; tissue type flower  
 C/Genetics:  
 A/Note: def2  
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo  
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>  
 Query Match 32.5%; Score 359; DB 2; Length 228;  
 Best Local Similarity 37.5%; Pred. No. 2.7e-16;  
 Matches 78; Conservative 43; Mismatches 73; Indels 14; Gaps 3;

QY 1 MGRGKVEIKRIENSSNQVYTSKRNGIIRKKEITVLCDAKVSLIYSSSGMVEYCSF 60  
 Db 1 MARGKIQIKRIENQTNQVYTSKRANGLFKKAHELTVLCDARVSIIMSSSNKLHEFISP 60  
 QY 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 Db 61 STTLTEILDKYHGSGGKLMADAKHENLSNEVDKVKDNDMSQVLEHLKGEDITSLNHVE 120  
 QY 121 LMALFEALENGSLTIRDKQSKF---VDMWRDNGKALEDENKRLTYELQKQEKIKENV 176  
 Db 121 LLSLEBEMENFTKLVREKFKSLGNQIETTKKNGSQODIQNLHLELBAE---DPHY 177  
 QY 177 RMWENG-----YHQRLGNYN 194  
 Db 178 GLVNDGQDYSLVGYQLRPHQNHHPY 207

## RESULT 15

A42095  
 floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana  
 N/Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
 C/Accession: A42095; S52633; T47593  
 R/Jack, T.; Brockman, L.L.; Meyerowitz, E.M.  
 Cell 68, 683-697, 1992  
 A/Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is ex  
 A/Reference number: A42095; MUID:92154682; PMID:1346756  
 A/Accession: A42095  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-232 <JAC>  
 A/Cross-references: GB:M66357; NID:9166607; PIDN:AAA32740.1; PID:9166608  
 A/Experimental source: petals, stems  
 A/Note: Sequence extracted from NCBI Backbone (NCBI:82520, NCBI:82521)  
 R/Okamoto, H.; Yano, A.; Shirasahi, H.; Okada, K.; Shimura, Y.  
 Plant Mol. Biol. 26, 465-472, 1994  
 A/Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid  
 A/Reference number: S52633; MUID:95036018; PMID:7948893  
 A/Accession: S52633  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-63 <OKA>  
 A/Cross-references: GB:D21125  
 R/Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Queller, F.; Salanoubat M.Mewes,  
 submitted to the Protein Sequence Database, March 2000  
 A/Reference number: 22469  
 A/Accession: T47593  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-232 <BLO>  
 A/Cross-references: EMBL:AL132971  
 A/Experimental source: cultivar Columbia; BAC clone T12E18  
 C/Genetics:  
 A/Map position: 3  
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3  
 A/Note: T12E18.30  
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo  
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation  
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 32.3%; Score 356.5; DB 2; Length 232;  
 Best Local Similarity 35.1%; Pred. No. 4e-16;  
 Matches 79; Conservative 46; Mismatches 73; Indels 27; Gaps 3;

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QY 1 MGRGKVEIKRIENSSNRQVTSKRRNGIIRKAKELTVLADAKVSLITSSSGKWEYCSP 60
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DB 1 MARGKIQIRIEVQTRQVTSRRRNGLPKKAHELTVLGDARVSIIMFSSSKLHEYISP 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 STTLREILDKYGQSGSKLMDAKHENTSNVDKNDSDMQVELRHLKGEDITSINHYE 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 NTTKEIVDLQYQTSIDVDYMATQYERMQETKRLLETNRNLRTQIKRLGECLELDIQE 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 LMALEALENGULSTRDKSKF---VDMRDNGKALDEPNKRLTYELQKQGEKIKENV 176
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 LRLLEDMENTFKLVKRFKSLGNQIETTKKRNKSQODIQKILHELELRAE---DPHY 177
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 177 RNMENG-----YHORQLGNYNNOQOIIPA 201
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 GLVDNGGDYDVLGYQIEGSRAYALRPFQNHNNHYYPNHGLHAFSA 222
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 Job time : 25.0492 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:22:22 ; Search time 76.0087 Seconds  
(without alignments) 6337.402 Million cell updates/sec

Title: US-10-069-527-1  
Perfect score: 868  
Sequence: 1 atggagacgtgggaaggtga.....aaaaaaaaaaaaaaaa 868

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCITUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	3.6	964	1 US-08-448-606-5	Sequence 5, Appl
2	31	3.6	1111	4 US-09-336-643A-29	Sequence 29, Appl
3	31	3.6	1246	4 US-09-336-643A-28	Sequence 28, Appl
4	30	3.5	197	4 US-09-621-976-16515	Sequence 16515, A
5	30	3.5	198	4 US-09-621-976-16515	Sequence 16515, A
6	30	3.5	451	4 US-09-621-976-2738	Sequence 2738, Ap
7	30	3.5	572	4 US-09-342-653-5	Sequence 5, Appl
8	30	3.5	1080	4 US-08-225-757B-1	Sequence 1, Appl
9	30	3.5	1080	2 US-08-722-050-1	Sequence 1, Appl
10	30	3.5	1080	2 US-09-883-985-1	Sequence 1, Appl
11	30	3.5	1300	4 US-09-501-115-19	Sequence 19, Appl
12	30	3.5	1411	3 US-08-864-127-5	Sequence 5, Appl
13	30	3.5	1411	3 US-09-496-692-5	Sequence 5, Appl
14	30	3.5	1411	4 US-10-000-273-5	Sequence 5, Appl
15	30	3.5	1414	4 US-09-404-296A-9	Sequence 9, Appl
16	30	3.5	2862	1 US-08-148-209A-1	Sequence 1, Appl
17	30	3.5	2864	1 US-08-148-209A-5	Sequence 1, Appl
18	30	3.5	3200	1 US-08-444-405-1	Sequence 1, Appl
19	30	3.5	3200	1 US-08-384-850-1	Sequence 1, Appl
20	30	3.5	71	4 US-09-816-089A-5	Sequence 1, Appl
21	29	3.3	82	4 US-09-621-976-12434	Sequence 12434, A
22	29	3.3	132	4 US-09-430-240-1	Sequence 1, Appl
23	29	3.3	132	4 US-09-466-994-1	Sequence 1, Appl
24	29	3.3	133	4 US-09-621-976-16514	Sequence 16514, A
25	29	3.3	220	4 US-09-322-575-20	Sequence 20, Appl
26	29	3.3	220	4 US-09-389-681-20	Sequence 20, Appl
27	29	3.3	290	4 US-09-620-405B-20	Sequence 20, Appl

C	28	29	3.3	290	4 US-09-339-338-20	Sequence 20, Appl
C	29	29	3.3	290	4 US-09-433-826B-20	Sequence 20, Appl
C	30	29	3.3	290	4 US-09-604-287A-20	Sequence 20, Appl
C	31	29	3.3	290	4 US-09-285-480-20	Sequence 20, Appl
C	32	29	3.3	290	4 US-09-834-759-20	Sequence 20, Appl
C	33	29	3.3	314	1 US-08-868-878A-25	Sequence 25, Appl
C	34	29	3.3	314	4 US-09-175-928-25	Sequence 25, Appl
C	35	29	3.3	651	4 US-09-800-729-13	Sequence 13, Appl
C	36	29	3.3	840	4 US-09-244-111-5	Sequence 5, Appl
C	37	29	3.3	917	2 US-08-924-759-17	Sequence 17, Appl
C	38	29	3.3	917	4 US-09-448-335-17	Sequence 17, Appl
C	39	29	3.3	963	1 US-08-886-765-1	Sequence 1, Appl
C	40	29	3.3	963	1 US-09-115-660-1	Sequence 1, Appl
C	41	29	3.3	1133	3 US-08-700-626-2	Sequence 2, Appl
C	42	29	3.3	1394	1 US-07-730-953-1	Sequence 1, Appl
C	43	29	3.3	1745	4 US-09-388-349-5	Sequence 5, Appl
C	44	29	3.3	1839	4 US-09-461-325-23	Sequence 23, Appl
C	45	29	3.3	1839	4 US-10-012-542-23	Sequence 23, Appl
C	46	29	3.3	1875	4 US-09-614-912-129	Sequence 129, App
C	47	29	3.3	1878	1 US-08-724-194-3	Sequence 3, Appl
C	48	29	3.3	2017	4 US-09-690-454-45	Sequence 45, Appl
C	49	29	3.3	2026	4 US-09-690-454-30	Sequence 30, Appl
C	50	29	3.3	2301	1 US-08-614-801A-5	Sequence 5, Appl
C	51	29	3.3	2308	4 US-09-835-654-4	Sequence 4, Appl
C	52	29	3.3	2537	4 US-09-835-654-1	Sequence 1, Appl
C	53	29	3.3	2608	4 US-09-504-615-16	Sequence 16, Appl
C	54	29	3.3	2730	4 US-09-215-450-6	Sequence 6, Appl
C	55	29	3.3	3720	4 US-09-342-681C-12	Sequence 12, Appl
C	56	28	3.2	52	4 US-09-611-627-20	Sequence 4, Appl
C	57	28	3.2	54	2 US-08-771-624B-4	Sequence 4, Appl
C	58	28	3.2	56	3 US-09-118-256-1	Sequence 1, Appl
C	59	28	3.2	56	3 US-09-118-256-2	Sequence 2, Appl
C	60	28	3.2	60	4 US-09-975-408-68	Sequence 68, Appl
C	61	28	3.2	87	4 US-09-621-976-14560	Sequence 14560, A
C	62	28	3.2	166	4 US-09-621-976-18390	Sequence 18390, A
C	63	28	3.2	204	4 US-09-621-976-16458	Sequence 16458, A
C	64	28	3.2	222	4 US-09-621-976-16409	Sequence 16409, A
C	65	28	3.2	246	4 US-09-621-976-13617	Sequence 13617, A
C	66	28	3.2	266	4 US-09-621-976-16988	Sequence 16988, A
C	67	28	3.2	261	4 US-09-051-097-21	Sequence 21, Appl
C	68	28	3.2	269	4 US-09-621-976-16936	Sequence 16936, A
C	69	28	3.2	270	2 US-08-520-678A-30	Sequence 30, Appl
C	70	28	3.2	270	3 US-08-897-126-30	Sequence 30, Appl
C	71	28	3.2	280	4 US-09-621-976-16932	Sequence 16932, A
C	72	28	3.2	280	4 US-09-621-976-14588	Sequence 14588, A
C	73	28	3.2	299	4 US-09-621-976-16226	Sequence 16226, A
C	74	28	3.2	300	4 US-09-621-976-16227	Sequence 16227, A
C	75	28	3.2	352	4 US-09-389-681-418	Sequence 418, App
C	76	28	3.2	352	4 US-09-620-405B-418	Sequence 418, App
C	77	28	3.2	352	4 US-09-433-826B-418	Sequence 418, App
C	78	28	3.2	352	4 US-09-604-287A-418	Sequence 418, App
C	79	28	3.2	352	4 US-09-834-759-418	Sequence 418, App
C	80	28	3.2	352	4 US-09-387-212-2	Sequence 2, Appl
C	81	28	3.2	403	4 US-09-948-802-2	Sequence 2, Appl
C	82	28	3.2	552	4 US-09-461-325-111	Sequence 111, App
C	83	28	3.2	552	4 US-10-012-542-111	Sequence 111, App
C	84	28	3.2	556	4 US-09-370-838-242	Sequence 242, App
C	85	28	3.2	558	4 US-09-280-116-185	Sequence 185, App
C	86	28	3.2	654	4 US-09-255-630-4	Sequence 4, Appl
C	87	28	3.2	664	4 US-09-904-615-66	Sequence 66, Appl
C	88	28	3.2	722	1 US-08-698-551-5	Sequence 5, Appl
C	89	28	3.2	722	1 US-08-602-228-5	Sequence 5, Appl
C	90	28	3.2	722	2 US-08-649-311A-5	Sequence 5, Appl
C	91	28	3.2	722	2 US-08-494-440B-5	Sequence 5, Appl
C	92	28	3.2	722	2 US-08-533-901B-5	Sequence 5, Appl
C	93	28	3.2	722	2 US-08-839-032A-5	Sequence 5, Appl
C	94	28	3.2	722	2 US-08-839-031A-5	Sequence 5, Appl
C	95	28	3.2	722	2 US-09-185-258C-5	Sequence 5, Appl
C	96	28	3.2	722	4 PCT-US95-12724-5	Sequence 5, Appl
C	97	28	3.2	774	4 US-09-833-381-411	Sequence 411, App
C	98	28	3.2	777	2 US-08-618-911-3	Sequence 3, Appl
C	99	28	3.2	777	2 US-08-618-911-3	Sequence 3, Appl
C	100	28	3.2	777	2 US-08-618-911-5	Sequence 5, Appl

101	28	3.2	798	4	US-09-118-554-57	Sequence 57, Appl	174	28	3.2	1802	3	US-09-032-523-5	Sequence 5, Appl
102	28	3.2	798	4	US-09-118-627-57	Sequence 57, Appl	175	28	3.2	1802	3	US-09-802-633-5	Sequence 5, Appl
103	28	3.2	798	4	US-09-602-877A-57	Sequence 57, Appl	176	28	3.2	1817	2	US-08-870-518-8	Sequence 8, Appl
104	28	3.2	809	4	US-09-149-476-244	Sequence 244, App	177	28	3.2	1826	4	US-09-799-877-13	Sequence 13, Appl
105	28	3.2	874	4	US-09-023-655-1377	Sequence 1377, Ap	178	28	3.2	1858	4	US-09-336-533-58	Sequence 56, Appl
106	28	3.2	875	4	US-09-589-733C-4	Sequence 4, Appl	179	28	3.2	1867	4	US-09-482-273-81	Sequence 46, Appl
107	28	3.2	898	4	US-09-857-556A-29	Sequence 29, Appl	180	28	3.2	1875	4	US-08-984-919A-86	Sequence 81, Appl
108	28	3.2	947	4	US-09-673-395A-8	Sequence 8, Appl	181	28	3.2	1875	4	US-08-984-919A-86	Sequence 46, Appl
109	28	3.2	966	2	US-08-921-362-1	Sequence 1, Appl	182	28	3.2	1881	4	US-08-874-102-46	Sequence 48, Appl
110	28	3.2	966	2	US-09-386-380-1	Sequence 1, Appl	183	28	3.2	1897	1	US-08-184-632-1	Sequence 15, Appl
111	28	3.2	1003	2	US-08-887-997B-1	Sequence 38, Appl	184	28	3.2	1948	4	US-09-419-627-15	Sequence 4, Appl
112	28	3.2	1048	4	US-09-489-847-38	Sequence 10, Appl	185	28	3.2	2010	2	US-07-864-475A-4	Sequence 4, Appl
113	28	3.2	1051	3	US-09-245-041-10	Sequence 161, Ap	186	28	3.2	2010	2	US-08-468-249A-4	Sequence 12, Appl
114	28	3.2	1064	4	US-09-833-381-1661	Sequence 10, Appl	187	28	3.2	2028	3	US-09-211-930-12	Sequence 12, Appl
115	28	3.2	1112	4	US-09-716-161A-10	Sequence 7, Appl	188	28	3.2	2028	3	US-09-340-993-12	Sequence 12, Appl
116	28	3.2	1126	4	US-09-389-956-7	Sequence 5, Appl	189	28	3.2	2028	3	US-09-468-442-12	Sequence 12, Appl
117	28	3.2	1142	1	US-08-006-082A-5	Sequence 20, Appl	190	28	3.2	2073	4	US-09-565-264-1	Sequence 1, Appl
118	28	3.2	1144	4	US-09-904-615-20	Sequence 84, Appl	191	28	3.2	2073	4	US-09-565-264-1	Sequence 1, Appl
119	28	3.2	1149	4	US-09-227-357-84	Sequence 5, Appl	192	28	3.2	2131	4	US-09-700-397-7	Sequence 3, Appl
120	28	3.2	1169	3	US-09-100-391-5	Sequence 5, Appl	193	28	3.2	2144	4	US-08-876-798A-3	Sequence 1, Appl
121	28	3.2	1169	3	US-09-616-614-5	Sequence 5, Appl	194	28	3.2	2153	4	US-08-876-798A-3	Sequence 3, Appl
122	28	3.2	1230	3	US-09-387-574-5	Sequence 5, Appl	195	28	3.2	2171	3	US-08-851-843A-100	Sequence 165, App
123	28	3.2	1230	3	US-09-668-096-5	Sequence 138, App	196	28	3.2	2171	3	US-08-974-549A-266	Sequence 266, App
124	28	3.2	1294	4	US-09-227-357-138	Sequence 29, Appl	197	28	3.2	2171	3	US-08-854-050-100	Sequence 100, App
125	28	3.2	1296	4	US-09-461-325-29	Sequence 11, Appl	198	28	3.2	2171	4	US-09-430-323-100	Sequence 266, App
126	28	3.2	1296	4	US-10-012-542-29	Sequence 11, Appl	199	28	3.2	2171	4	US-09-402-181B-266	Sequence 266, App
127	28	3.2	1302	3	US-09-100-391-11	Sequence 11, Appl	200	28	3.2	2171	4	US-09-721-456-266	Sequence 59, Appl
128	28	3.2	1302	4	US-09-616-614-11	Sequence 11, Appl	201	28	3.2	2202	4	US-09-465-558-59	Sequence 59, Appl
129	28	3.2	1305	4	US-09-907-794A-70	Sequence 70, Appl	202	28	3.2	2202	4	US-09-907-794A-3	Sequence 1, Appl
130	28	3.2	1305	4	US-09-905-125A-70	Sequence 70, Appl	203	28	3.2	2206	4	US-09-905-125A-3	Sequence 3, Appl
131	28	3.2	1305	4	US-09-902-775A-70	Sequence 70, Appl	204	28	3.2	2206	4	US-09-905-125A-3	Sequence 3, Appl
132	28	3.2	1335	4	US-09-740-028A-1	Sequence 1, Appl	205	28	3.2	2206	4	US-09-905-125A-3	Sequence 3, Appl
133	28	3.2	1348	4	US-09-485-632B-1	Sequence 248, App	206	28	3.2	2242	4	US-09-482-273-85	Sequence 35, Appl
134	28	3.2	1350	4	US-09-149-476-248	Sequence 174, App	207	28	3.2	2287	4	US-09-561-763-7	Sequence 7, Appl
135	28	3.2	1369	4	US-09-205-258-174	Sequence 7, Appl	208	28	3.2	2287	4	US-09-431-367B-7	Sequence 7, Appl
136	28	3.2	1374	2	US-08-758-621-7	Sequence 7, Appl	209	28	3.2	2310	4	US-09-800-729-66	Sequence 66, Appl
137	28	3.2	1374	3	US-09-107-858-7	Sequence 7, Appl	210	28	3.2	2320	4	US-09-202-904A-13	Sequence 13, Appl
138	28	3.2	1374	3	US-09-579-174-7	Sequence 7, Appl	211	28	3.2	2345	3	US-08-955-937A-1	Sequence 1, Appl
139	28	3.2	1382	4	US-09-820-005-1	Sequence 6, Appl	212	28	3.2	2345	3	US-09-300-985-1	Sequence 1, Appl
140	28	3.2	1383	3	US-09-400-742-7	Sequence 12, Appl	213	28	3.2	2394	4	US-09-482-273-85	Sequence 33, Appl
141	28	3.2	1383	3	US-08-618-651A-7	Sequence 1, Appl	214	28	3.2	2475	3	US-08-945-771-1	Sequence 1, Appl
142	28	3.2	1383	4	US-09-215-352-6	Sequence 1, Appl	215	28	3.2	2510	2	US-09-045-185-3	Sequence 1, Appl
143	28	3.2	1383	4	US-09-970-989A-6	Sequence 1, Appl	216	28	3.2	2510	4	US-08-888-982A-42	Sequence 42, Appl
144	28	3.2	1400	1	US-08-085-122-12	Sequence 12, Appl	217	28	3.2	2510	4	US-09-462-281-42	Sequence 42, Appl
145	28	3.2	1400	3	US-08-442-108B-22	Sequence 21, Appl	218	28	3.2	2532	4	US-09-506-073-89	Sequence 89, Appl
146	28	3.2	1420	4	US-09-227-357-21	Sequence 1, Appl	219	28	3.2	2581	4	US-09-962-276-1	Sequence 1, Appl
147	28	3.2	1425	1	US-08-464-148-1	Sequence 1, Appl	220	28	3.2	2581	4	US-09-363-708-1	Sequence 1, Appl
148	28	3.2	1425	1	US-08-385-500-1	Sequence 1, Appl	221	28	3.2	2629	2	US-09-083-597-1	Sequence 1, Appl
149	28	3.2	1465	4	US-08-984-919A-10	Sequence 10, Appl	222	28	3.2	2629	2	US-08-590-454-1	Sequence 1, Appl
150	28	3.2	1465	4	US-08-984-919A-10	Sequence 10, Appl	223	28	3.2	2630	3	US-08-890-980-1	Sequence 1, Appl
151	28	3.2	1472	3	US-08-781-420-10	Sequence 12, Appl	224	28	3.2	2630	3	US-08-890-980-1	Sequence 1, Appl
152	28	3.2	1472	3	US-08-781-420-10	Sequence 12, Appl	225	28	3.2	2630	3	US-09-032-894-1	Sequence 1, Appl
153	28	3.2	1472	4	US-08-874-102-10	Sequence 10, Appl	226	28	3.2	2630	3	US-09-031-826-1	Sequence 1, Appl
154	28	3.2	1472	4	US-08-874-102-10	Sequence 10, Appl	227	28	3.2	2643	3	US-09-100-391-9	Sequence 1, Appl
155	28	3.2	1472	4	US-09-006-595A-10	Sequence 10, Appl	228	28	3.2	2643	3	US-08-616-614-9	Sequence 9, Appl
156	28	3.2	1472	4	US-09-006-595A-10	Sequence 10, Appl	229	28	3.2	2668	2	US-08-909-655C-1	Sequence 9, Appl
157	28	3.2	1509	4	US-09-149-476-179	Sequence 179, App	230	28	3.2	2668	2	US-08-909-655C-1	Sequence 9, Appl
158	28	3.2	1605	4	US-09-106-464-1	Sequence 1, Appl	231	28	3.2	2968	4	US-09-404-879A-385	Sequence 385, App
159	28	3.2	1605	4	US-09-106-464-1	Sequence 1, Appl	232	28	3.2	2968	4	US-09-813-819-1	Sequence 1, Appl
160	28	3.2	1636	4	US-09-016-434-1433	Sequence 1433, Ap	233	28	3.2	3040	1	US-08-446-794A-1	Sequence 1, Appl
161	28	3.2	1733	4	US-09-741-154-1	Sequence 102, App	234	28	3.2	3040	1	US-08-700-007-2	Sequence 2, Appl
162	28	3.2	1733	4	US-09-482-273-102	Sequence 1, Appl	235	28	3.2	3040	1	US-08-945-024-1	Sequence 1, Appl
163	28	3.2	1733	4	US-09-482-273-102	Sequence 1, Appl	236	28	3.2	3047	1	US-07-927-851-2	Sequence 1, Appl
164	28	3.2	1747	1	US-08-993-260-2	Sequence 1, Appl	237	28	3.2	3047	1	US-08-453-323-2	Sequence 2, Appl
165	28	3.2	1747	1	US-08-176-620A-1	Sequence 1, Appl	238	28	3.2	3134	2	US-08-440-520-2	Sequence 2, Appl
166	28	3.2	1747	2	US-08-463-862-1	Sequence 1, Appl	239	28	3.2				
167	28	3.2	1747	2	US-08-461-985-1	Sequence 1, Appl	240	28	3.2				
168	28	3.2	1747	2	US-08-458-887-1	Sequence 1, Appl	241	28	3.2				
169	28	3.2	1747	3	US-08-932-787B-1	Sequence 1, Appl	242	28	3.2				
170	28	3.2	1747	3	US-08-932-787B-1	Sequence 1, Appl	243	28	3.2				
171	28	3.2	1747	4	US-08-888-818C-1	Sequence 1, Appl	244	28	3.2				
172	28	3.2	1798	4	US-09-797-906-1	Sequence 46, Appl	245	28	3.2				
173	28	3.2	1801	4	US-09-336-536-46	Sequence 46, Appl	246	28	3.2				



247	28	3.2	3134	4	US-09-183-861-1	Sequence 1, Appli	320	27	3.1	72	4	US-09-621-976-12390	Sequence 12390, A
248	28	3.2	3134	4	US-09-022-765-1	Sequence 1, Appli	321	27	3.1	73	4	US-09-621-976-14698	Sequence 14698, A
249	28	3.2	3134	4	US-09-551-974A-1	Sequence 1, Appli	322	27	3.1	77	4	US-09-621-976-12266	Sequence 12266, A
250	28	3.2	3134	4	US-09-565-501A-1	Sequence 1, Appli	323	27	3.1	81	3	US-09-014-616-57	Sequence 57, Appli
251	28	3.2	3134	4	US-09-639-206A-1	Sequence 1, Appli	324	27	3.1	81	4	US-09-621-976-12198	Sequence 12198, A
252	28	3.2	3134	4	US-09-874-923-1	Sequence 1, Appli	325	27	3.1	81	4	US-09-621-976-13601	Sequence 13601, A
253	28	3.2	3207	1	US-07-946-427-1	Sequence 1, Appli	326	27	3.1	82	4	US-09-621-976-11689	Sequence 11689, A
254	28	3.2	3207	1	US-08-483-322-1	Sequence 1, Appli	327	27	3.1	82	4	US-09-621-976-11841	Sequence 11841, A
255	28	3.2	3207	1	US-08-478-883-1	Sequence 1, Appli	328	27	3.1	82	4	US-09-621-976-11864	Sequence 11864, A
256	28	3.2	3319	3	US-08-335-844A-15	Sequence 15, Appli	329	27	3.1	82	4	US-09-621-976-11868	Sequence 11868, A
257	28	3.2	3319	4	US-09-129-366-15	Sequence 15, Appli	330	27	3.1	82	4	US-09-621-976-11944	Sequence 11944, A
258	28	3.2	3383	4	US-09-130-491-3	Sequence 3, Appli	331	27	3.1	82	4	US-09-621-976-11849	Sequence 11849, A
259	28	3.2	3635	1	US-08-252-626A-1	Sequence 1, Appli	332	27	3.1	82	4	US-09-621-976-12015	Sequence 12015, A
260	28	3.2	3652	4	US-08-936-135-5	Sequence 5, Appli	333	27	3.1	82	4	US-09-621-976-12088	Sequence 12088, A
261	28	3.2	3652	4	US-09-439-711C-5	Sequence 5, Appli	334	27	3.1	82	4	US-09-621-976-12103	Sequence 12103, A
262	28	3.2	3695	1	US-08-091-569-1	Sequence 1, Appli	335	27	3.1	82	4	US-09-621-976-12127	Sequence 12127, A
263	28	3.2	3695	1	US-08-203-676-1	Sequence 1, Appli	336	27	3.1	82	4	US-09-621-976-12131	Sequence 12131, A
264	28	3.2	3695	2	US-08-822-238-1	Sequence 1, Appli	337	27	3.1	82	4	US-09-621-976-12137	Sequence 12137, A
265	28	3.2	3736	2	US-08-480-473B-1	Sequence 1, Appli	338	27	3.1	82	4	US-09-621-976-12322	Sequence 12322, A
266	28	3.2	3736	2	US-08-915-213-1	Sequence 1, Appli	339	27	3.1	82	4	US-09-621-976-12368	Sequence 12368, A
267	28	3.2	3736	3	US-09-148-547-1	Sequence 1, Appli	340	27	3.1	82	4	US-09-621-976-13349	Sequence 13349, A
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269	28	3.2	3736	3	US-09-383-581-1	Sequence 1, Appli	342	27	3.1	83	4	US-09-621-976-12107	Sequence 12107, A
270	28	3.2	3736	5	PCR-US96-10251-1	Sequence 1, Appli	343	27	3.1	83	4	US-09-621-976-12175	Sequence 12175, A
271	28	3.2	3777	3	US-09-121-321-15	Sequence 15, Appli	344	27	3.1	83	4	US-09-621-976-12195	Sequence 12195, A
272	28	3.2	3777	3	US-08-933-803A-15	Sequence 15, Appli	345	27	3.1	83	4	US-09-621-976-12429	Sequence 12429, A
273	28	3.2	3902	4	US-09-389-956-1	Sequence 1, Appli	346	27	3.1	83	4	US-09-621-976-12450	Sequence 12450, A
274	28	3.2	3999	4	US-09-351-224E-9	Sequence 9, Appli	347	27	3.1	84	4	US-09-621-976-12510	Sequence 12510, A
275	28	3.2	3999	4	US-09-677-488A-9	Sequence 9, Appli	348	27	3.1	85	1	US-08-120-827-97	Sequence 97, Appli
276	28	3.2	3999	4	US-09-677-682B-9	Sequence 9, Appli	349	27	3.1	85	1	US-08-478-675-97	Sequence 97, Appli
277	28	3.2	4104	1	US-07-998-003A-94	Sequence 94, Appli	350	27	3.1	90	1	US-08-677-944-2	Sequence 2, Appli
278	28	3.2	4104	1	US-08-453-278B-94	Sequence 94, Appli	351	27	3.1	90	1	US-09-284-048A-1	Sequence 1, Appli
279	28	3.2	4104	1	US-08-453-695A-94	Sequence 94, Appli	352	27	3.1	90	3	US-09-921-203-1	Sequence 2, Appli
280	28	3.2	4104	1	US-08-268-161A-94	Sequence 94, Appli	353	27	3.1	90	4	US-09-616-089A-2	Sequence 2, Appli
281	28	3.2	4104	2	US-08-453-702A-94	Sequence 94, Appli	354	27	3.1	90	4	US-09-621-976-9330	Sequence 9330, Ap
282	28	3.2	4104	5	PCR-US93-12588-94	Sequence 94, Appli	355	27	3.1	90	4	US-10-106-832-1	Sequence 1, Appli
283	28	3.2	4104	5	PCR-US93-08071-94	Sequence 94, Appli	356	27	3.1	91	4	US-09-621-976-12161	Sequence 12161, A
284	28	3.2	4114	1	US-08-199-780-2	Sequence 2, Appli	357	27	3.1	93	4	US-09-616-089A-8	Sequence 8, Appli
285	28	3.2	4114	1	US-08-316-650-2	Sequence 2, Appli	358	27	3.1	97	1	US-08-120-827-87	Sequence 87, Appli
286	28	3.2	4114	2	US-08-476-062A-52	Sequence 52, Appli	359	27	3.1	97	1	US-08-478-675-87	Sequence 87, Appli
287	28	3.2	4704	4	US-09-023-655-1358	Sequence 1358, Ap	360	27	3.1	98	4	US-09-621-976-11444	Sequence 11444, A
288	28	3.2	4858	4	US-09-392-184-1	Sequence 1, Appli	361	27	3.1	105	2	US-08-735-381-2	Sequence 2, Appli
289	28	3.2	5984	4	US-09-705-872-2	Sequence 2, Appli	362	27	3.1	105	3	US-09-201-674-2	Sequence 2, Appli
290	28	3.2	5984	4	US-09-620-317D-823	Sequence 823, App	363	27	3.1	105	3	US-09-621-976-13820	Sequence 13820, A
291	28	3.2	43676	3	US-09-356-952-12	Sequence 12, Appli	364	27	3.1	106	4	US-09-621-976-12079	Sequence 12079, A
292	28	3.2	246240	2	US-08-724-394A-20	Sequence 20, Appli	365	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
293	28	3.2	246240	2	US-08-724-394A-21	Sequence 21, Appli	366	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
294	28	3.2	246240	2	US-08-724-394A-22	Sequence 22, Appli	367	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
295	28	3.2	246240	2	US-08-724-394A-11	Sequence 11, Appli	368	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
296	27	3.1	42	3	US-09-244-794A-12	Sequence 12, Appli	369	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
297	27	3.1	42	3	US-09-244-794A-13	Sequence 13, Appli	370	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
298	27	3.1	42	3	US-09-247-190-11	Sequence 11, Appli	371	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
299	27	3.1	42	3	US-09-247-190-12	Sequence 12, Appli	372	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
300	27	3.1	42	3	US-09-247-190-13	Sequence 13, Appli	373	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
301	27	3.1	42	3	US-09-238-710-11	Sequence 11, Appli	374	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
302	27	3.1	42	4	US-09-238-710-12	Sequence 12, Appli	375	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
303	27	3.1	42	4	US-09-238-710-13	Sequence 13, Appli	376	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
304	27	3.1	42	4	US-09-238-710-14	Sequence 14, Appli	377	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
305	27	3.1	44	1	US-08-664-596B-9	Sequence 9, Appli	378	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
306	27	3.1	44	4	US-09-619-103-5	Sequence 5, Appli	379	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
307	27	3.1	54	2	US-08-663-823B-73	Sequence 73, Appli	380	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
308	27	3.1	54	2	US-08-776-94A-8	Sequence 8, Appli	381	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
309	27	3.1	55	3	US-09-007-005-11	Sequence 11, Appli	382	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
310	27	3.1	55	3	US-09-007-005-12	Sequence 12, Appli	383	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
311	27	3.1	55	3	US-09-007-005-13	Sequence 13, Appli	384	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
312	27	3.1	55	3	US-09-244-796-11	Sequence 11, Appli	385	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
313	27	3.1	55	3	US-09-244-796-12	Sequence 12, Appli	386	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
314	27	3.1	55	3	US-09-244-796-13	Sequence 13, Appli	387	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
315	27	3.1	55	4	US-09-621-976-11651	Sequence 11651, A	388	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
316	27	3.1	59	4	US-09-621-976-11876	Sequence 11876, A	389	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
317	27	3.1	69	4	US-09-621-976-11887	Sequence 11887, A	390	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
318	27	3.1	69	4	US-09-621-976-12454	Sequence 12454, A	391	27	3.1	123	4	US-09-621-976-12330	Sequence 12330, A
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333	27	3.1	170	4	US-09-621-976-19172	Sequence 19172, A	466	27	3.1	282	4	US-09-621-976-18648	Sequence 18648, A
C 334	27	3.1	176	3	US-09-014-416-63	Sequence 63, Appl	467	27	3.1	289	4	US-09-621-976-16989	Sequence 16989, A
335	27	3.1	177	3	US-09-621-976-8073	Sequence 8073, Ap	468	27	3.1	283	4	US-09-621-976-15142	Sequence 15142, A
336	27	3.1	179	4	US-09-621-976-18054	Sequence 18054, A	469	27	3.1	291	3	US-09-329-796-1	Sequence 1, Appl1
337	27	3.1	180	4	US-09-621-976-18587	Sequence 18587, A	470	27	3.1	292	4	US-09-621-976-12039	Sequence 12039, A
338	27	3.1	182	4	US-09-621-976-16234	Sequence 16234, A	471	27	3.1	292	4	US-09-621-976-12050	Sequence 12050, A
C 339	27	3.1	183	3	US-09-014-416-60	Sequence 60, Appl	472	27	3.1	293	4	US-09-621-976-12696	Sequence 12696, A
400	27	3.1	184	4	US-09-621-976-13606	Sequence 13606, A	C 473	27	3.1	295	4	US-09-833-381-1263	Sequence 1263, Ap
401	27	3.1	184	4	US-09-480-921B-13	Sequence 13, Appl	474	27	3.1	297	4	US-09-621-976-16032	Sequence 16032, A
402	27	3.1	185	4	US-09-621-976-16538	Sequence 16538, A	475	27	3.1	297	4	US-09-621-976-16032	Sequence 16032, A
403	27	3.1	187	4	US-09-621-976-16539	Sequence 16539, A	C 476	27	3.1	298	2	US-08-520-678A-21	Sequence 21, Appl
404	27	3.1	188	4	US-09-621-976-16542	Sequence 16542, A	C 477	27	3.1	298	2	US-08-897-126-21	Sequence 21, Appl
405	27	3.1	189	4	US-09-621-976-14761	Sequence 14761, A	C 478	27	3.1	302	4	US-09-439-313-255	Sequence 255, App
406	27	3.1	190	4	US-09-621-976-16540	Sequence 16540, A	C 479	27	3.1	302	4	US-09-332-616A-255	Sequence 255, App
407	27	3.1	191	4	US-09-621-976-9448	Sequence 9448, Ap	C 480	27	3.1	302	4	US-09-232-149A-255	Sequence 255, App
408	27	3.1	191	4	US-09-621-976-16546	Sequence 16546, A	C 481	27	3.1	302	4	US-09-159-812-255	Sequence 255, App
409	27	3.1	193	4	US-09-621-976-10543	Sequence 10543, A	C 482	27	3.1	302	4	US-09-636-215-255	Sequence 255, App
410	27	3.1	193	4	US-09-621-976-16535	Sequence 16535, A	C 483	27	3.1	302	4	US-09-688-166A-255	Sequence 255, App
411	27	3.1	194	4	US-09-621-976-14889	Sequence 14889, A	C 484	27	3.1	302	4	US-09-688-489-255	Sequence 255, App
412	27	3.1	194	4	US-09-621-976-16537	Sequence 16537, A	485	27	3.1	305	4	US-09-621-976-16020	Sequence 16020, A
413	27	3.1	195	4	US-09-621-976-16062	Sequence 16062, A	486	27	3.1	306	4	US-09-621-976-16035	Sequence 16035, A
414	27	3.1	195	4	US-08-330-108-16	Sequence 16, Appl	C 487	27	3.1	321	2	US-08-520-678A-23	Sequence 23, Appl
415	27	3.1	198	5	PCT-US92-10087-16	Sequence 16, Appl	C 488	27	3.1	321	2	US-08-897-126-23	Sequence 23, Appl
416	27	3.1	199	4	US-09-736-457-102	Sequence 102, App	489	27	3.1	326	4	US-09-621-976-16024	Sequence 16024, A
417	27	3.1	199	4	US-09-736-457-102	Sequence 102, App	490	27	3.1	326	4	US-09-621-976-16012	Sequence 16012, A
418	27	3.1	199	4	US-09-614-124B-102	Sequence 102, App	491	27	3.1	329	4	US-09-621-976-16024	Sequence 16024, A
419	27	3.1	199	4	US-09-671-325-102	Sequence 102, App	492	27	3.1	330	4	US-09-621-976-16031	Sequence 16031, A
420	27	3.1	199	4	US-09-589-184-102	Sequence 102, App	493	27	3.1	332	4	US-09-621-976-16031	Sequence 16031, A
C 421	27	3.1	200	3	US-09-014-416-64	Sequence 64, Appl	494	27	3.1	332	4	US-09-621-976-16030	Sequence 16030, A
422	27	3.1	201	4	US-09-621-976-16551	Sequence 16551, A	495	27	3.1	333	3	US-08-946-026-35	Sequence 35, Appl
423	27	3.1	203	4	US-09-621-976-16454	Sequence 16454, A	496	27	3.1	333	3	US-09-621-976-16032	Sequence 16032, A
424	27	3.1	204	4	US-09-621-976-1323	Sequence 1323, Ap	497	27	3.1	333	4	US-09-621-976-16044	Sequence 16044, A
425	27	3.1	209	4	US-09-621-976-12930	Sequence 12930, A	498	27	3.1	334	4	US-09-621-976-16044	Sequence 16044, A
426	27	3.1	213	4	US-09-621-976-16536	Sequence 16536, A	499	27	3.1	334	4	US-09-621-976-16044	Sequence 16044, A
427	27	3.1	217	4	US-09-621-976-16285	Sequence 16285, A	500	27	3.1	336	4	US-09-621-976-16013	Sequence 16013, A
428	27	3.1	221	4	US-09-621-976-13585	Sequence 13585, A	501	27	3.1	336	4	US-09-621-976-16041	Sequence 16041, A
429	27	3.1	222	2	US-09-621-976-16293	Sequence 16293, A	502	27	3.1	337	4	US-09-621-976-16026	Sequence 16026, A
C 430	27	3.1	227	2	US-08-520-678A-28	Sequence 28, Appl	503	27	3.1	348	4	US-09-385-982-283	Sequence 283, App
C 431	27	3.1	227	3	US-08-897-126-28	Sequence 28, Appl	C 504	27	3.1	348	4	US-08-520-678A-22	Sequence 22, Appl
432	27	3.1	228	4	US-09-328-111-484	Sequence 111, App	C 505	27	3.1	356	2	US-08-897-126-22	Sequence 22, Appl
433	27	3.1	231	4	US-09-621-976-16317	Sequence 16317, A	C 506	27	3.1	356	3	US-09-621-976-16581	Sequence 16581, A
434	27	3.1	231	4	US-09-621-976-16536	Sequence 16536, A	507	27	3.1	356	4	US-09-621-976-16058	Sequence 16058, A
435	27	3.1	232	4	US-09-621-976-17701	Sequence 17701, A	508	27	3.1	357	4	US-09-621-976-16019	Sequence 16019, A
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438	27	3.1	235	4	US-09-621-976-16557	Sequence 16557, A	C 511	27	3.1	362	1	US-08-171-385-12	Sequence 12, Appl
439	27	3.1	235	4	US-09-621-976-16550	Sequence 16550, A	C 512	27	3.1	362	3	US-08-361-441B-12	Sequence 12, Appl
440	27	3.1	240	4	US-09-621-976-1324	Sequence 1324, Ap	513	27	3.1	362	4	US-09-621-976-16019	Sequence 16019, A
441	27	3.1	242	4	US-09-621-976-16320	Sequence 16320, A	514	27	3.1	365	4	US-09-621-976-14699	Sequence 14699, A
442	27	3.1	242	4	US-09-621-976-16324	Sequence 16324, A	515	27	3.1	365	4	US-09-621-976-16042	Sequence 16042, A
443	27	3.1	245	4	US-09-621-976-17945	Sequence 17945, A	516	27	3.1	367	3	US-09-328-111-446	Sequence 111, Appl
444	27	3.1	246	4	US-09-621-976-16288	Sequence 16288, A	517	27	3.1	371	4	US-09-621-976-16048	Sequence 16048, A
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446	27	3.1	248	4	US-09-621-976-9105	Sequence 9105, Ap	C 519	27	3.1	390	4	US-09-222-575-90	Sequence 90, Appl
447	27	3.1	249	4	US-09-621-976-1322	Sequence 1322, Ap	C 520	27	3.1	390	4	US-09-389-681-90	Sequence 90, Appl
448	27	3.1	249	4	US-09-621-976-16291	Sequence 16291, A	C 521	27	3.1	390	4	US-09-620-405B-90	Sequence 90, Appl
449	27	3.1	249	4	US-09-621-976-16292	Sequence 16292, A	C 522	27	3.1	390	4	US-09-339-338-90	Sequence 90, Appl
450	27	3.1	250	4	US-09-621-976-17371	Sequence 17371, A	C 523	27	3.1	390	4	US-09-433-826B-90	Sequence 90, Appl
451	27	3.1	250	4	US-09-621-976-18893	Sequence 18893, A	C 524	27	3.1	390	4	US-09-604-287A-90	Sequence 90, Appl
452	27	3.1	253	2	US-08-520-678A-25	Sequence 25, Appl	C 525	27	3.1	390	4	US-09-285-480-90	Sequence 90, Appl
C 453	27	3.1	253	2	US-08-897-126-25	Sequence 25, Appl	C 526	27	3.1	390	4	US-09-621-976-15352	Sequence 15352, A
C 454	27	3.1	257	2	US-08-520-678A-24	Sequence 24, Appl	C 527	27	3.1	390	4	US-09-834-759-90	Sequence 90, Appl
C 455	27	3.1	257	3	US-08-897-126-24	Sequence 24, Appl	C 528	27	3.1	394	4	US-09-621-976-15204	Sequence 15204, A
C 456	27	3.1	259	3	US-09-621-976-16294	Sequence 16294, A	C 529	27	3.1	395	4	US-09-195-106-21	Sequence 21, Appl
C 457	27	3.1	260	2	US-08-520-678A-29	Sequence 29, Appl	C 530	27	3.1	396	4	US-09-640-173-20	Sequence 173, Appl
C 458	27	3.1	260	2	US-08-897-126-29	Sequence 29, Appl	C 531	27	3.1	396	4	US-09-640-173-131	Sequence 131, Appl
459	27	3.1	261	4	US-09-621-976-17067	Sequence 17067, A	C 532	27	3.1	396	4	US-09-640-173-140	Sequence 140, Appl
460	27	3.1	266	4	US-09-621-976-16813	Sequence 16813, A	C 533	27	3.1	396	4	US-09-640-173-165	Sequence 165, App
461	27	3.1	267	2	US-08-924-838-3	Sequence 3, Appl1	C 534	27	3.1	396	4	US-09-713-550-20	Sequence 20, Appl
462	27	3.1	267	4	US-09-621-976-14155	Sequence 14155, A	C 535	27	3.1	396	4	US-09-713-550-131	Sequence 131, App
463	27	3.1	269	4	US-09-621-976-14781	Sequence 14781, A	C 536	27	3.1	396	4	US-09-713-550-140	Sequence 140, App
464	27	3.1	270	4	US-09-621-976-17049	Sequence 17049, A	C 537	27	3.1	396	4	US-09-713-550-165	Sequence 165, App
C 465	27	3.1	271	2	US-08-731-272A-29	Sequence 29, Appl	538	27	3.1	399	4	US-09-621-976-9484	Sequence 9484, A

C 539	27	3.1	413	3	US-09-328-111-25	Sequence 25, Appl	612	27	3.1	855	6	5223394-3	Patent No. 5223394
C 540	27	3.1	416	4	US-09-621-975-3320	Sequence 3320, Ap	613	27	3.1	859	2	US-09-347-773-47	Sequence 47, Appl
C 541	27	3.1	450	4	US-09-385-988-155	Sequence 155, App	614	27	3.1	861	2	US-08-524-759-15	Sequence 15, Appl
C 542	27	3.1	464	4	US-09-302-769-37	Sequence 37, Appl	615	27	3.1	861	3	US-09-248-335-15	Sequence 15, Appl
C 543	27	3.1	474	3	US-08-516-859A-97	Sequence 97, Appl	616	27	3.1	863	1	US-07-940-861-11	Sequence 11, Appl
C 544	27	3.1	474	4	US-09-586-472-97	Sequence 97, Appl	617	27	3.1	863	1	US-08-459-512-11	Sequence 11, Appl
C 545	27	3.1	474	4	US-09-528-706-97	Sequence 97, Appl	618	27	3.1	863	2	US-08-459-512-11	Sequence 11, Appl
C 546	27	3.1	495	4	US-09-220-132-186	Sequence 186, App	619	27	3.1	863	5	US-08-460-132-11	Sequence 11, Appl
C 547	27	3.1	504	4	US-09-796-766-11	Sequence 11, Appl	620	27	3.1	863	5	PCT-US92-02050-11	Sequence 11, Appl
C 548	27	3.1	520	4	US-09-220-132-111	Sequence 11, App	621	27	3.1	863	6	5185441-35	Patent No. 5185441
C 549	27	3.1	526	4	US-09-163-748C-2	Sequence 2, Appl1	622	27	3.1	863	6	5223394-5	Patent No. 5223394
C 550	27	3.1	531	4	US-09-105-542A-12	Sequence 12, Appl	623	27	3.1	872	3	US-09-248-335-63	Sequence 63, Appl
C 551	27	3.1	538	4	US-09-399-913-37	Sequence 37, Appl	624	27	3.1	873	3	US-09-475-116A-20	Sequence 20, Appl
C 552	27	3.1	536	1	US-08-341-568-1	Sequence 1, Appl1	625	27	3.1	873	4	US-09-704-640-420	Sequence 40, Appl
C 553	27	3.1	536	2	US-08-911-020-1	Sequence 1, Appl1	626	27	3.1	874	4	US-09-189-681-426	Sequence 426, Appl
C 554	27	3.1	537	4	US-09-720-201A-4	Sequence 4, Appl1	627	27	3.1	874	4	US-09-620-4055-426	Sequence 426, App
C 555	27	3.1	550	4	US-09-010-147B-5	Sequence 5, Appl1	628	27	3.1	874	4	US-09-433-826B-426	Sequence 426, App
C 556	27	3.1	564	4	US-09-702-705-1414	Sequence 1414, Ap	629	27	3.1	874	4	US-09-604-887A-426	Sequence 426, App
C 557	27	3.1	564	4	US-09-736-457-1414	Sequence 1414, Ap	630	27	3.1	874	4	US-09-604-887A-426	Sequence 426, App
C 558	27	3.1	564	4	US-09-614-124B-1414	Sequence 1414, Ap	631	27	3.1	879	1	US-08-158-682A-1	Sequence 1, Appl1
C 559	27	3.1	572	3	US-09-671-325-1414	Sequence 1414, Ap	632	27	3.1	879	1	US-08-015-203-1	Sequence 1, Appl1
C 560	27	3.1	572	3	US-09-328-111-644	Sequence 644, App	633	27	3.1	880	1	US-08-616-368A-7	Sequence 7, Appl1
C 561	27	3.1	572	3	US-09-357-251-7	Sequence 7, Appl1	634	27	3.1	880	3	US-09-054-298-7	Sequence 7, Appl1
C 562	27	3.1	578	3	US-09-385-982-465	Sequence 465, App	635	27	3.1	880	3	US-08-818-658-7	Sequence 7, Appl1
C 563	27	3.1	591	4	US-09-702-705-237	Sequence 237, App	636	27	3.1	880	4	US-09-305-839-7	Sequence 7, Appl1
C 564	27	3.1	591	4	US-09-736-457-237	Sequence 237, App	637	27	3.1	882	2	US-08-909-965C-9	Sequence 9, Appl1
C 565	27	3.1	591	4	US-09-614-124B-237	Sequence 237, App	638	27	3.1	882	4	US-09-188-930-13	Sequence 13, Appl
C 566	27	3.1	591	4	US-09-671-325-237	Sequence 237, App	639	27	3.1	888	4	US-09-612-283C-13	Sequence 13, Appl
C 567	27	3.1	591	4	US-09-589-184-237	Sequence 237, App	640	27	3.1	888	4	US-09-621-976-2725	Sequence 2725, Ap
C 568	27	3.1	599	3	US-09-328-111-147	Sequence 147, App	641	27	3.1	906	4	US-09-489-847-72	Sequence 72, Appl
C 569	27	3.1	603	3	US-09-385-982-251	Sequence 251, App	642	27	3.1	913	3	US-08-651-336C-13	Sequence 13, Appl
C 570	27	3.1	603	3	US-09-385-982-251	Sequence 251, App	643	27	3.1	913	4	US-09-229-911A-13	Sequence 13, Appl
C 571	27	3.1	607	3	US-09-328-111-531	Sequence 293, App	644	27	3.1	917	4	US-09-227-357-43	Sequence 43, Appl
C 572	27	3.1	615	4	US-09-328-111-371	Sequence 371, App	645	27	3.1	940	1	US-08-089-998B-1	Sequence 1, Appl1
C 573	27	3.1	615	4	US-09-105-542A-2	Sequence 2, Appl1	646	27	3.1	940	5	US-08-457-272-1	Sequence 1, Appl1
C 574	27	3.1	619	4	US-09-489-847-58	Sequence 58, Appl	647	27	3.1	940	5	PCT-US94-07595-1	Sequence 1, Appl1
C 575	27	3.1	623	6	5240847-1	Patent No. 5240847	648	27	3.1	944	4	US-09-227-357-122	Sequence 122, App
C 576	27	3.1	631	4	US-09-328-111-361	Sequence 361, App	649	27	3.1	953	1	US-08-137-793-3	Sequence 1, Appl1
C 577	27	3.1	644	4	US-09-720-201A-6	Sequence 6, Appl1	650	27	3.1	953	2	US-08-656-176-1	Sequence 1, Appl1
C 578	27	3.1	666	3	US-09-328-111-587	Sequence 587, App	651	27	3.1	953	5	PCT-US95-01618-1	Sequence 1, Appl1
C 579	27	3.1	669	3	US-09-328-111-342	Sequence 342, App	652	27	3.1	969	2	US-08-365-486A-27	Sequence 27, Appl
C 580	27	3.1	674	4	US-09-673-395A-94	Sequence 94, Appl	653	27	3.1	969	3	US-08-880-342-27	Sequence 27, Appl
C 581	27	3.1	685	4	US-09-489-847-103	Sequence 103, App	654	27	3.1	970	3	US-09-248-335-47	Sequence 47, Appl
C 582	27	3.1	688	4	US-09-148-545-73	Sequence 73, Appl	655	27	3.1	970	4	US-09-833-381-1294	Sequence 1294, Ap
C 583	27	3.1	699	4	US-09-690-454-31	Sequence 31, Appl	656	27	3.1	975	4	US-09-381-488-6	Sequence 6, Appl1
C 584	27	3.1	700	1	US-07-846-992-1	Sequence 1, Appl1	657	27	3.1	997	4	US-09-800-729-14	Sequence 14, Appl
C 585	27	3.1	700	1	US-08-469-555-1	Sequence 1, Appl1	658	27	3.1	999	4	US-09-699-266A-5	Sequence 5, Appl1
C 586	27	3.1	700	1	US-09-152-060-26	Sequence 26, Appl1	659	27	3.1	1007	3	US-09-248-335-31	Sequence 31, Appl
C 587	27	3.1	730	4	US-09-328-475C-283	Sequence 283, App	660	27	3.1	1009	6	5223394-8	Patent No. 5223394
C 588	27	3.1	737	4	US-09-148-545-127	Sequence 127, App	661	27	3.1	1019	4	US-09-288-143-33	Sequence 33, Appl
C 589	27	3.1	756	2	US-08-530-165-1	Sequence 1, Appl1	662	27	3.1	1023	3	US-08-554-385-4	Sequence 4, Appl1
C 590	27	3.1	775	3	US-09-361-434-6	Sequence 6, Appl1	663	27	3.1	1032	4	US-09-257-179-21	Sequence 21, Appl
C 591	27	3.1	775	3	US-09-361-434-8	Sequence 8, Appl1	664	27	3.1	1032	4	US-09-464-535-23	Sequence 23, Appl
C 592	27	3.1	775	4	US-09-635-025-6	Sequence 6, Appl1	665	27	3.1	1047	1	US-08-403-378B-3	Sequence 3, Appl1
C 593	27	3.1	775	4	US-09-635-025-8	Sequence 8, Appl1	666	27	3.1	1052	4	US-09-592-891A-8	Sequence 8, Appl1
C 594	27	3.1	776	4	US-09-902-331B-3	Sequence 3, Appl1	667	27	3.1	1057	4	US-09-716-129-16	Sequence 16, Appl
C 595	27	3.1	776	4	US-09-205-258-201	Sequence 20, App	668	27	3.1	1071	4	US-09-800-729-45	Sequence 45, Appl
C 596	27	3.1	782	4	US-09-621-976-1700	Sequence 1700, Ap	669	27	3.1	1078	6	5223394-10	Patent No. 5223394
C 597	27	3.1	790	4	US-09-363-970-4	Sequence 4, Appl1	670	27	3.1	1086	4	US-09-800-729-48	Sequence 48, Appl
C 598	27	3.1	813	4	US-09-308-386A-2	Sequence 2, Appl1	671	27	3.1	1097	4	US-09-461-325-84	Sequence 84, Appl
C 599	27	3.1	825	4	US-09-280-839-1	Sequence 1, Appl1	672	27	3.1	1097	4	US-10-012-542-84	Sequence 84, Appl
C 600	27	3.1	832	4	US-09-152-060-27	Sequence 27, Appl1	673	27	3.1	1109	4	US-09-372-422A-47	Sequence 47, Appl
C 601	27	3.1	836	2	US-08-698-805-7	Sequence 7, Appl1	674	27	3.1	1106	3	US-09-361-434-16	Sequence 16, Appl
C 602	27	3.1	841	3	US-09-004-731-40	Sequence 40, Appl	675	27	3.1	1106	3	US-09-361-434-18	Sequence 18, Appl
C 603	27	3.1	841	3	US-09-004-731-42	Sequence 42, Appl	676	27	3.1	1106	4	US-09-635-025-16	Sequence 16, Appl
C 604	27	3.1	841	3	US-09-032-215-46	Sequence 46, Appl	677	27	3.1	1106	4	US-09-635-025-16	Sequence 16, Appl
C 605	27	3.1	841	3	US-09-032-215-48	Sequence 48, Appl	678	27	3.1	1113	2	US-08-907-492A-13	Sequence 13, Appl1
C 606	27	3.1	841	3	US-08-749-699-40	Sequence 40, Appl	679	27	3.1	1115	3	US-08-190-802A-19	Sequence 19, Appl
C 607	27	3.1	841	3	US-08-749-699-42	Sequence 42, Appl	680	27	3.1	1115	3	US-08-477-346-19	Sequence 19, Appl
C 608	27	3.1	841	4	US-09-004-729-40	Sequence 40, Appl	681	27	3.1	1115	4	US-08-473-089-19	Sequence 19, Appl
C 609	27	3.1	847	4	US-09-004-729-42	Sequence 42, Appl	682	27	3.1	1117	4	US-08-487-072A-19	Sequence 19, Appl
C 610	27	3.1	847	4	US-09-149-476-205	Sequence 205, App	683	27	3.1	1117	4	US-09-148-545-54	Sequence 54, Appl
C 611	27	3.1	855	6	5185441-40	Patent No. 5185441	684	27	3.1	1124	4	US-09-386-149-11	Sequence 11, Appl

685	27	3.1	1127	4	US-09-391-741A-1	Sequence 1, Appl	758	27	3.1	1197	4	US-09-216-393B-345	Sequence 345, App
686	27	3.1	1127	4	US-09-391-741A-15	Sequence 15, Appl	759	27	3.1	1104	4	US-09-205-258-223	Sequence 223, App
687	27	3.1	1127	4	US-09-391-741A-25	Sequence 25, Appl	760	27	3.1	1408	1	US-08-254-404-21	Sequence 21, Appl
688	27	3.1	1133	3	US-08-983-409-5	Sequence 5, Appl	761	27	3.1	1408	2	US-08-327-451E-71	Sequence 21, Appl
689	27	3.1	1134	4	US-09-483-273-95	Sequence 95, Appl	762	27	3.1	1408	2	US-08-458-109-21	Sequence 27, Appl
690	27	3.1	1138	4	US-09-800-729-44	Sequence 44, Appl	763	27	3.1	1447	2	US-09-443-041A-27	Sequence 27, Appl
691	27	3.1	1143	4	US-09-220-132-166	Sequence 166, App	764	27	3.1	1454	2	US-08-713-000-7	Sequence 7, Appl
692	27	3.1	1147	1	US-08-665-716-1	Sequence 1, Appl	765	27	3.1	1454	2	US-08-973-316-7	Sequence 7, Appl
693	27	3.1	1149	4	US-09-800-729-47	Sequence 47, Appl	766	27	3.1	1454	4	US-09-211-710-7	Sequence 7, Appl
694	27	3.1	1153	4	US-09-372-448A-5	Sequence 5, Appl	767	27	3.1	1454	4	US-09-615-192A-7	Sequence 7, Appl
695	27	3.1	1153	4	US-09-149-476-41	Sequence 41, Appl	768	27	3.1	1454	4	US-09-169-789-7	Sequence 95, Appl
696	27	3.1	1172	4	US-09-461-325-106	Sequence 106, App	769	27	3.1	1460	4	US-09-615-192A-35	Sequence 95, Appl
697	27	3.1	1172	4	US-10-013-542-106	Sequence 106, App	770	27	3.1	1460	4	US-09-169-789-95	Sequence 95, Appl
698	27	3.1	1175	4	US-09-461-325-15	Sequence 15, Appl	771	27	3.1	1474	2	US-08-975-316-71	Sequence 71, Appl
699	27	3.1	1175	4	US-10-013-542-15	Sequence 15, Appl	772	27	3.1	1474	4	US-09-615-192A-71	Sequence 71, Appl
700	27	3.1	1179	4	US-09-149-476-267	Sequence 267, App	773	27	3.1	1474	4	US-09-615-192A-702	Sequence 402, App
701	27	3.1	1181	3	US-09-328-796-2	Sequence 2, Appl	774	27	3.1	1474	4	US-09-328-932A-102	Sequence 202, App
702	27	3.1	1192	4	US-09-439-554-23	Sequence 23, Appl	775	27	3.1	1474	4	US-09-169-789-71	Sequence 71, Appl
703	27	3.1	1193	4	US-09-372-442A-23	Sequence 23, Appl	776	27	3.1	1474	4	US-09-169-789-184	Sequence 184, App
704	27	3.1	1208	4	US-09-205-258-25	Sequence 25, Appl	777	27	3.1	1477	4	US-09-585-173B-7	Sequence 7, Appl
705	27	3.1	1215	1	US-08-593-214A-1	Sequence 1, Appl	778	27	3.1	1493	6	5340934-5	Parent No. 5340934
706	27	3.1	1215	3	US-09-148-976-1	Sequence 1, Appl	779	27	3.1	1500	5	PCT-US93-08386-3	Sequence 3, Appl
707	27	3.1	1215	4	US-09-220-132-184	Sequence 184, App	780	27	3.1	1503	4	US-09-907-794A-220	Sequence 220, App
708	27	3.1	1216	4	US-09-533-029-121	Sequence 121, App	781	27	3.1	1503	4	US-09-905-125A-220	Sequence 220, App
709	27	3.1	1217	3	US-09-225-244-1	Sequence 1, Appl	782	27	3.1	1503	4	US-09-902-775A-220	Sequence 220, App
710	27	3.1	1217	3	US-09-417-242-1	Sequence 1, Appl	783	27	3.1	1511	2	US-08-809-763-3	Sequence 3, Appl
711	27	3.1	1227	2	US-08-903-851-1	Sequence 1, Appl	784	27	3.1	1511	3	US-08-956-253-3	Sequence 3, Appl
712	27	3.1	1236	1	US-09-694-094-2	Sequence 2, Appl	785	27	3.1	1513	4	US-09-301-666A-9	Sequence 9, Appl
713	27	3.1	1240	1	US-08-388-756-1	Sequence 1, Appl	786	27	3.1	1513	4	US-09-301-217-9	Sequence 9, Appl
714	27	3.1	1240	2	US-08-748-428-1	Sequence 1, Appl	787	27	3.1	1527	4	US-09-244-111-7	Sequence 7, Appl
715	27	3.1	1243	1	US-08-178-606-1	Sequence 1, Appl	788	27	3.1	1536	4	US-09-082-358B-1	Sequence 1, Appl
716	27	3.1	1243	1	US-08-314-309A-24	Sequence 24, Appl	789	27	3.1	1537	2	US-08-839-008-1	Sequence 1, Appl
717	27	3.1	1263	1	US-08-140-797-1	Sequence 1, Appl	790	27	3.1	1541	4	US-09-149-476-65	Sequence 65, Appl
718	27	3.1	1267	4	US-08-466-670A-1	Sequence 1, Appl	791	27	3.1	1544	4	US-09-187-999-14	Sequence 14, Appl
719	27	3.1	1276	1	US-09-716-129-40	Sequence 40, Appl	792	27	3.1	1558	1	US-08-467-607-2	Sequence 2, Appl
720	27	3.1	1279	3	US-09-248-335-25	Sequence 25, Appl	793	27	3.1	1558	2	US-08-468-362-2	Sequence 2, Appl
721	27	3.1	1280	4	US-09-369-247-40	Sequence 40, Appl	794	27	3.1	1558	2	US-08-850-332-2	Sequence 2, Appl
722	27	3.1	1293	1	US-08-317-522A-6	Sequence 6, Appl	795	27	3.1	1559	2	US-08-417-174-1	Sequence 1, Appl
723	27	3.1	1293	1	US-08-439-818A-6	Sequence 6, Appl	796	27	3.1	1559	2	US-08-231-565A-1	Sequence 1, Appl
724	27	3.1	1293	2	US-08-751-965-6	Sequence 6, Appl	797	27	3.1	1559	2	US-09-007-961-1	Sequence 1, Appl
725	27	3.1	1293	2	US-08-728-975-6	Sequence 6, Appl	798	27	3.1	1559	3	US-09-267-439-1	Sequence 1, Appl
726	27	3.1	1293	2	US-08-728-636-6	Sequence 6, Appl	799	27	3.1	1559	4	US-09-073-138-1	Sequence 1, Appl
727	27	3.1	1293	2	US-08-808-559A-6	Sequence 6, Appl	800	27	3.1	1562	1	US-08-330-108-1	Sequence 1, Appl
728	27	3.1	1296	1	US-08-385-151A-1	Sequence 1, Appl	801	27	3.1	1562	5	PCT-US92-10087-1	Sequence 1, Appl
729	27	3.1	1296	1	US-08-472-402A-1	Sequence 1, Appl	802	27	3.1	1573	4	US-09-216-333B-292	Sequence 292, App
730	27	3.1	1298	1	US-08-361-708-1	Sequence 1, Appl	803	27	3.1	1573	4	US-09-216-333B-294	Sequence 294, App
731	27	3.1	1298	1	US-08-536-277-1	Sequence 1, Appl	804	27	3.1	1584	1	US-08-483-432-24	Sequence 24, Appl
732	27	3.1	1300	4	US-09-419-679-7	Sequence 7, Appl	805	27	3.1	1584	1	US-08-483-432-24	Sequence 24, Appl
733	27	3.1	1302	4	US-09-322-409-91	Sequence 91, Appl	806	27	3.1	1584	1	US-08-745-995A-1	Sequence 1, Appl
734	27	3.1	1302	4	US-09-322-409-93	Sequence 93, Appl	807	27	3.1	1584	4	US-08-745-995A-3	Sequence 3, Appl
735	27	3.1	1302	4	US-09-451-527-91	Sequence 91, Appl	808	27	3.1	1584	4	US-09-005-352-1	Sequence 1, Appl
736	27	3.1	1302	4	US-09-451-527-93	Sequence 93, Appl	809	27	3.1	1584	4	US-09-005-352-1	Sequence 1, Appl
737	27	3.1	1315	3	US-09-164-193-1	Sequence 1, Appl	810	27	3.1	1584	4	US-09-005-352-1	Sequence 1, Appl
738	27	3.1	1315	3	US-09-221-448A-1	Sequence 1, Appl	811	27	3.1	1587	4	US-09-724-864-5	Sequence 5, Appl
739	27	3.1	1325	1	US-08-306-691B-51	Sequence 51, Appl	812	27	3.1	1595	4	US-09-724-864-5	Sequence 13, Appl
740	27	3.1	1325	1	US-08-464-517-1	Sequence 1, Appl	813	27	3.1	1606	4	US-09-820-004-1	Sequence 1, Appl
741	27	3.1	1325	2	US-08-246-351A-1	Sequence 1, Appl	814	27	3.1	1619	4	US-09-522-714-11	Sequence 11, Appl
742	27	3.1	1325	3	US-08-463-772-1	Sequence 1, Appl	815	27	3.1	1630	4	US-10-162-012-39	Sequence 39, Appl
743	27	3.1	1325	3	US-09-412-102-3	Sequence 3, Appl	816	27	3.1	1652	4	US-09-627-650B-2	Sequence 2, Appl
744	27	3.1	1325	3	US-09-217-787-3	Sequence 3, Appl	817	27	3.1	1652	4	US-09-436-063C-2	Sequence 2, Appl
745	27	3.1	1325	5	PCT-US93-05000-1	Sequence 1, Appl	818	27	3.1	1654	4	US-08-991-426-3	Sequence 3, Appl
746	27	3.1	1335	4	US-09-482-273-80	Sequence 80, Appl	819	27	3.1	1654	3	US-09-147-470-3	Sequence 3, Appl
747	27	3.1	1342	4	US-09-500-569-9	Sequence 9, Appl	820	27	3.1	1654	4	US-08-648-006A-3	Sequence 3, Appl
748	27	3.1	1342	4	US-09-971-823B-9	Sequence 9, Appl	821	27	3.1	1654	4	US-09-771-023-3	Sequence 3, Appl
749	27	3.1	1354	4	US-09-097-319A-5	Sequence 5, Appl	822	27	3.1	1687	1	US-08-143-219-26	Sequence 26, Appl
750	27	3.1	1354	4	US-09-614-912-37	Sequence 37, Appl	823	27	3.1	1688	2	US-08-433-814-2	Sequence 2, Appl
751	27	3.1	1375	4	US-09-372-422A-37	Sequence 37, Appl	824	27	3.1	1699	4	US-09-153-060-19	Sequence 19, Appl
752	27	3.1	1377	3	US-09-461-474-5	Sequence 5, Appl	825	27	3.1	1700	4	US-09-833-381-1885	Sequence 1885, App
753	27	3.1	1378	4	US-09-149-476-208	Sequence 208, App	826	27	3.1	1703	2	US-08-794-795-1	Sequence 1, Appl
754	27	3.1	1384	4	US-09-227-357-142	Sequence 142, App	827	27	3.1	1703	4	US-09-248-200-1	Sequence 1, Appl
755	27	3.1	1393	1	US-08-174-467-18	Sequence 18, Appl	828	27	3.1	1713	4	US-09-000-062-1	Sequence 1, Appl
756	27	3.1	1393	3	US-08-452-071-18	Sequence 18, Appl	829	27	3.1	1713	4	US-08-945-144A-1	Sequence 1, Appl
757	27	3.1	1397	4	US-09-216-393B-343	Sequence 343, App	830	27	3.1	1716	2	US-08-954-333-3	Sequence 9, Appl

831	27	3.1	1721	5	PCT-US96-00994-3	Sequence 21, Appl	904	27	3.1	1941	4	US-09-468-702-2	Sequence 21, Appl
832	27	3.1	1761	4	US-09-369-247-21	Sequence 21, Appl	905	27	3.1	1945	4	US-09-149-476-164	Sequence 164, App
833	27	3.1	1766	1	US-07-991-587A-6	Sequence 6, Appl	906	27	3.1	1958	4	US-08-665-034A-3	Sequence 3, Appl
834	27	3.1	1766	4	US-08-309-985-6	Sequence 6, Appl	907	27	3.1	1964	4	US-09-434-613-2	Sequence 2, Appl
835	27	3.1	1766	4	US-09-904-615-29	Sequence 29, Appl	908	27	3.1	1969	1	US-07-937-609-28	Sequence 28, Appl
836	27	3.1	1772	2	US-08-960-022-13	Sequence 13, Appl	909	27	3.1	1969	3	US-08-029-170-28	Sequence 28, Appl
837	27	3.1	1780	4	US-09-202-548B-5	Sequence 5, Appl	910	27	3.1	1969	4	US-09-148-545-107	Sequence 107, App
838	27	3.1	1780	4	US-09-942-858-5	Sequence 5, Appl	911	27	3.1	1974	4	US-08-413-135-3	Sequence 3, Appl
839	27	3.1	1790	4	US-09-865-028-31	Sequence 31, Appl	912	27	3.1	1974	4	US-08-971-395-3	Sequence 3, Appl
840	27	3.1	1797	4	US-09-482-273-69	Sequence 69, Appl	913	27	3.1	1977	4	US-09-614-912-143	Sequence 143, App
841	27	3.1	1804	2	US-08-504-459-5	Sequence 5, Appl	914	27	3.1	1985	4	US-09-205-258-97	Sequence 97, Appl
842	27	3.1	1813	5	PCT-US94-12883-3	Sequence 3, Appl	915	27	3.1	2013	4	US-09-596-196-3	Sequence 3, Appl
843	27	3.1	1816	4	US-09-149-476-167	Sequence 167, App	916	27	3.1	2020	4	US-09-716-129-29	Sequence 29, Appl
844	27	3.1	1825	3	US-09-461-697-75	Sequence 75, Appl	917	27	3.1	2030	4	US-09-347-650-3	Sequence 3, Appl
845	27	3.1	1828	4	US-09-310-363C-5	Sequence 5, Appl	918	27	3.1	2061	4	US-09-800-960-1	Sequence 1, Appl
846	27	3.1	1843	4	US-09-328-925-49	Sequence 49, Appl	919	27	3.1	2061	4	US-10-096-960-1	Sequence 1, Appl
847	27	3.1	1848	4	US-09-205-238-18	Sequence 18, App	920	27	3.1	2071	4	US-09-816-088-1	Sequence 1, Appl
848	27	3.1	1866	4	US-09-224-048A-1	Sequence 1, Appl	921	27	3.1	2071	4	US-09-956-993-1	Sequence 1, Appl
849	27	3.1	1866	4	US-09-673-395A-24	Sequence 24, Appl	922	27	3.1	2075	4	US-09-966-993-1	Sequence 962, App
850	27	3.1	1868	3	US-08-392-367B-1	Sequence 1, Appl	923	27	3.1	2091	2	US-08-439-814-1	Sequence 1, Appl
851	27	3.1	1868	3	US-08-893-467A-1	Sequence 1, Appl	924	27	3.1	2091	4	US-09-813-818-1	Sequence 1, Appl
852	27	3.1	1873	1	US-07-841-646-24	Sequence 24, Appl	925	27	3.1	2096	3	US-09-008-481A-10	Sequence 10, Appl
853	27	3.1	1873	1	US-07-901-703-8	Sequence 8, Appl	926	27	3.1	2096	3	US-09-195-666A-16	Sequence 16, Appl
854	27	3.1	1873	1	US-08-147-023-24	Sequence 24, Appl	927	27	3.1	2096	3	US-09-309-592-10	Sequence 10, Appl
855	27	3.1	1873	1	US-08-278-729A-18	Sequence 18, Appl	928	27	3.1	2096	4	US-09-635-705-16	Sequence 16, Appl
856	27	3.1	1873	1	US-08-480-528A-5	Sequence 5, Appl	929	27	3.1	2096	4	US-09-634-858A-16	Sequence 16, Appl
857	27	3.1	1873	1	US-08-479-666-5	Sequence 5, Appl	930	27	3.1	2096	4	US-08-869-927C-16	Sequence 16, Appl
858	27	3.1	1873	1	US-08-155-343A-18	Sequence 18, Appl	931	27	3.1	2143	4	US-09-881-578A-3	Sequence 3, Appl
859	27	3.1	1873	1	US-08-406-672-18	Sequence 18, Appl	932	27	3.1	2152	1	US-07-779-890-1	Sequence 1, Appl
860	27	3.1	1873	1	US-08-643-563A-18	Sequence 18, Appl	933	27	3.1	2152	1	US-07-779-890-1	Sequence 1, Appl
861	27	3.1	1873	1	US-08-447-570-24	Sequence 24, Appl	934	27	3.1	2152	5	PCT-US93-05640-1	Sequence 1, Appl
862	27	3.1	1873	1	US-08-643-763A-18	Sequence 18, Appl	935	27	3.1	2173	2	US-08-036-624-1	Sequence 6, Appl
863	27	3.1	1873	1	US-08-462-623-18	Sequence 18, Appl	936	27	3.1	2173	4	US-08-449-610-6	Sequence 6, Appl
864	27	3.1	1873	1	US-08-451-953A-18	Sequence 18, Appl	937	27	3.1	2173	4	US-09-361-096A-6	Sequence 6, Appl
865	27	3.1	1873	2	US-08-459-346-3	Sequence 3, Appl	938	27	3.1	2187	4	US-09-302-769-7	Sequence 7, Appl
866	27	3.1	1873	2	US-08-445-468A-18	Sequence 18, Appl	939	27	3.1	2205	4	US-08-888-077A-41	Sequence 41, Appl
867	27	3.1	1873	2	US-08-901-200A-5	Sequence 5, Appl	940	27	3.1	2218	4	US-09-016-437A-1157	Sequence 1157, App
868	27	3.1	1873	2	US-08-449-700-24	Sequence 24, Appl	941	27	3.1	2223	1	US-08-286-624-1	Sequence 1, Appl
869	27	3.1	1873	2	US-08-449-699A-4	Sequence 4, Appl	942	27	3.1	2231	4	US-08-496-631-1	Sequence 1, Appl
870	27	3.1	1873	2	US-08-461-397A-18	Sequence 18, Appl	943	27	3.1	2241	4	US-09-673-395A-133	Sequence 133, Appl
871	27	3.1	1873	3	US-08-912-088-18	Sequence 18, Appl	944	27	3.1	2264	4	US-09-833-381-883	Sequence 883, App
872	27	3.1	1873	3	US-08-278-730A-18	Sequence 18, Appl	945	27	3.1	2264	4	US-09-394-645-1	Sequence 1, Appl
873	27	3.1	1873	3	US-08-889-419-3	Sequence 3, Appl	946	27	3.1	2269	4	US-09-243-650B-1	Sequence 1, Appl
874	27	3.1	1873	3	US-08-445-467-18	Sequence 18, Appl	947	27	3.1	2274	4	US-09-220-132-188	Sequence 188, App
875	27	3.1	1873	3	US-08-480-515A-18	Sequence 18, Appl	948	27	3.1	2285	2	US-08-967-101-136	Sequence 136, App
876	27	3.1	1873	3	US-09-219-391-5	Sequence 5, Appl	949	27	3.1	2285	3	US-08-592-541-136	Sequence 136, App
877	27	3.1	1873	4	US-09-170-936-18	Sequence 18, Appl	950	27	3.1	2285	2	US-09-124-698-136	Sequence 136, App
878	27	3.1	1873	4	US-08-402-542-3	Sequence 3, Appl	951	27	3.1	2285	4	US-09-127-480-136	Sequence 136, App
879	27	3.1	1873	4	US-08-461-113-18	Sequence 18, Appl	952	27	3.1	2285	4	US-09-124-523-136	Sequence 136, App
880	27	3.1	1873	4	US-08-456-031-18	Sequence 18, Appl	953	27	3.1	2285	4	US-09-656-796A-136	Sequence 136, App
881	27	3.1	1873	4	US-08-643-321-17	Sequence 17, Appl	954	27	3.1	2291	4	US-09-220-132-114	Sequence 114, App
882	27	3.1	1873	4	US-09-464-206-15	Sequence 15, Appl	955	27	3.1	2309	1	US-08-036-210-10	Sequence 10, Appl
883	27	3.1	1873	4	US-09-148-925C-24	Sequence 24, Appl	956	27	3.1	2309	2	US-08-449-609-9	Sequence 9, Appl
884	27	3.1	1873	4	US-08-404-113A-15	Sequence 15, Appl	957	27	3.1	2309	4	US-09-026-001A-13	Sequence 13, Appl
885	27	3.1	1873	5	US-08-957-425-24	Sequence 24, Appl	958	27	3.1	2309	4	US-09-361-096A-10	Sequence 10, Appl
886	27	3.1	1873	5	PCT-US90-07654-1	Sequence 1, Appl	959	27	3.1	2330	4	US-09-016-434-1054	Sequence 1054, Ap
887	27	3.1	1873	5	PCT-US92-01968-18	Sequence 18, Appl	960	27	3.1	2333	4	US-09-149-476-24	Sequence 24, Appl
888	27	3.1	1873	5	PCT-US93-05446-8	Sequence 8, Appl	961	27	3.1	2360	1	US-08-145-681-1	Sequence 1, Appl
889	27	3.1	1873	5	PCT-US93-07189-3	Sequence 3, Appl	962	27	3.1	2360	1	US-08-250-308-1	Sequence 1, Appl
890	27	3.1	1873	5	PCT-US93-07190-18	Sequence 18, Appl	963	27	3.1	2360	1	US-08-453-703-3	Sequence 1, Appl
891	27	3.1	1873	5	PCT-US93-07231-18	Sequence 18, Appl	964	27	3.1	2360	2	US-08-456-106-1	Sequence 1, Appl
892	27	3.1	1873	5	PCT-US93-08742-18	Sequence 18, Appl	965	27	3.1	2360	3	US-08-456-108-1	Sequence 1, Appl
893	27	3.1	1873	5	PCT-US93-08808-18	Sequence 18, Appl	966	27	3.1	2360	3	US-08-856-567-9	Sequence 9, Appl
894	27	3.1	1873	5	PCT-US93-08885-18	Sequence 18, Appl	967	27	3.1	2360	3	US-09-265-577-1	Sequence 1, Appl
895	27	3.1	1873	5	PCT-US93-10520-5	Sequence 5, Appl	968	27	3.1	2360	4	US-09-606-304-9	Sequence 9, Appl
896	27	3.1	1889	4	US-09-675-018B-9	Sequence 9, Appl	969	27	3.1	2360	4	US-09-633-739-1	Sequence 1, Appl
897	27	3.1	1898	1	US-08-342-411A-1	Sequence 1, Appl	970	27	3.1	2360	5	PCT-US93-03614-1	Sequence 1, Appl
898	27	3.1	1908	2	US-08-909-965C-17	Sequence 17, Appl	971	27	3.1	2401	4	US-09-724-864-1	Sequence 1, Appl
899	27	3.1	1910	3	US-08-974-691-7	Sequence 7, Appl	972	27	3.1	2406	4	US-09-594-506-37	Sequence 37, Appl
900	27	3.1	1932	4	US-09-518-386B-2	Sequence 2, Appl	973	27	3.1	2407	4	US-09-370-807-7	Sequence 7, Appl
901	27	3.1	1941	4	US-09-920-759-3	Sequence 3, Appl	974	27	3.1	2427	4	US-09-921-259-7	Sequence 7, Appl
902	27	3.1	1941	4	US-09-008-960-2	Sequence 2, Appl	975	27	3.1	2431	1	US-09-833-381-1993	Sequence 1993, Ap
903	27	3.1	1941	3	US-09-368-240-2	Sequence 2, Appl	976	27	3.1	2431	1	US-07-847-743B-25	Sequence 25, Appl

977 27 3.1 2431 1 US-08-456-201-25 Sequence 25, Appl  
978 27 3.1 2431 2 US-08-456-241-25 Sequence 25, Appl  
979 27 3.1 2431 5 PCT-US92-04295A-25 Sequence 25, Appl  
980 27 3.1 2444 3 US-08-906-791-1 Sequence 1, Appl  
981 27 3.1 2454 4 US-08-890-615-1 Sequence 1, Appl  
982 27 3.1 2454 4 US-09-246-290A-1 Sequence 1, Appl  
983 27 3.1 2469 3 US-09-111-730-5 Sequence 5, Appl  
984 27 3.1 2469 4 US-09-848-334-1 Sequence 1, Appl  
985 27 3.1 2469 4 US-10-274-878-1 Sequence 1, Appl  
986 27 3.1 2481 2 US-08-630-118A-1 Sequence 1, Appl  
987 27 3.1 2481 2 US-08-838-399-1 Sequence 1, Appl  
988 27 3.1 2481 4 US-09-235-839-1 Sequence 1, Appl  
989 27 3.1 2481 4 US-09-327-035-1 Sequence 1, Appl  
990 27 3.1 2485 4 US-09-889-463A-9 Sequence 9, Appl  
991 27 3.1 2524 1 US-08-317-522A-1 Sequence 1, Appl  
992 27 3.1 2524 1 US-08-433-818A-1 Sequence 1, Appl  
993 27 3.1 2524 2 US-08-751-965-1 Sequence 1, Appl  
994 27 3.1 2524 2 US-08-738-975-1 Sequence 1, Appl  
995 27 3.1 2524 2 US-08-728-626-1 Sequence 1, Appl  
996 27 3.1 2524 3 US-08-808-599A-1 Sequence 1, Appl  
997 27 3.1 2535 4 US-09-672-749-10 Sequence 10, Appl  
998 27 3.1 2550 1 US-08-245-295-10 Sequence 10, Appl  
999 27 3.1 2550 1 US-08-481-130-10 Sequence 10, Appl  
1000 27 3.1 2550 1 US-08-656-984A-10 Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-448-606-5  
; Sequence 5, Application US/08448606  
; Patent No. 5721114  
; GENERAL INFORMATION:  
; APPLICANT: Abrahams n, Lars  
; APPLICANT: Kalden n, Christina  
; APPLICANT: Lake, Mats  
; APPLICANT: Mikaelsson, sa  
; APPLICANT: Seilitz, Torsten  
; TITLE OF INVENTION: Expression System For Producing  
; TITLE OF INVENTION: Apolipoprotein AI-M  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pollock, Vande Sande & Priddy  
; STREET: 1990 M Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,606  
; FILING DATE: 25-AUG-1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE93/01061  
; FILING DATE: 09-DEC-1993  
; PRIOR APPLICATION DATA: SE 9203753-0  
; FILING DATE: 11-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amernick, Burton A.  
; REGISTRATION NUMBER: 24,852  
; REFERENCE/DOCKET NUMBER: 0151/00121  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)331-7111  
; TELEFAX: (202) 293-6229  
; INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 964 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 117..847  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 54..116  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 54..847  
US-08-448-606-5  
Query Match 3.6%; Score 31; DB 1; Length 964;  
Best Local Similarity 100.0%; Pred. No. 0.00047;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 838 GTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868  
DB 899 GTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 929

RESULT 2  
US-09-336-643A-29  
; Sequence 29, Application US/09336643A  
; Patent No. 639761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.  
; APPLICANT: Curran, Mark Edward  
; APPLICANT: Hu, Ping  
; APPLICANT: Rutler, Marc  
; APPLICANT: Wang, Jian-Wang  
; TITLE OF INVENTION: No. 639761e1 Human Potassium Channels  
; FILE REFERENCE: SEQ-15P  
; CURRENT APPLICATION NUMBER: US/09/336,643A  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: 60/076,687  
; PRIOR FILING DATE: 1998-08-07  
; PRIOR APPLICATION NUMBER: 60/116,448  
; PRIOR FILING DATE: 1998-01-19  
; PRIOR APPLICATION NUMBER: PCT/US99/03826  
; PRIOR FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 1111  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (297)...(957)  
; OTHER INFORMATION: K-hov44, splice 2  
US-09-336-643A-29  
Query Match 3.6%; Score 31; DB 4; Length 1111;  
Best Local Similarity 100.0%; Pred. No. 0.00046;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 837 TGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 867  
DB 1081 TGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1111  
RESULT 3  
US-09-336-643A-28  
; Sequence 28, Application US/09336643A  
; Patent No. 639761  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Andrew P.

```
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Ruteer, Marc
APPLICANT: Wang, Jian-Wang
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION NUMBER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1246
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (432)...(1092)
OTHER INFORMATION: K+hov44, splice 1
US-09-336-643A-28
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 837 TGTGGGAAAAAAAAAAAAAAAAAAAAA 867
DB 1216 TGTGGGAAAAAAAAAAAAAAAAAAAAA 1246
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RESULT 4
US-09-621-976-16516
Sequence 16516, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16516
LENGTH: 197
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16516
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 165 TGGGAAAAAAAAAAAAAAAAAAAAA 194
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RESULT 5
US-09-621-976-16515
Sequence 16515, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
```

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FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 16515
LENGTH: 198
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-16515
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 839 TGGGAAAAAAAAAAAAAAAAAAAAA 868
DB 165 TGGGAAAAAAAAAAAAAAAAAAAAA 194
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RESULT 6
US-09-621-976-2738
Sequence 2738, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2738
LENGTH: 451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 13..162
US-09-621-976-2738
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 839 TGGGAAAAAAAAAAAAAAAAAAAAA 868
DB 410 TGGGAAAAAAAAAAAAAAAAAAAAA 439
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RESULT 7
US-09-342-653-5
Sequence 5, Application US/09342653
Patent No. 6306632
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Chromatin Associated Proteins
FILE REFERENCE: BB-1118
CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,841
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 572
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-342-653-5
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Query Match 3.5%; Score 30; DB 4; Length 572;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868  
DB 470 TGGGAAAAAAAAAAAAAAAAAAAA 499

RESULT 8  
US-08-225-757B-1  
Sequence 1, Application US/08225757B  
Patent No. 5506133  
GENERAL INFORMATION:  
APPLICANT: YU, ET AL.  
TITLE OF INVENTION: Superoxide Dismutase-4  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,757B  
FILING DATE: 11 APR-94  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-106  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1080 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
US-08-225-757B-1

Query Match 3.5%; Score 30; DB 1; Length 1080;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868  
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAA 1071

RESULT 9  
US-08-722-050-1  
Sequence 1, Application US/08722050  
Patent No. 5871729  
GENERAL INFORMATION:  
APPLICANT: YU, GUO-LIANG  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: ROSEN, CLAIRE M.  
APPLICANT: COCCAYNE, JEANNINE D.  
TITLE OF INVENTION: SUPEROXIDE DISMUTASE-4  
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,050  
FILING DATE: 23-JAN-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/225,757  
FILING DATE: 11-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFF, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1020001/EKS/AJK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1080 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (CDNA)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 115..879  
US-08-722-050-1

Query Match 3.5%; Score 30; DB 2; Length 1080;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAA 868  
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAA 1071

RESULT 10  
US-09-883-985-1  
Sequence 1, Application US/09883985  
Patent No. 6635252  
GENERAL INFORMATION:  
APPLICANT: YU, GUO-LIANG  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: FRASER, CLAIRE M.  
APPLICANT: COCCAYNE, JEANNINE D.  
TITLE OF INVENTION: SUPEROXIDE DISMUTASE-4  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,985  
FILING DATE: 20-Jan-2001

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 09/203,607
  FILING DATE: 02-DEC-1998
  APPLICATION NUMBER: US 08/722,050
  FILING DATE: 23-JAN-1997
  APPLICATION NUMBER: US 08/225,757
  FILING DATE: 11-APR-1994
ATTORNEY/AGENT INFORMATION:
  NAME: STEFFE, ERIC K.
  REGISTRATION NUMBER: 36,688
  REFERENCE/DOCKET NUMBER: 1488.1020003
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1080 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
  NAME/KEY: CDS
  LOCATION: 115..879
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-883-985-1

Query Match
Best Local Similarity 100.0%; Score 30; DB 4; Length 1080;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868
DB 1042 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1071

RESULT 11
US-09-501-115-19
  Sequence 19, Application US/09501115
  Patent No. 6552249
  GENERAL INFORMATION:
    APPLICANT: Caloon, Rebecca E.
    APPLICANT: Fader, Gary M.
    APPLICANT: Rafalski, Antoni
    TITLE OF INVENTION: Plant Cinnamyl-Alcohol Dehydrogenase Homologs
    FILE REFERENCE: B01328 US NA
    CURRENT APPLICATION NUMBER: US/09/501,115
    EARLIER FILING DATE: 2000-02-09
    EARLIER APPLICATION NUMBER: 60/119,585
    NUMBER OF SEQ ID NOS: 48
    SOFTWARE: Microsoft Office 97
    SEQ ID NO: 19
    LENGTH: 1310
    TYPE: DNA
    ORGANISM: Glycine max
US-09-501-115-19

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Best Local Similarity 100.0%; Score 30; DB 4; Length 1310;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868
DB 1272 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1301

RESULT 12
US-08-964-127-5
  Sequence 5, Application US/08964127
  Patent No. 6277565
  GENERAL INFORMATION:

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  APPLICANT: Grandearl, Andrew David John
  TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
  TITLE OF INVENTION: MOLECULES
  NUMBER OF SEQUENCES: 17
  CORRESPONDENCE ADDRESS:
    ADDRESSER: Fish & Richardson P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02110-2804
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
  OPERATING SYSTEM: Windows 95
  SOFTWARE: FASTSEQ for Windows Version 2.0b
  CURRENT APPLICATION DATA:
    FILING DATE: 06-NOV-1997
    APPLICATION NUMBER:
    FILING DATE:
    FILING DATE: 06-NOV-1997
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
    ATTORNEY/AGENT INFORMATION:
      NAME: Crews, Ph.D., L. Lee
      REGISTRATION NUMBER: P-43,567
      REFERENCE/DOCKET NUMBER: 07334/038001
      TELEPHONE: 617/542-5070
      TELEFAX: 617/542-8906
      TELEX: 200154
    INFORMATION FOR SEQ ID NO: 5:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 1411 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      FEATURE:
        NAME/KEY: Coding Sequence
        LOCATION: 1...966
US-08-964-127-5

Query Match
Best Local Similarity 100.0%; Score 30; DB 3; Length 1411;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 839 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868
DB 1309 TGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1338

RESULT 13
US-09-496-692-5
  Sequence 5, Application US/09496692
  Patent No. 6313271
  GENERAL INFORMATION:
    APPLICANT: Grandearl, Andrew David John
    TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
    TITLE OF INVENTION: MOLECULES
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
      ADDRESSER: Fish & Richardson P.C.
      STREET: 225 Franklin Street
      CITY: Boston
      STATE: MA
      COUNTRY: USA
      ZIP: 02110-2804
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette
    OPERATING SYSTEM: Windows 95
    SOFTWARE: FASTSEQ for Windows Version 2.0b
    CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/496,692  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/964,127  
FILING DATE: 06-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Crews, Ph.D., L. Lee  
REGISTRATION NUMBER: P-43,567  
REFERENCE/DOCKET NUMBER: 07334/038001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1411 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...966  
US-09-496-692-5

Query Match 3.5%; Score 30; DB 4; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

839 TGGGAAAAAAAAAAAAAAAAAAAAAAAA 868  
1309 TGGGAAAAAAAAAAAAAAAAAAAAAAAA 1338

Db

RESULT 14  
US-10-000-273-5  
Sequence 5, Application US/10000273  
Patent No. 6573057  
GENERAL INFORMATION:  
APPLICANT: Grandearl, Andrew David John  
TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE MOLECULES  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/000,273  
FILING DATE: 02-NOV-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/964,127  
FILING DATE: 06-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Crews, Ph.D., L. Lee  
REGISTRATION NUMBER: P-43,567  
REFERENCE/DOCKET NUMBER: 07334/038001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1411 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...966  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-10-000-273-5

Query Match 3.5%; Score 30; DB 4; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

839 TGGGAAAAAAAAAAAAAAAAAAAAAAAA 868  
1309 TGGGAAAAAAAAAAAAAAAAAAAAAAAA 1338

Db

RESULT 15  
US-09-404-296B-9  
Sequence 9, Application US/09404296B  
Patent No. 6559358  
GENERAL INFORMATION:  
APPLICANT: MURRAY, James Augustus Henry  
TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH  
FILE REFERENCE: 2121-0151P  
CURRENT APPLICATION NUMBER: US/09/404,296B  
CURRENT FILING DATE: 1999-09-24  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 1414  
TYPE: DNA  
ORGANISM: Helianthus tuberosus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (48)..(1118)  
OTHER INFORMATION: cDNA encoding CYCD3;1  
US-09-404-296B-9

Query Match 3.5%; Score 30; DB 4; Length 1414;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

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Job time : 93.0087 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 20:24:57; Search time 403.034 Seconds  
(without alignments)  
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Title: US-10-069-527-1

Perfect score: 868

Sequence: 1 atggagacgtgggaagcttga.....aaaaaaaaaaaaaaaaaaaa 868

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 3373863 seqs, 2124059041 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

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- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2003as.\*
- 8: geneseqn2003bs.\*
- 9: geneseqn2003cs.\*
- 10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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7	70	8.1	121 6 ABK25465	ABK25465 Male-ster
8	70	8.1	121 6 ABK25461	ABK25461 Male-ster
9	70	8.1	121 6 ABK25457	ABK25457 Male-ster
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11	34	3.9	3130 8 ADA02946	ADA02946 Mouse Nek
12	34	3.9	3130 9 ADH72684	ADH72684 Mouse Nek
13	34	3.9	3130 9 ADG5426	ADG5426 Mouse Nek
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17	34	3.6	370 7 ABK42887	ABK42887 Bovine ES
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24	31	3.6	1111 2 AAZ11913	AAZ11913 Human pot
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28	31	3.6	1808 6 ABX92004	ABX92004 lung spec
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31	31	3.6	2045 3 AAA33283	AAA33283 Human col
32	31	3.6	2045 6 ABK69105	ABK69105 DNA encod
33	31	3.6	2396 6 ABLS5754	ABLS5754 Human ctn
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36	31	3.6	2714 7 ACA66851	ACA66851 CDNA enco
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104	30	3.5	46	6	ABK30184	ABK30184 CYP2D6 ge	177	30	3.5	1166	3	AAC98204	Aac98204 Human col
105	30	3.5	68	5	ABV34579	ABV34579 Human pro	178	30	3.5	1199	9	ADDA6756	Add6756 Human gen
106	30	3.5	68	5	ABV43435	ABV43435 Human pro	179	30	3.5	1199	9	ADBS5553	Adbs5553 Human gen
107	30	3.5	79	6	ABG95007	ABG95007 Tumour su	180	30	3.5	1232	2	AAV40526	Aav40526 Homo sap1
108	30	3.5	139	6	AA24170	AA24170 Human bre	181	30	3.5	1310	8	ADA38394	Ada38394 Soybean c
109	30	3.5	141	6	ABL81058	ABL81058 Human ova	182	30	3.5	1312	9	ADDA4858	Add4858 Rat gene
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111	30	3.5	165	5	ABV61544	ABV61544 Human pro	184	30	3.5	1327	6	AACT7734	Aact7734 Human can
112	30	3.5	166	6	ABG94997	ABG94997 Tumour su	185	30	3.5	1351	4	AA526200	Aa526200 Human cDN
113	30	3.5	169	6	ABG95000	ABG95000 Tumour su	186	30	3.5	1351	4	ABX73541	Abx73541 Human nov
114	30	3.5	198	5	ABV61836	ABV61836 Human pro	187	30	3.5	1351	7	ABBS57071	Abbs57071 Mouse cDN
115	30	3.5	217	4	AA507780	AA507780 Cervical	188	30	3.5	1384	3	AAA64190	Aaa64190 Nucleotid
116	30	3.5	222	5	ABV56932	ABV56932 Human pro	189	30	3.5	1400	4	AAH34413	Aah34413 Human col
117	30	3.5	234	4	AA115324	AA115324 Human bre	190	30	3.5	1411	2	AAV33888	Aav33888 H.tuberos
118	30	3.5	245	4	AA125924	AA125924 Human pro	191	30	3.5	1414	2	AAV33888	Aav33888 H.tuberos
119	30	3.5	268	5	ABV57845	ABV57845 Human pro	192	30	3.5	1534	4	AA541556	Aa541556 cDNA enco
120	30	3.5	284	5	ABV57877	ABV57877 Human pro	193	30	3.5	1534	4	AA535046	Aa535046 cDNA enco
121	30	3.5	294	5	ABG98609	ABG98609 Human col	194	30	3.5	1534	4	ADC46204	Adc46204 Human theo
122	30	3.5	294	5	ABV61758	ABV61758 Human pro	195	30	3.5	1534	9	AA526079	Aa526079 Human cDN
123	30	3.5	304	5	ABV07230	ABV07230 Human pro	196	30	3.5	1613	4	ABX73420	Abx73420 Human nov
124	30	3.5	352	5	ABV46492	ABV46492 Human pro	197	30	3.5	1613	4	AA562515	Aa562515 cDNA secu
125	30	3.5	363	4	AA180642	AA180642 Human pol	198	30	3.5	1643	6	ABX91984	Abx91984 Lung spec
126	30	3.5	367	4	AA180642	AA180642 Human pol	199	30	3.5	1794	3	AACT6186	Aact6186 Human ORF
127	30	3.5	377	5	ABV61233	ABV61233 Human pro	200	30	3.5	1853	6	AA597011	Aa597011 DNA enco
128	30	3.5	382	4	AA183142	AA183142 Human pol	201	30	3.5	1861	6	ABX04194	Abx04194 Human mRN
129	30	3.5	384	4	AA191176	AA191176 Human pol	202	30	3.5	1891	4	AA502543	Aa502543 Human sec
130	30	3.5	387	4	AA186392	AA186392 Human pol	203	30	3.5	1928	6	ABK69104	Abk69104 DNA enco
131	30	3.5	405	4	AA192234	AA192234 Human pol	204	30	3.5	2015	2	AA224904	Aa224904 Human sec
132	30	3.5	406	6	ABK64145	ABK64145 Human ben	205	30	3.5	2015	2	ABE50334	ABe50334 Human can
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134	30	3.5	406	8	ACH21552	ACH21552 Human adu	207	30	3.5	2265	7	ABL86428	ABl86428 Human DNA
135	30	3.5	408	8	ACH35167	ACH35167 Human end	208	30	3.5	2265	6	ABL86428	ABl86428 Human DNA
136	30	3.5	414	4	AA186277	AA186277 Human pol	209	30	3.5	2265	6	ABL86428	ABl86428 Human DNA
137	30	3.5	415	3	AA659163	AA659163 Human sec	210	30	3.5	2265	6	ABL95732	ABl95732 Human ang
138	30	3.5	416	5	ABV60942	ABV60942 Human pro	211	30	3.5	2265	7	ABX78831	ABx78831 Human PRO
139	30	3.5	419	4	AA188389	AA188389 Human pol	212	30	3.5	2265	7	ACA75803	AcA75803 Novel hum
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141	30	3.5	425	8	ACH18956	ACH18956 Human adu	214	30	3.5	2265	7	ACC87811	ACC87811 Human sec
142	30	3.5	428	6	ABK34922	ABK34922 Human cDN	215	30	3.5	2265	7	ACC87197	ACC87197 Human sec
143	30	3.5	432	8	ACH27134	ACH27134 Human adu	216	30	3.5	2265	7	ACD04370	ACd04370 cDNA enco
144	30	3.5	433	8	ACH17038	ACH17038 Human adu	217	30	3.5	2265	7	ACA69701	ACA69701 cDNA enco
145	30	3.5	457	4	AA193105	AA193105 Human pol	218	30	3.5	2265	7	ACA90546	ACA90546 Novel hum
146	30	3.5	459	8	ACH40535	ACH40535 Human foe	219	30	3.5	2265	7	ACC89653	ACC89653 Human sec
147	30	3.5	472	8	ACH34420	ACH34420 Human end	220	30	3.5	2265	7	ACA98444	ACA98444 Novel hum
148	30	3.5	481	4	AA119882	AA119882 Human bre	221	30	3.5	2265	7	ACH94086	ACH94086 Human sec
149	30	3.5	483	4	AA182236	AA182236 Human pol	222	30	3.5	2265	7	ACD15479	ACd15479 Human sec
150	30	3.5	487	4	AA192639	AA192639 Human pol	223	30	3.5	2265	7	ACD09066	ACd09066 Human sec
151	30	3.5	491	8	ACH35435	ACH35435 Human end	224	30	3.5	2265	7	ACC96986	ACC96986 Human sec
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153	30	3.5	503	5	ABV60802	ABV60802 Human pro	226	30	3.5	2265	7	ACA73074	ACA73074 Human PRO
154	30	3.5	520	6	ABN61470	ABN61470 Human can	227	30	3.5	2265	7	ACD03246	ACd03246 Novel hum
155	30	3.5	521	5	ABV60685	ABV60685 Human pro	228	30	3.5	2265	7	ACD02061	ACd02061 Novel hum
156	30	3.5	536	5	ABV61310	ABV61310 Human pro	229	30	3.5	2265	7	ACA92253	ACA92253 Novel hum
157	30	3.5	543	5	ABV61361	ABV61361 Human pro	230	30	3.5	2265	7	ACA89678	ACA89678 cDNA enco
158	30	3.5	565	3	AACT5891	AACT5891 Human ORF	231	30	3.5	2265	7	ACA73688	ACA73688 Human sec
159	30	3.5	659	3	AACT7234	AACT7234 Human ORF	232	30	3.5	2265	7	ACA06003	ACA06003 Human sec
160	30	3.5	669	6	ABG75346	ABG75346 Human lun	233	30	3.5	2265	7	ACA66837	ACA66837 cDNA enco
161	30	3.5	722	4	AA123666	AA123666 Human bre	234	30	3.5	2265	7	ACF20412	ACf20412 cDNA enco
162	30	3.5	791	6	ABT08076	ABT08076 Human bre	235	30	3.5	2265	7	ACF19798	ACf19798 Human sec
163	30	3.5	805	4	AA196132	AA196132 Human neu	236	30	3.5	2265	7	ACD22086	ACd22086 Human sec
164	30	3.5	814	3	AAAF21759	AAAF21759 Human bre	237	30	3.5	2265	7	ACF11351	ACf11351 Human sec
165	30	3.5	816	7	ABT42385	ABT42385 Toxicity	238	30	3.5	2265	7	ACD25354	ACd25354 Human sec
166	30	3.5	817	6	ABL90239	ABL90239 Human pol	239	30	3.5	2265	7	ACF00403	ACf00403 Human sec
167	30	3.5	840	5	ABV04294	ABV04294 Human pro	240	30	3.5	2265	7	ACA72460	ACA72460 Novel hum
168	30	3.5	846	4	AAFT4194	AAFT4194 DNA enco	241	30	3.5	2265	7	ACD04984	ACd04984 Novel hum
169	30	3.5	868	5	ABV13463	ABV13463 Human pro	242	30	3.5	2265	7	ACD18445	ACd18445 Human sec

243	30	3.5	2265	7	ACD08452	Human	sec	316	30	3.5	2265	7	ACA91946	Human	PRO
244	30	3.5	2265	7	ACA88886	Novel	hum	317	30	3.5	2265	7	ACA71590	Human	sec
245	30	3.5	2265	7	ACA70328	Human	sec	318	30	3.5	2265	7	ACC09090	Human	sec
246	30	3.5	2265	7	ACD12550	Novel	hum	319	30	3.5	2265	7	ACA66000	CDNA	enco
247	30	3.5	2265	7	ACCT4465	Human	sec	320	30	3.5	2265	7	ACA95145	CDNA	enco
248	30	3.5	2265	7	ACD16093	Human	sec	321	30	3.5	2265	7	ACD16707	Human	sec
249	30	3.5	2265	7	ACD25661	Novel	hum	322	30	3.5	2265	7	ACD15786	Human	sec
250	30	3.5	2265	7	ACD18138	Human	sec	323	30	3.5	2265	7	ABX16889	Human	CDN
251	30	3.5	2265	7	ACC88425	Human	sec	324	30	3.5	2265	7	ACA97830	Human	PRO
252	30	3.5	2265	7	ACD21779	Human	sec	325	30	3.5	2265	8	ACA99279	Human	sec
253	30	3.5	2265	7	ACD18846	Human	sec	326	30	3.5	2265	8	ACG91911	Novel	hum
254	30	3.5	2265	7	ABX98456	Human	CDN	327	30	3.5	2265	8	ACD11322	Human	sec
255	30	3.5	2265	7	ACD14207	Human	PRO	328	30	3.5	2265	8	ACD15172	Human	sec
256	30	3.5	2265	7	ACD09987	Human	sec	329	30	3.5	2265	8	ACD11936	Human	sec
257	30	3.5	2265	7	ACC88732	Human	sec	330	30	3.5	2265	8	ACC96065	Human	sec
258	30	3.5	2265	7	ACD21472	Human	sec	331	30	3.5	2265	8	ACF16628	Human	sec
259	30	3.5	2265	7	ABX75844	Human	CDN	332	30	3.5	2265	8	ACF02746	Human	sec
260	30	3.5	2265	7	ABX98047	Human	PRO	333	30	3.5	2265	8	ACF03053	Human	sec
261	30	3.5	2265	7	ACA97523	Novel	hum	334	30	3.5	2265	8	ACF21640	Human	sec
262	30	3.5	2265	7	ACA57986	Human	PRO	335	30	3.5	2265	8	ACF10324	Human	sec
263	30	3.5	2265	7	ACD14514	Human	PRO	336	30	3.5	2265	8	ACF78217	Human	sec
264	30	3.5	2265	7	ACC91297	Human	sec	337	30	3.5	2265	8	ACD46922	Human	sec
265	30	3.5	2265	7	ACC89039	Human	sec	338	30	3.5	2265	8	ACD49685	Human	sec
266	30	3.5	2265	7	ACD07236	Human	PRO	339	30	3.5	2265	8	ACF28452	Human	sec
267	30	3.5	2265	7	ACA67687	Human	PRO	340	30	3.5	2265	8	ACD89142	Human	sec
268	30	3.5	2265	7	ACC81742	Human	sec	341	30	3.5	2265	8	ACD84537	Human	sec
269	30	3.5	2265	7	ACC89346	Human	sec	342	30	3.5	2265	8	ACD99311	CDNA	enco
270	30	3.5	2265	7	ACC86702	Human	sec	343	30	3.5	2265	8	ADA78359	Human	sec
271	30	3.5	2265	7	ACC89960	Human	sec	344	30	3.5	2265	8	ACF49053	Human	sec
272	30	3.5	2265	7	ACC93139	Human	sec	345	30	3.5	2265	8	ACD09373	Human	sec
273	30	3.5	2265	7	ACA72767	Human	PRO	346	30	3.5	2265	8	ACF12166	Human	sec
274	30	3.5	2265	7	ACA92825	Human	sec	347	30	3.5	2265	8	ACF41400	Human	sec
275	30	3.5	2265	7	ACA70021	Human	sec	348	30	3.5	2265	8	ACF16014	Human	sec
276	30	3.5	2265	7	ACA97164	Novel	hum	349	30	3.5	2265	8	ACF16321	Human	sec
277	30	3.5	2265	7	ACA91160	Novel	hum	350	30	3.5	2265	8	ACD32148	Human	sec
278	30	3.5	2265	7	ACA70942	Human	sec	351	30	3.5	2265	8	ACF18956	Human	sec
279	30	3.5	2265	7	ACA95452	Novel	hum	352	30	3.5	2265	8	ACF09403	Human	sec
280	30	3.5	2265	7	ACC86395	Human	sec	353	30	3.5	2265	8	ACF78524	Human	sec
281	30	3.5	2265	7	ACC90267	Human	sec	354	30	3.5	2265	8	ACF52123	Human	sec
282	30	3.5	2265	7	ACD12875	Human	sec	355	30	3.5	2265	8	ACF26610	Human	sec
283	30	3.5	2265	7	ACFP0105	Human	sec	356	30	3.5	2265	8	ACF24403	Human	sec
284	30	3.5	2265	7	ABX77049	Human	PRO	357	30	3.5	2265	8	ACF63714	Human	sec
285	30	3.5	2265	7	ACA73381	Novel	hum	358	30	3.5	2265	8	ACF50588	Human	sec
286	30	3.5	2265	7	ACA68924	Novel	hum	359	30	3.5	2265	8	ACH08059	Human	sec
287	30	3.5	2265	7	ACA74768	CDNA	enco	360	30	3.5	2265	8	ACF13865	Human	sec
288	30	3.5	2265	7	ACA70635	Human	sec	361	30	3.5	2265	8	ACD41791	Human	sec
289	30	3.5	2265	7	ACD14821	Human	PRO	362	30	3.5	2265	8	ACF32204	Human	sec
290	30	3.5	2265	7	ACA68493	Novel	hum	363	30	3.5	2265	8	ACF23482	Human	sec
291	30	3.5	2265	7	ABX88958	Novel	hum	364	30	3.5	2265	8	ACF40172	Human	sec
292	30	3.5	2265	7	ACC81435	Human	sec	365	30	3.5	2265	8	ACD45694	Human	sec
293	30	3.5	2265	7	ACA95759	Novel	hum	366	30	3.5	2265	8	ACF53351	Human	sec
294	30	3.5	2265	7	ACD04677	Novel	hum	367	30	3.5	2265	8	ACF27531	Human	sec
295	30	3.5	2265	7	ACC88118	Human	sec	368	30	3.5	2265	8	ACF45369	Human	sec
296	30	3.5	2265	7	ACFI2780	Human	sec	369	30	3.5	2265	8	ACF29987	Human	sec
297	30	3.5	2265	7	ACA96495	Human	PRO	370	30	3.5	2265	8	ACD90063	Human	sec
298	30	3.5	2265	7	ACA95259	Human	PRO	371	30	3.5	2265	8	ACD84844	Human	PRO
299	30	3.5	2265	7	ACA73995	Human	sec	372	30	3.5	2265	8	ACD99004	CDNA	enco
300	30	3.5	2265	7	ACA74407	Novel	hum	373	30	3.5	2265	8	ACF77296	Human	sec
301	30	3.5	2265	7	ACA96802	Human	PRO	374	30	3.5	2265	8	ACF76989	Human	sec
302	30	3.5	2265	7	ACD10908	CDNA	enco	375	30	3.5	2265	8	ACF49974	Human	sec
303	30	3.5	2265	7	ACCG1604	Human	sec	376	30	3.5	2265	8	ACF50281	Human	sec
304	30	3.5	2265	7	ACD02939	CDNA	enco	377	30	3.5	2265	8	ACD09680	Human	sec
305	30	3.5	2265	7	ACC87504	Human	sec	378	30	3.5	2265	8	ACD08759	Human	sec
306	30	3.5	2265	7	ACC86088	Human	sec	379	30	3.5	2265	8	ACF12473	Human	sec
307	30	3.5	2265	7	ACA65576	Human	PRO	380	30	3.5	2265	8	ACC94981	Human	sec
308	30	3.5	2265	7	ACA94393	Human	sec	381	30	3.5	2265	8	ACD22700	Human	sec
309	30	3.5	2265	7	ACA98137	Human	PRO	382	30	3.5	2265	8	ACF15400	Human	sec
310	30	3.5	2265	7	ACA91639	Novel	hum	383	30	3.5	2265	8	ACC97495	Human	sec
311	30	3.5	2265	7	ACA90853	Novel	hum	384	30	3.5	2265	8	ACC92525	Human	sec
312	30	3.5	2265	7	ACD16400	Human	sec	385	30	3.5	2265	8	ACF14172	Human	sec
313	30	3.5	2265	7	ACD17561	Human	sec	386	30	3.5	2265	8	ACF14479	Human	sec
314	30	3.5	2265	7	ACC92218	Human	sec	387	30	3.5	2265	8	ACF09710	Human	sec
315	30	3.5	2265	7	ACA75075	CDNA	enco	388	30	3.5	2265	8	ACD46001	Human	sec

389	30	3.5	2265	8	ACD48150	Human sec	462	30	3.5	2265	8	ACH05241	CDNA enco
390	30	3.5	2265	8	ACD67881	CDNA enco	463	30	3.5	2265	8	ACF44738	Human sec
391	30	3.5	2265	8	ACF25689	Human sec	464	30	3.5	2265	8	ADA81878	Human sec
392	30	3.5	2265	8	ACF29373	Human sec	465	30	3.5	2265	8	ACD22393	Human sec
393	30	3.5	2265	8	ACD85151	Human sec	466	30	3.5	2265	8	ACD24740	Human sec
394	30	3.5	2265	8	ACD84230	Human PRO	467	30	3.5	2265	8	ACD39943	CDNA enco
395	30	3.5	2265	8	ACD88321	Human sec	468	30	3.5	2265	8	ACD40250	CDNA enco
396	30	3.5	2265	8	ACF30908	Human sec	469	30	3.5	2265	8	ACF13558	Human sec
397	30	3.5	2265	8	ACF32511	Human sec	470	30	3.5	2265	8	ACF03360	Human sec
398	30	3.5	2265	8	ACH12171	CDNA enco	471	30	3.5	2265	8	ACF78831	Human sec
399	30	3.5	2265	8	ACH12478	CDNA enco	472	30	3.5	2265	8	ACF11552	Human sec
400	30	3.5	2265	8	ACD40870	Human sec	473	30	3.5	2265	8	ACF50895	Human sec
401	30	3.5	2265	8	ACF18342	Human sec	474	30	3.5	2265	8	ACF34390	Human sec
402	30	3.5	2265	8	ACF08789	Human sec	475	30	3.5	2265	8	ACD46615	Human sec
403	30	3.5	2265	8	ACF31590	Human sec	476	30	3.5	2265	8	ACD48457	Human sec
404	30	3.5	2265	8	ACF52430	Human sec	477	30	3.5	2265	8	ACF27838	Human sec
405	30	3.5	2265	8	ACD50299	Human sec	478	30	3.5	2265	8	ACF24710	Human sec
406	30	3.5	2265	8	ACF39002	Human sec	479	30	3.5	2265	8	ACD85765	Human sec
407	30	3.5	2265	8	ACF26917	Human sec	480	30	3.5	2265	8	ACD90370	Human sec
408	30	3.5	2265	8	ACF25017	Human sec	481	30	3.5	2265	8	ACD83923	Human sec
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410	30	3.5	2265	8	ACF28145	Human sec	483	30	3.5	2265	8	ACH07445	Human sec
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412	30	3.5	2265	8	ACF64021	Human sec	485	30	3.5	2265	8	ACH08366	Human sec
413	30	3.5	2265	8	ACF60661	Human sec	486	30	3.5	2265	8	ACH11557	CDNA enco
414	30	3.5	2265	8	ACH12785	CDNA enco	487	30	3.5	2265	8	ACH11864	CDNA enco
415	30	3.5	2265	8	ACH10208	Human sec	488	30	3.5	2265	8	ACH10515	Human sec
416	30	3.5	2265	8	ACD04063	Human sec	489	30	3.5	2265	8	ACF01518	Human sec
417	30	3.5	2265	8	ACD10601	Human sec	490	30	3.5	2265	8	ACF41093	Human sec
418	30	3.5	2265	8	ACF42628	Human sec	491	30	3.5	2265	8	ACD24433	Human sec
419	30	3.5	2265	8	ACF18649	Human sec	492	30	3.5	2265	8	ACD31534	Human sec
420	30	3.5	2265	8	ACF02439	Human sec	493	30	3.5	2265	8	ACF18035	Human sec
421	30	3.5	2265	8	ACF21947	Human sec	494	30	3.5	2265	8	ACF32818	Human sec
422	30	3.5	2265	8	ACF10631	Human sec	495	30	3.5	2265	8	ACF40479	Human sec
423	30	3.5	2265	8	ACF34083	Human sec	496	30	3.5	2265	8	ACF48439	Human sec
424	30	3.5	2265	8	ACF45045	Human sec	497	30	3.5	2265	8	ACF38388	Human sec
425	30	3.5	2265	8	ACD90677	Human sec	498	30	3.5	2265	8	ACF23524	Human sec
426	30	3.5	2265	8	ACD91290	Human sec	499	30	3.5	2265	8	ACF27224	Human sec
427	30	3.5	2265	8	ACF30601	Human sec	500	30	3.5	2265	8	ACF29680	Human sec
428	30	3.5	2265	8	ACD87300	Human sec	501	30	3.5	2265	8	ACD87914	Human sec
429	30	3.5	2265	8	ACF60354	Human sec	502	30	3.5	2265	8	ACF76375	Human sec
430	30	3.5	2265	8	ACF46904	Human sec	503	30	3.5	2265	8	ACF49667	Human sec
431	30	3.5	2265	8	ACF75761	Human sec	504	30	3.5	2265	8	ACF44124	Human sec
432	30	3.5	2265	8	ADA80151	Human sec	505	30	3.5	2265	8	ACH06469	CDNA enco
433	30	3.5	2265	8	ACF17421	Human sec	506	30	3.5	2265	8	ACH06776	CDNA enco
434	30	3.5	2265	8	ACF23175	Human sec	507	30	3.5	2265	8	ADA83676	Human sec
435	30	3.5	2265	8	ACF08175	Human sec	508	30	3.5	2265	8	ACF92832	Human sec
436	30	3.5	2265	8	ACF08482	Human sec	509	30	3.5	2265	8	ACF93446	Human sec
437	30	3.5	2265	8	ACF40786	Human sec	510	30	3.5	2265	8	ACF19491	Human sec
438	30	3.5	2265	8	ACF53965	Human sec	511	30	3.5	2265	8	ACD13182	Human sec
439	30	3.5	2265	8	ACD47229	Human sec	512	30	3.5	2265	8	ACH06840	Human sec
440	30	3.5	2265	8	ACF48132	Human sec	513	30	3.5	2265	8	ACF94674	Human sec
441	30	3.5	2265	8	ACF47518	Human sec	514	30	3.5	2265	8	ACC98102	Human sec
442	30	3.5	2265	8	ACF46290	Human sec	515	30	3.5	2265	8	ACC94367	Human sec
443	30	3.5	2265	8	ACD86379	Human sec	516	30	3.5	2265	8	ACF42321	Human sec
444	30	3.5	2265	8	ACF52737	Human sec	517	30	3.5	2265	8	ACD31227	Human sec
445	30	3.5	2265	8	ACF53044	Human sec	518	30	3.5	2265	8	ACD43256	CDNA enco
446	30	3.5	2265	8	ACF65037	Human sec	519	30	3.5	2265	8	ACD43563	CDNA enco
447	30	3.5	2265	8	ACF76682	Human sec	520	30	3.5	2265	8	ACF15093	Human sec
448	30	3.5	2265	8	ACF61582	Human sec	521	30	3.5	2265	8	ACF01825	Human sec
449	30	3.5	2265	8	ACF61889	Human sec	522	30	3.5	2265	8	ACF31897	Human sec
450	30	3.5	2265	8	ACD30920	Human sec	523	30	3.5	2265	8	ACD67574	CDNA enco
451	30	3.5	2265	8	ACD31841	Human sec	524	30	3.5	2265	8	ACD48764	CDNA enco
452	30	3.5	2265	8	ACD33762	Human sec	525	30	3.5	2265	8	ACD49071	Human sec
453	30	3.5	2265	8	ACF17728	Human sec	526	30	3.5	2265	8	ACF51509	Human sec
454	30	3.5	2265	8	ACF07561	Human sec	527	30	3.5	2265	8	ACF54272	Human sec
455	30	3.5	2265	8	ACF20719	Human sec	528	30	3.5	2265	8	ACF25966	Human sec
456	30	3.5	2265	8	ACF21026	Human sec	529	30	3.5	2265	8	ACF39309	Human sec
457	30	3.5	2265	8	ACF21333	Human sec	530	30	3.5	2265	8	ACF29066	Human sec
458	30	3.5	2265	8	ACD47843	Human sec	531	30	3.5	2265	8	ACD90983	Human sec
459	30	3.5	2265	8	ACF47825	Human sec	532	30	3.5	2265	8	ACH06686	Human sec
460	30	3.5	2265	8	ACF53658	Human sec	533	30	3.5	2265	8	ACH05548	CDNA enco
461	30	3.5	2265	8	ACD86993	Human sec	534	30	3.5	2265	8	ACF65344	Human sec



535	30	3.5	2265	8	ADB20719	AdB20719	Human	sec	608	30	3.5	2265	8	ACD23007	AcD23007	Human	sec
536	30	3.5	2265	8	ACF43817	ACf43817	Human	sec	609	30	3.5	2265	8	ACF41707	ACf41707	Human	sec
537	30	3.5	2265	8	ACH09287	ACh09287	Human	sec	610	30	3.5	2265	8	ACF07254	ACf07254	Human	sec
538	30	3.5	2265	8	ACH09594	ACh09594	Human	sec	611	30	3.5	2265	8	ACF77910	ACf77910	Human	sec
539	30	3.5	2265	8	ADA78971	ADa78971	Human	sec	612	30	3.5	2265	8	ACD46308	ACd46308	Human	sec
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541	30	3.5	2265	8	ACF51202	ACf51202	Human	sec	614	30	3.5	2265	8	ACF54579	ACf54579	Human	sec
542	30	3.5	2265	8	ACF24096	ACf24096	Human	sec	615	30	3.5	2265	8	ACF45983	ACf45983	Human	sec
543	30	3.5	2265	8	ACD88528	ACd88528	Human	sec	616	30	3.5	2265	8	ACF45676	ACf45676	Human	sec
544	30	3.5	2265	8	ACH09901	ACh09901	Human	sec	617	30	3.5	2265	8	ACF38695	ACf38695	Human	sec
545	30	3.5	2265	8	ACH10822	ACh10822	Human	sec	618	30	3.5	2265	8	ACD89756	ACd89756	Human	sec
546	30	3.5	2265	8	ACH11629	ACh11629	Human	sec	619	30	3.5	2265	8	ACD85458	ACd85458	Human	sec
547	30	3.5	2265	8	ACCG6679	ACc66679	Human	sec	620	30	3.5	2265	8	ACD86072	ACd86072	Human	sec
548	30	3.5	2265	8	ACCG8709	ACc8709	Human	sec	621	30	3.5	2265	8	ACF76068	ACf76068	Human	sec
549	30	3.5	2265	8	ACF42014	ACf42014	Human	sec	622	30	3.5	2265	8	ACF60968	ACf60968	Human	sec
550	30	3.5	2265	8	ACF16935	ACf16935	Human	sec	623	30	3.5	2265	8	ACH05855	ACh05855	Human	sec
551	30	3.5	2265	8	ACD32455	ACd32455	Human	sec	624	30	3.5	2265	8	ADA83042	ADa83042	Human	sec
552	30	3.5	2265	8	ACD30613	ACd30613	Human	sec	625	30	3.5	2265	8	ACF56114	ACf56114	Human	sec
553	30	3.5	2265	8	ACD41484	ACd41484	Human	sec	626	30	3.5	2265	8	ACF55500	ACf55500	Human	sec
554	30	3.5	2265	8	ACF07868	ACf07868	Human	sec	627	30	3.5	2265	9	ADB86350	ADb86350	Human	sec
555	30	3.5	2265	8	ACF31283	ACf31283	Human	sec	628	30	3.5	2265	9	ACF56421	ACf56421	Human	sec
556	30	3.5	2265	8	ACF77603	ACf77603	Human	sec	629	30	3.5	2265	9	ACF56728	ACf56728	Human	sec
557	30	3.5	2265	8	ACF11245	ACf11245	Human	sec	630	30	3.5	2265	9	ACF55807	ACf55807	Human	sec
558	30	3.5	2265	8	ACF33125	ACf33125	Human	sec	631	30	3.5	2265	9	ACF55193	ACf55193	Human	sec
559	30	3.5	2265	8	ACF26303	ACf26303	Human	sec	632	30	3.5	2265	9	ADD06080	ADd06080	Human	sec
560	30	3.5	2265	8	ACD83616	ACd83616	Human	PRO	633	30	3.5	2265	9	ADD10632	ADd10632	Human	sec
561	30	3.5	2265	8	ACF23789	ACf23789	Human	sec	634	30	3.5	2265	9	ADD11592	ADd11592	Human	sec
562	30	3.5	2265	8	ACF43203	ACf43203	Human	sec	635	30	3.5	2265	9	ADD37385	ADd37385	Human	sec
563	30	3.5	2265	8	ACF43510	ACf43510	Human	sec	636	30	3.5	2265	10	ADE41593	ADe41593	Human	sec
564	30	3.5	2265	8	ACH06162	ACh06162	CDNA	enco	637	30	3.5	2265	10	ADB47474	ADb47474	Human	sec
565	30	3.5	2265	8	ACH08980	ACh08980	Human	sec	638	30	3.5	2265	10	ADE75356	ADe75356	Human	sec
566	30	3.5	2265	8	ACCG0574	ACc0574	Human	sec	639	30	3.5	2307	3	ACF77488	ACf77488	Human	ORF
567	30	3.5	2265	8	ACF10938	ACf10938	Human	sec	640	30	3.5	2329	5	AACT5989	AAcT5989	Human	ORF
568	30	3.5	2265	8	ACCG3753	ACc3753	Human	sec	641	30	3.5	2376	5	AAD17002	AAd17002	Human	arg
569	30	3.5	2265	8	ACCG6372	ACc6372	Human	sec	642	30	3.5	2613	9	ADB62364	ADb62364	Human	CDN
570	30	3.5	2265	8	ACD25047	ACd25047	Human	sec	643	30	3.5	2627	7	ADA83753	ADa83753	Human	ZNF
571	30	3.5	2265	8	ACF02132	ACf02132	Human	sec	644	30	3.5	2725	4	AAFA37048	AAfA37048	Human	PRO
572	30	3.5	2265	8	ACF22254	ACf22254	Human	sec	645	30	3.5	2725	4	AAFA54262	AAfA54262	Human	PRO
573	30	3.5	2265	8	ACF22868	ACf22868	Human	sec	646	30	3.5	2725	4	AAD02922	AAd02922	Human	PRO
574	30	3.5	2265	8	ACF09096	ACf09096	Human	sec	647	30	3.5	2725	4	AAAS21483	AAaS21483	Human	CDN
575	30	3.5	2265	8	ACF33432	ACf33432	Human	sec	648	30	3.5	2725	5	AAC91482	AAc91482	Human	PRO
576	30	3.5	2265	8	ACF54886	ACf54886	Human	sec	649	30	3.5	2725	5	ACD24092	ACd24092	Novel	hum
577	30	3.5	2265	8	ACF48746	ACf48746	Human	sec	650	30	3.5	2725	7	ACA67233	ACa67233	CDNA	enco
578	30	3.5	2265	8	ACD47536	ACd47536	Human	sec	651	30	3.5	2725	7	ACA03842	ACa03842	CDNA	enco
579	30	3.5	2265	8	ACD49378	ACd49378	Human	sec	652	30	3.5	2725	7	ABX89380	ABx89380	DNA	encod
580	30	3.5	2265	8	ACF38081	ACf38081	Human	sec	653	30	3.5	2725	7	ABX13478	ABx13478	Human	DNA
581	30	3.5	2265	8	ACF30294	ACf30294	Human	sec	654	30	3.5	2725	7	ACD42034	ACd42034	Human	sec
582	30	3.5	2265	8	ACD87607	ACd87607	Human	sec	655	30	3.5	2725	7	ACA04263	ACa04263	Human	CDN
583	30	3.5	2265	8	ACF62196	ACf62196	Human	sec	656	30	3.5	2725	8	ADA45968	ADa45968	Novel	hum
584	30	3.5	2265	8	ACH11129	ACh11129	Human	sec	657	30	3.5	2725	8	ADA76429	ADa76429	Human	PRO
585	30	3.5	2265	8	ACD10294	ACd10294	Human	sec	658	30	3.5	2725	8	ADA19079	ADa19079	Human	PRO
586	30	3.5	2265	8	ACD17019	ACd17019	CDNA	enco	659	30	3.5	2725	8	ADA61702	ADa61702	Homo sapi	
587	30	3.5	2265	8	ACCG9316	ACc9316	Human	sec	660	30	3.5	2725	8	ADB19487	ADb19487	Novel	hum
588	30	3.5	2265	8	ACF00710	ACf00710	Human	sec	661	30	3.5	2725	8	ADB28028	ADb28028	CDNA	enco
589	30	3.5	2265	8	ACD41177	ACd41177	Human	sec	662	30	3.5	2725	8	ADA86507	ADa86507	Novel	hum
590	30	3.5	2265	8	ACF44786	ACf44786	Human	sec	663	30	3.5	2725	8	ADB16071	ADb16071	Human	PRO
591	30	3.5	2265	8	ACF22561	ACf22561	Human	sec	664	30	3.5	2725	8	ADA74857	ADa74857	Human	PRO
592	30	3.5	2265	8	ACF79138	ACf79138	Human	sec	665	30	3.5	2725	8	ACD68299	ACd68299	Novel	hum
593	30	3.5	2265	8	ACF11859	ACf11859	Human	sec	666	30	3.5	2725	8	ADA67652	ADa67652	Human	PRO
594	30	3.5	2265	8	ACF51816	ACf51816	Human	sec	667	30	3.5	2725	8	ADB30659	ADb30659	CDNA	enco
595	30	3.5	2265	8	ACF31739	ACf31739	Human	sec	668	30	3.5	2725	8	ADA85955	ADa85955	Novel	hum
596	30	3.5	2265	8	ACD49992	ACd49992	Human	sec	669	30	3.5	2725	8	ADA97167	ADa97167	Human	PRO
597	30	3.5	2265	8	ACF37774	ACf37774	Human	sec	670	30	3.5	2725	8	ADA79471	ADa79471	Human	PRO
598	30	3.5	2265	8	ACF28759	ACf28759	Human	sec	671	30	3.5	2725	8	ADA87610	ADa87610	Novel	hum
599	30	3.5	2265	8	ACD88835	ACd88835	Human	sec	672	30	3.5	2725	8	ADA916812	ADa916812	Human	PRO
600	30	3.5	2265	8	ACF75454	ACf75454	Human	sec	673	30	3.5	2725	8	ADA91904	ADa91904	Novel	hum
601	30	3.5	2265	8	ACF61275	ACf61275	Human	sec	674	30	3.5	2725	8	ADB14967	ADb14967	Human	PRO
602	30	3.5	2265	8	ACF44431	ACf44431	Human	sec	675	30	3.5	2725	8	ADB18928	ADb18928	Human	PRO
603	30	3.5	2265	8	ACH08673	ACh08673	Human	sec	676	30	3.5	2725	8	ADA94143	ADa94143	Human	PRO
604	30	3.5	2265	8	ACCG4060	ACc4060	Human	sec	677	30	3.5	2725	8	ADB20039	ADb20039	Novel	hum
605	30	3.5	2265	8	ACD21165	ACd21165	Human	sec	678	30	3.5	2725	8	ADB13351	ADb13351	Human	PRO
606	30	3.5	2265	8	ACF06947	ACf06947	Human	sec	679	30	3.5	2725	8	ACD98663	ACd98663	Novel	hum
607	30	3.5	2265	8	ACD20858	ACd20858	Human	sec	680	30	3.5	2725	8	ADA74605	ADa74605	Human	PRO

681	30	3.5	2725	8	ADB24838	Adh24838	Human	PRO	754	30	3.5	2725	9	ADD04708	Adh04708	Novel	hum
682	30	3.5	2725	8	ADA82362	Ada82362	Human	PRO	755	30	3.5	2725	9	ADC80664	Adc80664	Novel	hum
683	30	3.5	2725	8	ADA75325	Ada75325	Human	PRO	756	30	3.5	2725	9	ADD11171	Add11171	Human	PRO
684	30	3.5	2725	8	ADA85403	Ada85403	Novel	hum	757	30	3.5	2725	9	ADC48052	Adc48052	Human	PRO
685	30	3.5	2725	8	ADA84851	Ada84851	Novel	hum	758	30	3.5	2725	9	ADC80112	Adc80112	Novel	hum
686	30	3.5	2725	8	ADB30107	Adb30107	CDNA	enco	759	30	3.5	2725	9	ADD09581	Add09581	Human	PRO
687	30	3.5	2725	8	ADA80635	Ada80635	Human	PRO	760	30	3.5	2725	9	ADD41294	Add41294	Novel	hum
688	30	3.5	2725	8	ADA75877	Ada75877	Human	PRO	761	30	3.5	2725	9	ADD52433	Add52433	CDNA	enco
689	30	3.5	2725	8	ADA47102	Ada47102	Human	PRO	762	30	3.5	2725	9	ADD15375	Add15375	Novel	hum
690	30	3.5	2725	8	ADB25398	Adb25398	Human	PRO	763	30	3.5	2725	9	ADD70602	Add70602	Human	CDN
691	30	3.5	2725	8	ADA93574	Ada93574	Human	PRO	764	30	3.5	2725	9	ADD39679	Add39679	Human	CDN
692	30	3.5	2725	8	ADB26924	Adb26924	CDNA	enco	765	30	3.5	2725	9	ADD53173	Add53173	CDNA	enco
693	30	3.5	2725	8	ADB31211	Adb31211	CDNA	enco	766	30	3.5	2725	9	ADD53725	Add53725	Novel	hum
694	30	3.5	2725	8	ADA61139	Ada61139	Human	PRO	767	30	3.5	2725	9	ADD70125	Add70125	Human	CDN
695	30	3.5	2725	8	ADB24286	Adb24286	Human	PRO	768	30	3.5	2725	9	ADD38246	Add38246	Human	CDN
696	30	3.5	2725	8	ADA96615	Ada96615	Human	PRO	769	30	3.5	2725	9	ADD39202	Add39202	Human	CDN
697	30	3.5	2725	8	ADA81187	Ada81187	Human	PRO	770	30	3.5	2725	9	ADD51681	Add51681	CDNA	enco
698	30	3.5	2725	8	ADA96063	Ada96063	Human	PRO	771	30	3.5	2725	9	ADD02680	Add02680	Human	PRO
699	30	3.5	2725	8	ADB26372	Adb26372	CDNA	enco	772	30	3.5	2725	9	ADD02114	Add02114	Human	PRO
700	30	3.5	2725	8	ADB21857	Adb21857	Novel	hum	773	30	3.5	2725	9	ADD54296	Add54296	Novel	hum
701	30	3.5	2725	8	ADA77636	Ada77636	Human	PRO	774	30	3.5	2725	9	ADD35875	Add35875	Human	CDN
702	30	3.5	2725	8	ADB18376	Adb18376	CDNA	enco	775	30	3.5	2725	9	ADD40156	Add40156	Human	CDN
703	30	3.5	2725	8	ADA87059	Ada87059	Novel	hum	776	30	3.5	2725	9	ADD50377	Add50377	Human	CDN
704	30	3.5	2725	8	ACH04401	Ach04401	Human	CDN	777	30	3.5	2725	9	ADD92613	Add92613	Human	PRO
705	30	3.5	2725	8	ADA88162	Ada88162	Novel	hum	778	30	3.5	2725	9	ADD91509	Add91509	Human	PRO
706	30	3.5	2725	8	ADA46550	Ada46550	Novel	hum	779	30	3.5	2725	9	ADE04123	Ade04123	Human	PRO
707	30	3.5	2725	8	ADB28580	Adb28580	CDNA	enco	780	30	3.5	2725	9	ADE19989	Ade19989	Human	CDN
708	30	3.5	2725	8	ADB29132	Adb29132	CDNA	enco	781	30	3.5	2725	9	ADD53240	Add53240	Novel	hum
709	30	3.5	2725	8	ADA77084	Ada77084	Human	PRO	782	30	3.5	2725	9	ADD22252	Add22252	CDNA	enco
710	30	3.5	2725	8	ACD67945	Acd67945	Novel	hum	783	30	3.5	2725	9	ADD79576	Add79576	CDNA	enco
711	30	3.5	2725	8	ADA88714	Ada88714	Novel	hum	784	30	3.5	2725	9	ADE42112	Ade42112	Human	PRO
712	30	3.5	2725	8	ADA97719	Ada97719	Novel	hum	785	30	3.5	2725	9	ADE17929	Ade17929	Human	PRO
713	30	3.5	2725	8	ADB27476	Adb27476	CDNA	enco	786	30	3.5	2725	9	ADD92061	Add92061	Human	PRO
714	30	3.5	2725	8	ADB22409	Adb22409	Novel	hum	787	30	3.5	2725	9	ADD33524	Add33524	Novel	hum
715	30	3.5	2725	8	ADA67100	Ada67100	Human	PRO	788	30	3.5	2725	9	ADB34076	Adb34076	Novel	hum
716	30	3.5	2725	8	ADB22961	Adb22961	Human	PRO	789	30	3.5	2725	9	ADD80128	Add80128	CDNA	enco
717	30	3.5	2725	8	ADB23734	Adb23734	Human	PRO	790	30	3.5	2725	9	ADD49900	Add49900	Human	CDN
718	30	3.5	2725	8	ADA92456	Ada92456	Novel	hum	791	30	3.5	2725	9	ADD93165	Add93165	Human	PRO
719	30	3.5	2725	8	ADB15519	Adb15519	Novel	hum	792	30	3.5	2725	9	ADE19585	Ade19585	Human	PRO
720	30	3.5	2725	8	ADB38771	Adb38771	Novel	hum	793	30	3.5	2725	9	ADE21458	Ade21458	Human	CDN
721	30	3.5	2725	8	ADB38219	Adb38219	Novel	hum	794	30	3.5	2725	9	ADE19033	Ade19033	Human	PRO
722	30	3.5	2725	8	ADB66691	Adb66691	Novel	hum	795	30	3.5	2725	9	ADD43329	Add43329	Human	PRO
723	30	3.5	2725	8	ADB89771	Adb89771	Human	PRO	796	30	3.5	2725	9	ADD96018	Add96018	Human	PRO
724	30	3.5	2725	8	ADB90503	Adb90503	Human	PRO	797	30	3.5	2725	9	ADD22804	Add22804	CDNA	enco
725	30	3.5	2725	8	ADB34604	Adb34604	Novel	hum	798	30	3.5	2725	9	ADD79022	Add79022	CDNA	enco
726	30	3.5	2725	8	ADB47227	Adb47227	Novel	hum	799	30	3.5	2725	9	ADD32972	Add32972	Novel	hum
727	30	3.5	2725	8	ADB86834	Adb86834	Human	PRO	800	30	3.5	2725	9	ADE42664	Ade42664	Human	PRO
728	30	3.5	2725	8	ADB77439	Adb77439	Novel	hum	801	30	3.5	2725	9	ADD80680	Add80680	CDNA	enco
729	30	3.5	2725	8	ADB34596	Adb34596	Human	PRO	802	30	3.5	2725	9	ADD89708	Add89708	Human	PRO
730	30	3.5	2725	8	ADB35700	Adb35700	Human	PRO	803	30	3.5	2725	9	ADD40992	Add40992	Human	PRO
731	30	3.5	2725	8	ADB34044	Adb34044	Human	PRO	804	30	3.5	2725	9	ADB04791	Adb04791	Novel	hum
732	30	3.5	2725	8	ADB35148	Adb35148	Human	PRO	805	30	3.5	2725	10	ADD81216	Add81216	Novel	hum
733	30	3.5	2725	8	ADB3252	Adb3252	Human	PRO	806	30	3.5	2725	10	ADD76664	Add76664	Human	PRO
734	30	3.5	2725	8	ADB46647	Adb46647	Novel	hum	807	30	3.5	2725	10	ADD88028	Add88028	Human	PRO
735	30	3.5	2725	8	ADB17956	Adb17956	Human	PRO	808	30	3.5	2725	10	ADD86432	Add86432	Human	PRO
736	30	3.5	2725	8	ADC50520	Adc50520	Novel	hum	809	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
737	30	3.5	2725	8	ADC72067	Adc72067	Novel	hum	810	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
738	30	3.5	2725	8	ADC60046	Adc60046	Novel	hum	811	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
739	30	3.5	2725	8	ADC3053	Adc3053	Novel	hum	812	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
740	30	3.5	2725	8	ADC57407	Adc57407	Novel	hum	813	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
741	30	3.5	2725	8	ADC60598	Adc60598	Novel	hum	814	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
742	30	3.5	2725	8	ADC51073	Adc51073	Novel	hum	815	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
743	30	3.5	2725	8	ADC65600	Adc65600	Human	PRO	816	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
744	30	3.5	2725	8	ADC54698	Adc54698	Novel	hum	817	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
745	30	3.5	2725	8	ADC53659	Adc53659	Novel	hum	818	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
746	30	3.5	2725	8	ADC59182	Adc59182	Novel	hum	819	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
747	30	3.5	2725	8	ADC56060	Adc56060	Novel	hum	820	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
748	30	3.5	2725	8	ADC88630	Adc88630	Novel	hum	821	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
749	30	3.5	2725	8	ADC03304	Adc03304	Novel	hum	822	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
750	30	3.5	2725	8	ADC90296	Adc90296	Novel	hum	823	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
751	30	3.5	2725	8	ADC69715	Adc69715	CDNA	enco	824	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
752	30	3.5	2725	8	ADC48604	Adc48604	Human	PRO	825	30	3.5	2725	10	AD75880	Ad75880	Human	PRO
753	30	3.5	2725	8	ADD10133	Add10133	Human	PRO	826	30	3.5	2725	10	AD75880	Ad75880	Human	PRO

827	30	3.5	2848	7	ACA60411	Novel	hum	900	30	3.5	2848	10	ADC52235	Adc52235	Novel	hum
828	30	3.5	2848	7	ACA58858	CDNA	enco	901	30	3.5	2848	10	Adc21061	Adc21061	Novel	hum
829	30	3.5	2848	7	ACA64034	CDNA	enco	902	30	3.5	2848	10	Adc05905	Adc05905	Human	PRO
830	30	3.5	2848	7	ACA91298	CDNA	enco	903	30	3.5	2848	10	Adc755134	Adc755134	Human	PRO
831	30	3.5	2848	7	ACD45197	Human	sec	904	30	3.5	2848	10	Adc75880	Adc75880	Novel	hum
832	30	3.5	2848	7	ACA93745	Human	CDN	905	30	3.5	2848	10	Adc85112	Adc85112	Novel	hum
833	30	3.5	2848	7	ACA67319	CDNA	enco	906	30	3.5	2848	10	Adc86938	Adc86938	Novel	hum
834	30	3.5	2848	7	ACA68590	Novel	hum	907	30	3.5	2848	10	Adc20815	Adc20815	Novel	hum
835	30	3.5	2848	7	ACH66292	Novel	hum	908	30	3.5	2848	10	Adc39112	Adc39112	Novel	hum
836	30	3.5	2848	7	ACH02346	Novel	hum	909	30	3.5	2848	10	Adc056559	Adc056559	Human	PRO
837	30	3.5	2848	7	ACH89337	Novel	hum	910	30	3.5	2848	10	Adc73644	Adc73644	Human	PRO
838	30	3.5	2848	7	ACA89374	Novel	hum	911	30	3.5	2848	10	Adc78484	Adc78484	Novel	hum
839	30	3.5	2848	7	ACA98496	CDNA	enco	912	30	3.5	2848	10	Adc21307	Adc21307	Novel	hum
840	30	3.5	2848	8	ACA63421	CDNA	enco	913	30	3.5	2848	10	Adc77422	Adc77422	Novel	hum
841	30	3.5	2848	8	Adc44319	Human	PRO	914	30	3.5	2848	10	Adc20569	Adc20569	Novel	hum
842	30	3.5	2848	8	Adc17154	Human	CDN	915	30	3.5	2848	10	Adc75634	Adc75634	Human	PRO
843	30	3.5	2848	8	ACH03624	Human	sec	916	30	3.5	2848	10	Adc74150	Adc74150	Novel	hum
844	30	3.5	2848	8	ACH068401	Novel	hum	917	30	3.5	2848	10	Adc74396	Adc74396	Human	PRO
845	30	3.5	2848	8	Adc19959	Novel	hum	918	30	3.5	2848	10	Adc76126	Adc76126	Novel	hum
846	30	3.5	2848	8	Adc17342	Human	CDN	919	30	3.5	2848	10	Adc05618	Adc05618	Novel	hum
847	30	3.5	2848	8	Adc20131	Novel	hum	920	30	3.5	2848	10	Adc05167	Adc05167	Human	PRO
848	30	3.5	2848	8	Adc82138	Human	sec	921	30	3.5	2848	10	Adc75380	Adc75380	Human	PRO
849	30	3.5	2848	8	Adc44602	Human	PRO	922	30	3.5	2848	10	Adc76924	Adc76924	Novel	hum
850	30	3.5	2848	8	Adc82269	Human	sec	923	30	3.5	2848	10	Adc86692-	Adc86692-	Novel	hum
851	30	3.5	2848	8	Adc04503	Human	sec	924	30	3.5	2848	10	Adc77914	Adc77914	Novel	hum
852	30	3.5	2848	8	Adc04503	Human	CDN	925	30	3.5	2848	10	Adc77914	Adc77914	Novel	hum
853	30	3.5	2848	8	Adc68047	Novel	hum	926	30	3.5	2848	10	Adc85372	Adc85372	Novel	hum
854	30	3.5	2848	8	Adc43975	Human	mem	927	30	3.5	2848	10	Adc73904	Adc73904	Human	PRO
855	30	3.5	2848	8	Adc85677	Novel	hum	928	30	3.5	2848	10	Adc74642	Adc74642	Human	PRO
856	30	3.5	2848	8	Adc80783	Novel	hum	929	30	3.5	2848	10	Adc77170	Adc77170	Novel	hum
857	30	3.5	2848	8	Adc73324	Novel	hum	930	30	3.5	2848	10	Adc85864	Adc85864	Novel	hum
858	30	3.5	2848	8	Adc78406	Novel	hum	931	30	3.5	2848	10	Adc05413	Adc05413	Human	PRO
859	30	3.5	2848	8	Adc85054	Human	PRO	932	30	3.5	2848	10	Adc05413	Adc05413	Human	PRO
860	30	3.5	2848	9	Adc78160	Novel	hum	933	30	3.5	2848	10	Adc17232	Adc17232	CDNA	sequ
861	30	3.5	2848	9	Adc87226	Human	PRO	934	30	3.5	2848	9	Adc14930	Adc14930	Novel	hum
862	30	3.5	2848	9	Adc84808	Human	PRO	935	30	3.5	2848	9	Adc084612	Adc084612	Mouse	AT2
863	30	3.5	2848	9	Adc868349	Human	PRO	936	30	3.5	2848	4	Adc17208	Adc17208	Human	cat
864	30	3.5	2848	9	Adc68156	Human	PRO	937	30	3.5	2848	4	Adc84613	Adc84613	Rat	AT2
865	30	3.5	2848	9	Adc83923	Novel	hum	938	30	3.5	2848	9	Adc67631	Adc67631	Human	Lyl
866	30	3.5	2848	9	Adc73078	Novel	hum	939	30	3.5	2848	2	Adc07076	Adc07076	Cancer	su
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871	30	3.5	2848	9	Adc52425	Novel	hum	944	30	3.5	2848	5	Adc14483	Adc14483	Human	net
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874	30	3.5	2848	9	Adc49136	Novel	hum	947	29	3.3	201143	2	Adc02146	Adc02146	Human	sec
875	30	3.5	2848	9	Adc49653	Novel	hum	948	29	3.3	49	6	Adc08080	Adc08080	3' portio	
876	30	3.5	2848	9	Adc47514	Novel	hum	949	29	3.3	49	6	Adc5636	Adc5636	DNA	detc
877	30	3.5	2848	9	Adc47259	Novel	hum	950	29	3.3	53	2	Adc57442	Adc57442	Probe	oli
878	30	3.5	2848	9	Adc78134	Novel	hum	951	29	3.3	56	6	Adc129341	Adc129341	Colon	tum
879	30	3.5	2848	9	Adc06369	Novel	hum	952	29	3.3	58	4	Adc52233	Adc52233	Human	col
880	30	3.5	2848	9	Adc78888	Novel	hum	953	29	3.3	58	6	Adc53527	Adc53527	Human	col
881	30	3.5	2848	9	Adc50851	Novel	hum	954	29	3.3	64	7	Adc55108	Adc55108	Human	col
882	30	3.5	2848	9	Adc51097	Novel	hum	955	29	3.3	71	6	Adc141039	Adc141039	GUS	mRNA
883	30	3.5	2848	9	Adc10743	Human	CDN	956	29	3.3	74	6	Adc095005	Adc095005	Tumour	su
884	30	3.5	2848	9	Adc39820	Human	CDN	957	29	3.3	76	6	Adc54688	Adc54688	Human	col
885	30	3.5	2848	9	Adc70266	Human	CDN	958	29	3.3	125	3	Adc096267	Adc096267	Tumour	su
886	30	3.5	2848	9	Adc36101	Novel	hum	959	29	3.3	132	6	Adc49498	Adc49498	Molecular	
887	30	3.5	2848	9	Adc38387	Human	CDN	960	29	3.3	132	3	Adc096172	Adc096172	DNA	oligo
888	30	3.5	2848	9	Adc39343	Human	CDN	961	29	3.3	132	6	Adc096172	Adc096172	Tumour	su
889	30	3.5	2848	9	Adc50578	Human	PRO	962	29	3.3	140	5	Adc61779	Adc61779	Human	pro
890	30	3.5	2848	9	Adc50332	Human	PRO	963	29	3.3	148	6	Adc186280	Adc186280	Human	ova
891	30	3.5	2848	9	Adc38866	Human	CDN	964	29	3.3	148	6	Adc186553	Adc186553	Human	ova
892	30	3.5	2848	9	Adc40297	Human	CDN	965	29	3.3	150	6	Adc23026	Adc23026	Breast	ca
893	30	3.5	2848	9	Adc51343	Novel	hum	966	29	3.3	156	7	Adc723026	Adc723026	Human	pro
894	30	3.5	2848	9	Adc050518	Human	CDN	967	29	3.3	160	5	Adc56034	Adc56034	Human	pro
895	30	3.5	2848	9	Adc05010	Human	CDN	968	29	3.3	167	2	Adc071129	Adc071129	Human	gen
896	30	3.5	2848	9	Adc050041	Human	CDN	969	29	3.3	190	5	Adc60741	Adc60741	Human	pro
897	30	3.5	2848	9	Adc15859	Human	CDN	970	29	3.3	200	5	Adc61292	Adc61292	Human	pro
898	30	3.5	2848	10	Adc48890	Novel	hum	971	29	3.3	202	5	Adc19743	Adc19743	Human	pro
899	30	3.5	2848	10	Adc48890	Novel	hum	972	29	3.3	202	5	Adc19743	Adc19743	Human	pro

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C 973 29 3.3 210 5 AB056326 Abv56326 Human col
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C 975 29 3.3 213 5 ABV18738 Abv18738 Human pro
C 976 29 3.3 225 5 ABV61751 Abv61751 Human pro
C 977 29 3.3 229 5 ABV61677 Abv61677 Human pro
C 978 29 3.3 231 4 AAS60677 Aas60677 Human pro
C 979 29 3.3 233 5 ABV48411 Abv48411 Human pro
C 980 29 3.3 233 5 ABV58773 Abv58773 Human pro
C 981 29 3.3 234 5 ABV61612 Abv61612 Human pro
C 982 29 3.3 235 5 ABV60731 Abv60731 Human pro
C 983 29 3.3 241 5 ABV57667 Abv57667 Human pro
C 984 29 3.3 244 5 ABV19785 Abv19785 Human pro
C 985 29 3.3 247 5 ABV45142 Abv45142 Human pro
C 986 29 3.3 247 5 ABV57985 Abv57985 Human pro
C 987 29 3.3 252 5 ABV58215 Abv58215 Human pro
C 988 29 3.3 254 5 ABV49550 Abv49550 Human pro
C 989 29 3.3 255 5 AAH82121 AAH82121 Rat diffe
C 990 29 3.3 255 5 ABV52319 Abv52319 Human pro
C 991 29 3.3 257 5 ABV51610 Abv51610 Human pro
C 992 29 3.3 262 5 ABV58430 Abv58430 Human pro
C 993 29 3.3 262 5 ABV58178 Abv58178 Human pro
C 994 29 3.3 263 6 AB187048 AB187048 Human ova
C 995 29 3.3 265 5 ABV57910 Abv57910 Human pro
C 996 29 3.3 266 7 ABX46302 ABX46302 Bovine ES
C 997 29 3.3 269 4 AAL10304 Aal10304 Human bre
C 998 29 3.3 271 5 ABV56376 Abv56376 Human pro
C 999 29 3.3 276 5 ABV61340 Abv61340 Human pro
1000 29 3.3 276 6 ABN62408 ABn62408 Human can

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## ALIGNMENTS

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RESULT 1
AAS00103 standard; cDNA; 868 BP.
XX
AC AAS00103;
XX
DT 11-SEP-2003 (revised)
DT 17-MAY-2001 (first entry)
XX
DE Granny Smith apple cDNA encoding MdPI.
XX
KM Granny Smith apple, MdPI; seedless fruit; horticulture;
KM accelerated breeding programme; cross pollination; transgenic plant;
KM biennial bearing tendency; coding moth; ss.
XX
OS Malus x domestica; var. Granny Smith.
XX
FH Key Location/Qualifiers
FT CDS 1..648
FT FT /*tag= a
FT FT /product= "MdPI"
FT FT primer_bind 1..15
FT FT /*tag= b
FT FT /label= PCR primer_P1_binding_site
FT FT 19..41
FT FT /*tag= c
FT FT /label= PCR primer_P5_binding_site
FT FT 291..312
FT FT /*tag= d
FT FT /label= PCR primer_P3_binding_site
FT FT 314..334
FT FT /*tag= e
FT FT /label= PCR primer_P4_binding_site
FT FT complement(609..626)
FT FT /*tag= f
FT FT /label= PCR primer_P2_binding_site
FT FT complement(770..791)
FT FT /*tag= g
FT FT /label= PCR primer_P7_binding_site
FT FT complement(818..840)
FT primer_bind

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FT FT /*tag= h
FT FT /label= PCR primer_P6_binding_site
XX
XX MO200117334-A1.
XX
XX 15-MAR-2001.
PD
PF 07-SEP-2000; 2000MO-NZ000176.
XX
XX 07-SEP-1999; 99NZ-00337688.
PR
PR (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
PA
XX
XX Yao J, Morris BA;
XX
XX WFI, 2001-235145/24.
DR
DR P-PSDB; AAU00186.
XX
PT New genetically modified fruiting plants that does not functionally
PT express MdPI or MdAP3 peptides, useful for producing seedless fruits,
PT specifically apple and its related species.
XX
XX Claim 10, Fig 2; 41pp; English.
PS
XX
XX The sequence encodes Granny Smith apple MdPI. The invention concerns a
XX fruiting plant that has been genetically modified so that it does not
XX functionally express the MdPI or MdAP3 peptide, producing seedless
XX fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
XX may be used to transform fruiting plants, specifically apple and pear.
XX The polynucleotides may be used in modulating, reducing or eliminating
XX seed-bearing capacity in fruiting plants, used in horticulture, and in
XX breeding programmes to monitor the progress in breeding a stable seedless
XX fruiting plant. The polynucleotides may also be used in programmes for
XX identifying nucleic acid variants from fruiting plants. They can be used
XX for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
XX for use in an accelerated breeding programme to produce seedless fruit.
XX They may also be used in designing probes and primers for MdPI or MdAP3,
XX or their variants. The seedless fruiting plant is more convenient than
XX seeded fruit since these can be cropped without pollination, reducing
XX dependence on bees, pollinator varieties and warm weather at flowering.
XX The absence of pollen is also advantageous to alleviate environmental
XX concerns regarding the transfer of transgenes to non-transgenics by cross
XX pollination. Seedless cultivars can also avoid or reduce biennial bearing
XX tendencies that have been attributed to the inhibition of flower bud
XX formation by developing seeds and are less susceptible to coding moth
XX compared to seeded fruit. (updated on 11-SEP-2003 to standardise OS
XX field)
XX
SQ Sequence 868 BP; 296 A; 152 C; 208 G; 212 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 868; DB 4; Length 868;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGCGTGGAGGAGTTGAGATCAAGAGGATTGGAAGCTCAATACAGGACAGTACC 60
Db 1 ATGGAGCGTGGAGGAGTTGAGATCAAGAGGATTGGAAGCTCAATACAGGACAGTACC 60
QY 61 TACTCAGAGAGAGGAGATGATTAACAAGGCAAGAGAGATCACTGTTCTATGTGAT 120
Db 61 TACTCAGAGAGAGGAGATGATTAACAAGGCAAGAGAGATCACTGTTCTATGTGAT 120
QY 121 GCTAAGAGATCTCTATCTATTATTTAGCTCTGGGAAGATGGTGAATCTGAGGCCCT 180
Db 121 GCTAAGAGATCTCTATCTATTATTTAGCTCTGGGAAGATGGTGAATCTGAGGCCCT 180
QY 181 TCAACTAGCTGAGAGAAATCTTGAACAATACCATGAGCAATCTGGGAAGAGTTGTGG 240
Db 181 TCAACTAGCTGAGAGAAATCTTGAACAATACCATGAGCAATCTGGGAAGAGTTGTGG 240
QY 241 GATGCTAGCGATGGAACCTTACGCAATGAAGTGATGAGTCAAGAAAGCAATGACAC 300
Db 241 GATGCTAGCGATGGAACCTTACGCAATGAAGTGATGAGTCAAGAAAGCAATGACAC 300

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QY 301 ATGCAAGTATGAGCTCAGCATCTGAAAGGAGAGATATCATCATTTGACCATGTAGAG 360  
 DB 301 ATGCAAGTATGAGCTCAGCATCTGAAAGGAGAGATATCATCATTTGACCATGTAGAG 360  
 QY 361 CTGATGGCTTTAGAGAGACCTTTGAAATGAGCTTTACAGATATCCGGACAGCATGCC 420  
 DB 361 CTGATGGCTTTAGAGAGACCTTTGAAATGAGCTTTACAGATATCCGGACAGCATGCC 420  
 QY 421 AAGTTCGTGATGATGAGAGCAATGAGAAAGGACCTGAGATGAGAAATGAGCGCTC 480  
 DB 421 AAGTTCGTGATGATGAGAGCAATGAGAAAGGACCTGAGATGAGAAATGAGCGCTC 480  
 QY 481 ACTTATGAGCTGCAAAAACACAGAGATGAAATTAAGAGATGTGAGAAACATGGA 540  
 DB 481 ACTTATGAGCTGCAAAAACACAGAGATGAAATTAAGAGATGTGAGAAACATGGA 540  
 QY 541 AATGGGTATCATCAGAGAGAGCTGGGAACTACAAACAACACAGACAGATACCTTT 600  
 DB 541 AATGGGTATCATCAGAGAGAGCTGGGAACTACAAACAACACAGACAGATACCTTT 600  
 QY 601 GCGTCCGCGTCAAGCTTATTCAGCCAAATCTCCAGAGAGATCTAAATGATATATCT 660  
 DB 601 GCGTCCGCGTCAAGCTTATTCAGCCAAATCTCCAGAGAGATCTAAATGATATATCT 660  
 QY 661 TGCATTTGATGCTCTTTCTAACTGATATATATCTCTCCAGCTCTCTCTTTTCA 720  
 DB 661 TGCATTTGATGCTCTTTCTAACTGATATATATCTCTCCAGCTCTCTCTTTTCA 720  
 QY 721 TCTGTCAGAGAGTCTTAACTGATATATATCTCTCCAGCTCTCTCTTTTCA 780  
 DB 721 TCTGTCAGAGAGTCTTAACTGATATATATCTCTCCAGCTCTCTCTTTTCA 780  
 QY 781 CGTTATGAGGCTTTGTTGTAACCTTTGTAATTAAGGCGTGAATGAGCTGTTG 840  
 DB 781 CGTTATGAGGCTTTGTTGTAACCTTTGTAATTAAGGCGTGAATGAGCTGTTG 840  
 QY 841 GGAAG 868  
 DB 841 GGAAG 868

## RESULT 2

ABRK25454/C  
 ID ABRK25454 standard; DNA; 121 BP.

ABRK25454;

09-APR-2002 (first entry)

Male-sterile plant producing genome altering oligonucleotide #354.

KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KM o-methyl modification; DNA modification; phosphorothioate linkage;  
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KM abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KM amino acid over production; herbicide resistance; glyphosate resistance;  
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KM modified oil production; modified starch production; waxy starch;  
 KM altered floral morphology; male-sterile plant; albino mutant;  
 KM modified fatty acid content; reduced palmitate production; albino plant;  
 KM increased stearate production; reduced linoleic acid production;  
 KM photosynthetic process.

OS Malus x domestica.

XX Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-0081887S.  
 XX (UYDE ) UNIV DELAWARE.  
 XX Kmiec EB, Gamper HB, Rice MC, Kim J;  
 DR WPI; 2002-106307/14.  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 PS Claim 7; Page 90; 220pp; English.

CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an RNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 CC  
 XX Sequence 121 BP; 24 A; 41 C; 16 G; 40 T; 0 U; 0 Other;

Query Match 8.1%; Score 70; DB 6; Length 121;  
 Best Local Similarity 99.2%; Pred. No. 7,7e-18;  
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGAAGTGGAGAGGTTGATGATCAAGAGATTGAGAACTCAAGTAAAGGAGGTGACTTA 62  
 DB 121 GGAAGTGGAGAGGTTGATGATCAAGAGATTGAGAACTCAAGTAAAGGAGGTGACTTA 62  
 QY 63 CTCGAAGAGAGAGGATGAGATTCAGAGAGGAAAGGAGATACGTTTATGTGATGC 122  
 DB 61 GTCGAAGAGAGGATGAGATTCAGAGAGGAAAGGAGATACGTTTATGTGATGC 2  
 QY 123 T 123  
 DB 1 T 1

## RESULT 3

ABRK25462/C  
 ID ABRK25462 standard; DNA; 121 BP.

ABRK25462;

09-APR-2002 (first entry)

Male-sterile plant producing genome altering oligonucleotide #362.

KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KM o-methyl modification; DNA modification; phosphorothioate linkage;  
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
KW amino acid over production; herbicide resistance; glyphosate resistance;  
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
KW modified oil production; modified starch production; waxy starch;  
KW altered floral morphology; male-sterile plant; albino mutant;  
KW modified fatty acid content; reduced palmitate production; albino plant;  
KW increased stearate production; reduced linolenic acid production;  
KW photosynthetic process.  
XX  
XX Malus x domestica.  
OS Synthetic.  
XX WO200192512-A2.  
XX  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-US017672.  
XX  
XX 01-JUN-2000; 2000US-0208538P.  
XX 30-OCT-2000; 2000US-0244989P.  
XX 27-MAR-2001; 2001US-00818875.  
XX  
XX (UYDE ) UNIV DELAWARE.  
XX  
XX Kmiec EB, Gamper HB, Rice MC, Kim J;  
XX WPI; 2002-106307/14.  
XX  
XX New oligonucleotides with modified nuclease-resistant termini, useful for  
XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
XX nutritional value, herbicide or disease resistance, or modified oil  
XX production.  
XX  
XX Claim 7; Page 91; 220pp; English.  
XX  
XX The invention relates to an oligonucleotide for targeted alteration of a  
XX genetic sequence, which comprises a single-stranded oligonucleotide  
XX having a DNA domain. The DNA domain has at least one mismatch with  
XX respect to the genetic sequence to be altered and further comprises  
XX chemical modifications of the oligonucleotide. The chemical modifications  
XX consist of o-methyl modification, an RNA modification, two or more  
XX phosphorothioate linkages on a terminus, or a combination of any two or  
XX more of these modifications. The oligonucleotides are useful for  
XX directing repair or alteration of plant genetic information. The  
XX oligonucleotides are particularly useful for creating plants with desired  
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved  
XX nutritional value (e.g. altering amino acid content of plants or  
XX conferring amino acid over production), herbicide resistance (e.g.  
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide  
XX resistance), porphyrin herbicide resistance or triazine resistance),  
XX disease resistance, modified oil production, modified starch production  
XX (e.g. increased starch or production of waxy starch), altered floral  
XX morphology (e.g. male-sterile plants) or modified fatty acid content  
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
XX The oligonucleotides are also useful for producing albino mutants for the  
XX analysis of photosynthetic processes. This sequence represents a genome  
XX altering oligonucleotide of the invention  
SQ Sequence 121 BP; 33 A; 29 C; 19 G; 40 T; 0 U; 0 Other;  
Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 7.7e-18;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 148 A 148  
Db 1 A 1  
RESULT 4  
ID ABK25466/c  
ABK25466 standard; DNA; 121 BP.  
XX  
XX ABK25466;  
XX  
XX 09-APR-2002 (first entry)  
XX  
XX Male-sterile plant producing genome altering oligonucleotide #366.  
XX  
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
XX o-methyl modification; RNA modification; phosphorothioate linkage;  
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
KW amino acid over production; herbicide resistance; glyphosate resistance;  
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
KW modified oil production; modified starch production; waxy starch;  
KW altered floral morphology; male-sterile plant; albino mutant;  
KW modified fatty acid content; reduced palmitate production; albino plant;  
KW increased stearate production; reduced linolenic acid production;  
KW photosynthetic process.  
XX  
XX Malus x domestica.  
OS Synthetic.  
XX WO200192512-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-US017672.  
XX  
XX 01-JUN-2000; 2000US-0208538P.  
XX 30-OCT-2000; 2000US-0244989P.  
XX 27-MAR-2001; 2001US-00818875.  
XX  
XX (UYDE ) UNIV DELAWARE.  
XX  
XX Kmiec EB, Gamper HB, Rice MC, Kim J;  
XX WPI; 2002-106307/14.  
XX  
XX New oligonucleotides with modified nuclease-resistant termini, useful for  
XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
XX nutritional value, herbicide or disease resistance, or modified oil  
XX production.  
XX  
XX Claim 7; Page 91; 220pp; English.  
XX  
XX The invention relates to an oligonucleotide for targeted alteration of a  
XX genetic sequence, which comprises a single-stranded oligonucleotide  
XX having a DNA domain. The DNA domain has at least one mismatch with  
XX respect to the genetic sequence to be altered and further comprises  
XX chemical modifications of the oligonucleotide. The chemical modifications  
XX consist of o-methyl modification, an RNA modification, two or more  
XX phosphorothioate linkages on a terminus, or a combination of any two or  
XX more of these modifications. The oligonucleotides are useful for  
XX directing repair or alteration of plant genetic information. The  
XX oligonucleotides are particularly useful for creating plants with desired  
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved  
XX nutritional value (e.g. altering amino acid content of plants or  
XX conferring amino acid over production), herbicide resistance (e.g.  
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide  
XX resistance), porphyrin herbicide resistance or triazine resistance),  
XX disease resistance, modified oil production, modified starch production  
XX (e.g. increased starch or production of waxy starch), altered floral  
XX morphology (e.g. male-sterile plants) or modified fatty acid content  
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).

CC The oligonucleotides are also useful for producing albino mutants for the  
CC analysis of photosynthetic processes. This sequence represents a genome  
CC altering oligonucleotide of the invention

SQ Sequence 121 BP; 34 A; 28 C; 20 G; 39 T; 0 U; 0 Other;

Query Match 8.1%; Score 70; DB 6; Length 121;

Best Local Similarity 99.2%; Pred. No. 7,7e-18;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 ATTGAGACTCAATACAGAGGAGTGCCTACTCCAGAGGAGGATGGATTATACAG 90

DB 121 ATTGAGACTCAATACAGAGGAGGAGTGCCTACTCCAGAGGAGGATGGATTATACAG 62

QY 91 AAGGCAAGAGATCTCTTCTATGTATGCTTAAGTCTCTTATCTTATCTTACG 150

DB 61 TAGGCAAGAGATCTCTTCTATGTATGCTTAAGTCTCTTATCTTATCTTACG 2

QY 151 T 151

DB 1 T 1

SQ Sequence 121 BP; 25 A; 38 C; 17 G; 41 T; 0 U; 0 Other;

Query Match 8.1%; Score 70; DB 6; Length 121;

Best Local Similarity 99.2%; Pred. No. 7,7e-18;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGAGGTTGATCATCAGAGGATTCAGACTCAAGTACAGGCGGAGCTTATCC 66

DB 121 CGTGGAGGTTGATCATCAGAGGATTCAGACTCAAGTACAGGCGGAGCTTATCC 62

QY 67 AAGAGGAGATGGGATTCATCAAGAGGAGGATCTCTGTATGTGATGCTTAA 126

DB 61 TAGGCAAGAGATGGGATTCATCAAGAGGAGGATCTCTGTATGTGATGCTTAA 2

QY 127 G 127

DB 1 G 1

RESULT 6

ABK25453

ID ABK25453 standard; DNA; 121 BP.

ABK25453;

09-APR-2002 (first entry)

Male-sterile plant producing genome altering oligonucleotide #353.

Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

o-methyl modification; DNA modification; phosphorothioate linkage;

DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

abiotic stress tolerance; improved nutritional value; hygromycin; primer;

amino acid over production; herbicide resistance; glyphosate resistance;

imidazolinone herbicide resistance; sulphonylurea herbicide resistance;

porphyric herbicide resistance; triazine resistance; disease resistance;

modified oil production; modified starch production; waxy starch;

altered floral morphology; male-sterile plant; albino mutant;

modified fatty acid content; reduced palmitate production; albino plant;

increased stearate production; reduced linolenic acid production;

photosynthetic process.

Malus x domestica.

Synthetic.

WO200192512-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US017672.

01-JUN-2000; 2000US-0206538P.

30-OCT-2000; 2000US-0244989P.

27-MAR-2001; 2001US-0081887S.

(UYDE ) UNIV DELAWARE.

Kmiec EB, Gampier HB, Rice MC, Kim U;

WPI; 2002-106307/14.

New oligonucleotides with modified nuclease-resistant termini, useful for

creating plants with desired phenotypes, e.g. stress tolerance, improved

nutritional value, herbicide or disease resistance, or modified oil

production.

Claim 7, Page 91; 220pp; English.

The invention relates to an oligonucleotide for targeted alteration of a





Db 121 T 121

RESULT 8  
ABK25461  
ID ABK25461 standard; DNA, 121 BP.  
XX  
XX  
AC ABK25461;  
XX  
DT 09-APR-2002 (first entry)  
DE Male-sterile plant producing genome altering oligonucleotide #361.  
XX  
KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
KM o-methyl modification; LNA modification; phosphorothioate linkage;  
KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
KM abiotic stress tolerance; improved nutritional value; hygromycin-B;  
KM amino acid over production; herbicide resistance; glyphosate resistance;  
KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
KM porphyrin herbicide resistance; triazine resistance; disease resistance;  
KM modified oil production; modified starch production; waxy starch;  
KM altered floral morphology; male-sterile plant; albino mutant;  
KM modified fatty acid content; reduced palmitate production; albino plant;  
KM increased stearate production; reduced linolenic acid production;  
KM photosynthetic process.  
OS Malus x domestica.  
XX Synthetic.  
XX WO200192512-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-US017672.  
XX  
XX 01-JUN-2000; 2000US-0208538P.  
XX 30-OCT-2000; 2000US-0244989P.  
XX 27-MAR-2001; 2001US-00818875.  
XX  
XX (UYDE ) UNIV DELAWARE.  
XX  
XX Kmiec EB, Gamber HB, Rice MC, Kim U;  
XX  
XX WPI; 2002-106307/14.  
XX  
XX  
XX New oligonucleotides with modified nuclease-resistant termini, useful for  
XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
XX nutritional value, herbicide or disease resistance, or modified oil  
XX production.  
XX  
XX Claim 7, Page 91, 220pp; English.  
XX  
XX The invention relates to an oligonucleotide for targeted alteration of a  
XX genetic sequence, which comprises a single-stranded oligonucleotide  
XX having a DNA domain. The DNA domain has at least one mismatch with  
XX respect to the genetic sequence to be altered and further comprises  
XX chemical modifications of the oligonucleotide. The chemical modifications  
XX consist of o-methyl modification, an LNA modification, two or more  
XX phosphorothioate linkages on a terminus, or a combination of any two or  
XX more of these modifications. The oligonucleotides are useful for  
XX directing repair or alteration of plant genetic information. The  
XX oligonucleotides are particularly useful for creating plants with desired  
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved  
XX nutritional value (e.g. altering amino acid content of plants or  
XX conferring amino acid over production), herbicide resistance (e.g.  
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide  
XX resistance), porphyrin herbicide resistance or triazine resistance),  
XX disease resistance, modified oil production, modified starch production  
XX (e.g. increased starch or production of waxy starch), altered floral  
XX morphology (e.g. male-sterile plants) or modified fatty acid content  
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
XX The oligonucleotides are also useful for producing albino mutants for the

CC analysis of photosynthetic processes. This sequence represents a genome  
CC altering oligonucleotide of the invention  
XX  
XX Sequence 121 BP; 40 A; 19 C; 29 G; 33 T; 0 U; 0 Other;  
SQ  
Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 7,7e-18;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 28 AGATTAGAACTCAAGTAAGGACGAGTACCTACTCCAGAGGAGGAAATGGATTATC 87  
DB 1 AGGATTAGAACTCAAGTAAGGACGAGTACCTACTCCAGAGGAGGAAATGGATTATC 60  
OY 88 AGAAGGCAAGGAGATCACTGTTCTATGATGCTAAAGTATCTTATCATTTATCT 147  
DB 61 TAGAAGCAAGGAGATCACTGTTCTATGATGCTAAAGTATCTTATCATTTATCT 120  
OY 148 A 148  
DB 121 A 121  
RESULT 9  
ABK25457  
ID ABK25457 standard; DNA, 121 BP.  
XX  
XX  
AC ABK25457;  
XX  
DT 09-APR-2002 (first entry)  
DE Male-sterile plant producing genome altering oligonucleotide #357.  
XX  
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
XX o-methyl modification; LNA modification; phosphorothioate linkage;  
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
XX abiotic stress tolerance; improved nutritional value; hygromycin-B;  
XX amino acid over production; herbicide resistance; glyphosate resistance;  
XX imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
XX porphyrin herbicide resistance; triazine resistance; disease resistance;  
XX modified oil production; modified starch production; waxy starch;  
XX altered floral morphology; male-sterile plant; albino mutant;  
XX modified fatty acid content; reduced palmitate production; albino plant;  
XX increased stearate production; reduced linolenic acid production;  
XX photosynthetic process.  
OS Malus x domestica.  
XX Synthetic.  
XX WO200192512-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 01-JUN-2001; 2001WO-US017672.  
XX  
XX 01-JUN-2000; 2000US-0208538P.  
XX 30-OCT-2000; 2000US-0244989P.  
XX 27-MAR-2001; 2001US-00818875.  
XX  
XX (UYDE ) UNIV DELAWARE.  
XX  
XX Kmiec EB, Gamber HB, Rice MC, Kim U;  
XX  
XX WPI; 2002-106307/14.  
XX  
XX  
XX New oligonucleotides with modified nuclease-resistant termini, useful for  
XX creating plants with desired phenotypes, e.g. stress tolerance, improved  
XX nutritional value, herbicide or disease resistance, or modified oil  
XX production.  
XX  
XX Claim 7, Page 91, 220pp; English.  
XX  
XX The invention relates to an oligonucleotide for targeted alteration of a  
XX genetic sequence, which comprises a single-stranded oligonucleotide

CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of 0-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 CC  
 SQ Sequence 121 BP; 41 A; 17 C; 38 G; 25 T; 0 U; 0 Other;

Query Match 8.1%; Score 70; DB 6; Length 121;  
 Best Local Similarity 99.2%; Pred. No. 7.7e-16;  
 Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGGAAGTTGAGATCAAGAGTTGAGAACTCAAGTAAACAGGAGTGACTACTCC 66  
 DB 1 CTTGGGAAGTTGAGATCAAGAGTTGAGAACTCAAGTAAACAGGAGTGACTACTCC 60  
 QY 67 AAGAGAGCAATGGGATTATCAAGAGCAAGAGATCACTGTTATGTGATCTAA 126  
 DB 61 TAGAGAGCAATGGGATTATCAAGAGCAAGAGATCACTGTTATGTGATCTAA 120  
 QY 127 G 127  
 DB 121 G 121

RESULT 10  
 ID AAX27168 standard; DNA; 1964 BP.

XX AAX27168;  
 AC 27-MAY-1999 (first entry)  
 DT 27-MAY-1999 (first entry)  
 XX Rat GMEB-2 coding sequence.  
 DE Rat GMEB-2 coding sequence.  
 KM GMEB-1, glucocorticoid modulating element binding protein;  
 KM glucocorticoid receptor; GR dose-response curve; glucocorticoid hormone;  
 KM rat; ss.  
 OS Rattus norvegicus.  
 XX  
 XX W09905273-A1.  
 PN 04-FEB-1999.  
 PD 04-FEB-1999.  
 XX 14-JUL-1998; 98WO-US014423.  
 PF 25-JUL-1997; 97US-0053846P.  
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 PA Simons SS, Kaul S, Jackson DA, Zeng H, Hiseaji O,  
 XX MPI, 1999-153319/13.  
 DR P-PSDB; AAY00894.  
 XX  
 PT New nucleic acid encoding glucocorticoid modulatory element binding  
 PT protein - useful to increase the expression of genes that are linked to a

PT glucocorticoid modulatory element.  
 XX  
 PS Claim 2, Page 60-61, 78pp; English.  
 XX

CC This sequence encodes the rat glucocorticoid modulating element binding  
 CC protein, GMEB-2, of the invention. The polypeptides interact with a GME  
 CC (glucocorticoid modulatory element), linked to a nucleic acid sequence,  
 CC resulting in increased expression of the nucleic acid sequence. The  
 CC polypeptides may be supplied as such or provided by expression of the  
 CC nucleic acid sequences, particularly to treat cells that do not produce  
 CC sufficient, or functional, GME-binding protein. The nucleic acid  
 CC sequences and the polypeptides of the invention can also be used to  
 CC screen for presence of GME bound to a gene in a cell. Fragments of the  
 CC nucleic acid sequences are useful as primers and probes to isolate the  
 CC corresponding genomic sequence. The polypeptides may be used in two-  
 CC hybrid screens to identify other proteins involved in modulating the  
 CC glucocorticoid receptor (GR) dose-response curve. The polypeptides bind  
 CC to GME, enhancing expression by a GR of a gene regulated by a GME  
 CC (glucocorticoid responsive element). This results in increased expression  
 CC of the GR-regulated gene (which may be endogenous or introduced by gene  
 CC therapy) in presence of physiological levels of a glucocorticoid hormone  
 CC  
 SQ Sequence 1964 BP; 515 A; 539 C; 526 G; 384 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 2; Length 1964;  
 Best Local Similarity 100.0%; Pred. No. 0.00071;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTTTGGGAAAAA  
 DB 1930 TTTTGGGAAAAA  
 1963

RESULT 11

ID ADA02946 standard; cDNA; 3130 BP.

XX ADA02946;  
 AC 06-NOV-2003 (first entry)  
 DT 06-NOV-2003 (first entry)  
 XX Mouse Nek2 carcinoma associated cDNA, SEQ ID NO:1464.  
 DE Mouse Nek2 carcinoma associated cDNA, SEQ ID NO:1464.  
 XX  
 XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
 KM prostate; lymphoma; leukemia; cytoskeletal; gene therapy; drug screening;  
 KM gene; ss.  
 OS Mus sp.  
 XX  
 XX M02003057146-A2.  
 PN 17-JUL-2003.  
 PD 17-JUL-2003.  
 XX 26-DEC-2002; 2002WO-US041414.  
 PF 26-DEC-2001; 2001US-00035832.  
 PR (SAGR-) SAGRES DISCOVERY.  
 PA Morris DW;  
 XX MPI, 2003-587068/55.  
 DR  
 XX  
 PT New recombinant nucleic acid encoding carcinoma associated protein,  
 PT useful for preparing compositions for treating carcinomas.  
 PS Claim 1, SEQ ID NO 1464, 245pp; English.  
 XX  
 XX The invention relates to recombinant carcinoma associated (CA) nucleic  
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
 CC invention also encompasses expression vectors and host cells comprising a  
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically

CC binds to the protein, and a biochip comprising CA nucleic acid or  
 CC fragments thereof. The sequences of the invention were identified using  
 CC oncogenic retroviruses, which insert into the genome of the host organism  
 CC at random. Many of these do not carry transduced host oncogenes or  
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
 CC direct consequence of the effects of proviral integration into host  
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
 CC leukemia (especially breast cancer, prostate cancer, lymphoma or  
 CC carcinoma) or a propensity to carcinoma by determination of the sequence  
 CC of a CA gene, or by determination of CA gene expression in particular  
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
 CC therapeutic agents and in screening and evaluating drug candidates. The  
 CC present sequence represents a specifically claimed murine CA nucleic acid  
 CC sequence of the invention. Note: The complete sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 8; Length 3130;  
 Best Local Similarity 100.0%; Pred. No. 0.00067;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 868  
 |||||  
 DB 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 3117

#### RESULT 12

ADB72684  
 ID ADB72684 standard; mRNA; 3130 BP.

XX ADB72684;

XX 04-DEC-2003 (first entry)

DE Mouse Nek2 mRNA.

XX mouse; ss; cytosolic; gene therapy; vaccine; carcinoma; lymphomas;  
 KW cancer; neoplasm; adenocarcinoma; sarcoma.

XX Mus sp.

XX WO2003008583-A2.

XX 30-JAN-2003.

XX 26-DEC-2001; 2001WO-US051291.

XX 02-MAR-2001; 2001US-00798586.

XX 23-OCT-2001; 2001US-00084113.

XX 08-NOV-2001; 2001US-00052482.

XX 30-NOV-2001; 2001US-00997722.

XX 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX Claim 1; SEQ ID NO 512; 2304bp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a  
 CC nucleotide sequence selected from any of the 660 sequences fully defined  
 CC in the specification. A polynucleotide of the invention has cytosolic  
 CC activity, and may have a use in gene therapy, or in a vaccine. The  
 CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and

CC sarcomas. The present sequence represents a mouse mRNA of the invention.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 9; Length 3130;  
 Best Local Similarity 100.0%; Pred. No. 0.00067;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 868  
 |||||  
 DB 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 3117

#### RESULT 13

ADC85426  
 ID ADC85426 standard; DNA; 3130 BP.

XX ADC85426;

XX 01-JAN-2004 (first entry)

DE Mouse Nek2 mRNA sequence.

XX Cytosolic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;  
 KW secreted; transmembrane; intracellular; ds.

XX Mus sp.

XX WO2003045230-A2.

XX 05-JUN-2003.

XX 02-DEC-2002; 2002WO-US038582.

XX 30-NOV-2001; 2001US-00997722.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-513603/48.

XX New recombinant nucleic acid comprising a nucleotide sequence of any of  
 PT the carcinoma-associated (CA) genes; useful for screening for drug  
 PT candidates for diagnosing or treating carcinomas.

XX Claim 1; SEQ ID NO 212; 983bp; English.

XX The invention relates to a recombinant nucleic acid comprising a  
 CC nucleotide sequence selected from any of the fully defined carcinoma-  
 CC associated (CA) genes from the 50 tables given in the specification. The  
 CC CA proteins are secreted, transmembrane or intracellular proteins. The  
 CC recombinant nucleic acids are useful for screening for drug candidates  
 CC for diagnosing or treating carcinomas. Sequences given in ADC85215-  
 CC ADC85514 represent CA genes of the invention.

XX Sequence 3130 BP; 801 A; 692 C; 869 G; 768 T; 0 U; 0 Other;

Query Match 3.9%; Score 34; DB 9; Length 3130;  
 Best Local Similarity 100.0%; Pred. No. 0.00067;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 868  
 |||||  
 DB 3084 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 3117

#### RESULT 14

ABL93464/C  
 ID ABL93464 standard; cDNA; 469 BP.

XX ABL93464;

XX

DT 10-JUN-2002 (first entry)  
 XX Arabidopsis thaliana nucleic acid sequence Ref:2027229 SEQ ID NO:229.  
 DE Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;  
 KW genetic modification; gene; ss.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX US200203280-A1.  
 XX 21-FEB-2002.  
 PD 26-JAN-2001; 2001US-00770444.  
 XX 27-JAN-2000; 2000US-0178502P.  
 PR  
 XX (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.  
 XX  
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,  
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD,  
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N,  
 PI Hurban P;  
 XX WPI: 2002-267486/31.  
 DR  
 XX  
 PT New Arabidopsis thaliana nucleic acid, for identifying homologous genes,  
 PT producing compositions that modulate the expression or function of its  
 PT encoded protein, and mapping functional regions of a protein.  
 XX  
 PS Claim 1; SEQ ID NO 229; 44bp; English.  
 XX  
 CC The present invention describes an Arabidopsis thaliana nucleic acid (I)  
 CC comprising a sequence capable of hybridizing under stringent conditions  
 CC to a sequence (SI) selected from any one of the 399 sequences given in  
 CC ABL93236 to ABL94234. (I) have insecticide and fungicide activities, and  
 CC they can be used as protein expression modulators. (I) can be used in  
 CC identifying homologous or related genes, in producing compositions that  
 CC modulate the expression or function of their encoded proteins, mapping  
 CC functional regions of the proteins, and in studying associated  
 CC physiological pathways. (I) can also be used: (1) for the genetic  
 CC manipulation of cells, particularly plant cells; (2) in screening assays  
 CC of various plant strains to determine the strains that are best capable  
 CC of withstanding a particular disease or environmental stress; (3) for  
 CC enhancing or inhibiting production of a biosynthetic product in a plant;  
 CC (4) as probes in mapping and in diagnosis, in genetic modification and  
 CC for screening purposes, to generate additional copies of the nucleic  
 CC acids, to generate ribozymes or antisense oligonucleotides, and as single  
 CC stranded DNA probes or as triple-strand forming oligonucleotides; and (5)  
 CC for generating genetically modified transgenic organisms. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC USPTO web site  
 XX  
 SQ Sequence 469 BP; 120 A; 88 C; 93 G; 168 T; 0 U; 0 Other;

Query Match 3.8%; Score 33; DB 6; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 836 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 868  
 DB 65 TTGTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33  
 RESULT 15  
 ABX60840/C  
 ID ABX60840 standard; DNA; 469 BP.  
 XX  
 AC ABX60840;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Arabidopsis thaliana polynucleotide #186.  
 XX  
 KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;  
 KW genetic modification; environmental stress; disease resistance;  
 KW fungicide; insecticide; stress tolerance.  
 XX  
 OS Arabidopsis thaliana.  
 OS US2002142319-A1.  
 XX  
 PN 03-OCT-2002.  
 XX  
 PD 07-AUG-2001; 2001US-00924035.  
 XX  
 PF 13-AUG-1999; 99US-0148784P.  
 PR 11-AUG-2000; 2000US-00638258.  
 XX  
 XX (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAM/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 XX  
 XX Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y;  
 PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
 PI Garcia CA;  
 XX  
 DR WPI: 2003-102509/09.  
 XX  
 PT Novel Arabidopsis thaliana nucleic acid useful for constructing a  
 PT transgenic plant with enhanced disease resistance and enhanced traits of  
 PT interest, as probes, and in diagnosis and screening purposes.  
 XX  
 PS Claim 1; Page 67; 277bp; English.  
 XX  
 CC The invention relates to Arabidopsis thaliana nucleic acid sequences. The  
 CC DNA sequences and the polypeptides they encode are useful for identifying  
 CC homologous or related genes, for producing compositions that modulate the  
 CC expression or function of the polypeptides, for mapping functional  
 CC regions of the proteins, in diagnosis, for studying associated  
 CC physiological pathways, for genetic manipulation of cells, preferably  
 CC plant cells, in screening assays of various plant strains to determine  
 CC the strains that are capable of withstanding a particular disease or  
 CC environmental stress, for enhancing or inhibiting production of  
 CC biosynthetic products in plants and to create genetically modified and  
 CC transgenic organisms, such as plant cells and plants. Transgenic plants  
 CC are useful for introducing or improving disease resistance and stress

CC tolerance in plants, screening biologically active agents, such as  
 CC fungicides and insecticides, and for identifying factors involved in  
 CC biosynthetic pathways of nutritional, commercial or medicinal value.  
 CC Sequences ABX6065-ABX6154 represent Arabidopsis thaliana  
 CC polynucleotides of the invention  
 XX

SQ Sequence 469 BP; 120 A; 88 C; 93 G; 168 T; 0 U; 0 Other;

Query Match 3.8%; Score 33; DB 7; Length 469;  
 Best Local Similarity 100.0%; Pred. No. 0.0022;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 836 TTGTGGGAAAAAAAAAAAAAAAAAAAA 868  
 Db 65 TTGTGGGAAAAAAAAAAAAAAAAAAAA 33

Search completed: September 25, 2004, 22:55:31  
 Job time : 452.034 secs





score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

(without alignments)  
10259.034 Million cell updates/sec

Sequence: 1 atggtgacgtgtgtgaaagttgaa...aaaaaa 866

Scoring table: OLIGO\_NUC

Searched: 3470272 seqs, 21671516995 residues

word size :

Total number of hits satisfying chosen parameters: 6940544

Maximum DB seq length: 200000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl : \*

Result No.	Score	Query Match	Length	DB	ID	Description
1	868	100.0	868	8	MDC291490	AJ791490 Maltus dom
2	691	79.6	890	8	AB081092	AB081092 Maltus x d
3	323	31.0	3130	8	MDC291491	AJ791491 Maltus dom
4	70	8.1	121	6	AX324675	AX324675 Sequence
5	70	8.1	121	6	AX324676	AX324676 Sequence
6	70	8.1	121	6	AX324677	AX324677 Sequence
7	70	8.1	121	6	AX324680	AX324680 Sequence
8	70	8.1	121	6	AX324683	AX324683 Sequence
9	70	8.1	121	6	AX324684	AX324684 Sequence
10	70	8.1	121	6	AX324687	AX324687 Sequence
11	70	8.1	121	6	AX324688	AX324688 Sequence
12	36	4.1	1811	5	BC043631	BC043631 Xenopus 1
13	34	3.9	967	8	AB038462	AB038462 Rosa rugo
14	34	3.9	1929	9	BC043508	BC043508 Homo sapi
15	34	3.9	1964	10	AF059273	AF059273 Rattus no
16	34	3.9	2572	9	HSW802300	AI137558 Homo sapi
17	34	3.9	3130	6	AX95837	AX95837 Sequence
18	34	3.9	3130	10	NC095610	U95610 Mus musculu
19	34	3.9	189394	2	AC115933	AC115933 Mus muscu
20	34	3.9	189394	2	AC115933	AC115933 Mus muscu
21	33	3.8	899	8	BYNCALMOD	L14071 Byxonia dio
22	33	3.8	110000	3	AC116957_1	Continuation (2 of
23	33	3.8	179498	9	AC009831	AC009831 Homo sapi
24	33	3.8	182428	2	AC036167	AC036167 Homo sapi
25	33	3.8	213753	2	AC1336743	AC1336743 Mus muscu
26	32	3.7	597	5	AB033882	AB033882 Coccurnix
27	32	3.7	875	8	BPE488589	AJ488589 Betula pe
28	32	3.7	1667	9	BC005291	BC005291 Homo sapi
29	32	3.7	1350	9	BC007417	BC007417 Homo sapi
30	32	3.7	1399	9	BC047953	BC047953 Homo sapi
31	32	3.7	1311	9	BC036708	BC036708 Homo sapi
32	32	3.7	2334	4	BC039824	BC039824 Homo sapi
33	32	3.7	2600	10	BC037001	BC037001 Mus muscu
34	32	3.7	3575	9	BC030693	BC030693 Homo sapi
35	32	3.7	110000	2	AC098456_0	AC098456 Rattus no
36	32	3.7	166073	2	AL772241	AL772241 Danto rer
37	32	3.7	199337	2	BX649267	BX649267 Danto rer
38	32	3.7	205964	2	AC145960	AC145960 Gallus ga
39	32	3.7	220420	5	BX000452	BX000452 Zebrafish
40	32	3.7	225764	2	AC133209	AC133209 Mus muscu
41	32	3.7	234502	2	BX322654	BX322654 Danto rer
42	32	3.7	238530	5	BX539310	BX539310 Zebrafish
43	32	3.7	250264	2	AC109870	AC109870 Rattus no
44	32	3.7	251762	3	AB014851	AB014851 Plasmodu
45	32	3.7	261251	2	AC098618	AC098618 Rattus no
46	32	3.7	310779	2	AC005140	AC005140 Plasmodu
47	32	3.7	734	10	BC048516	BC048516 Mus muscu
48	32	3.6	784	10	BC031634	BC031634 Mus muscu
49	31	3.6	853	6	AX548546	AX548546 Sequence
50	31	3.6	1033	6	189264	189264 Sequence 5
51	31	3.6	1013	9	BC002831	BC002831 Homo sapi
52	31	3.6	1065	5	GCNKA8	Y11948 G.gallus NR
53	31	3.6	1111	5	GCNKA8	Y1065 G.gallus NK
54	31	3.6	1111	6	AR212368	AR212368 Sequence
55	31	3.6	1136	10	BC048473	BC048473 Mus muscu
56	31	3.6	1246	6	AR21267	AR21267 Sequence
57	31	3.6	1257	6	AX478035	AX478035 Sequence
58	31	3.6	1333	8	AF268422	AF268422 Brassaica
59	31	3.6	1358	9	AK026217	AK026217 Homo sapi
60	31	3.6	1416	10	RNMCMR1	Y

66	31	3.5	1897	9	BC002586	BC002586 Homo sapi	139	30	3.5	763	9	BC003540	BC003540 Homo sapi
67	31	3.6	1898	10	BC031885	BC031885 Mus muscu	140	30	3.5	763	9	BC009428	BC009428 Homo sapi
68	31	3.6	1951	9	BC027930	BC027930 Homo sapi	141	30	3.5	803	10	AF169156	AF169156 Mus muscu
69	31	3.6	1953	9	AB053326	AB053326 Homo sapi	142	30	3.5	805	6	BD019969	BD019969 Novel gen
70	31	3.6	1963	10	BC030492	BC030492 Mus muscu	143	30	3.5	805	6	BD099907	BD099907 Novel gen
71	31	3.6	1988	9	AB053325	AB053325 Homo sapi	144	30	3.5	816	10	AF402772	AF402772 Rattus no
72	31	3.6	1999	9	AB053324	AB053324 Homo sapi	145	30	3.5	822	8	AB101439	AB101439 Prunus mu
73	31	3.6	2227	9	BC043620	BC043620 Homo sapi	146	30	3.5	845	9	BC044653	BC044653 Homo sapi
74	31	3.6	2263	10	BC031747	BC031747 Mus muscu	147	30	3.5	846	6	BD084043	BD084043 Homo sapi
75	31	3.6	2396	6	AX398420	AX398420 Sequence	148	30	3.5	846	6	BD093358	BD093358 Envtromne
76	31	3.6	2714	6	AX358768	AX358768 Sequence	149	30	3.5	879	8	AY428650	AY428650 Helianthu
77	31	3.6	2714	6	AX362261	AX362261 Sequence	150	30	3.5	912	3	AY069269	AY069269 Drosophil
78	31	3.6	2714	6	AY358452	AY358452 Homo sapi	151	30	3.5	916	9	BC000308	BC000308 Homo sapi
79	31	3.6	2798	9	BC017174	BC017174 Homo sapi	152	30	3.5	916	9	BC019312	BC019312 Homo sapi
80	31	3.6	3227	4	AF010191	AF010191 Fells cat	153	30	3.5	918	5	OMY580843	OMY580843 Oncorhync
81	31	3.6	3250	9	HSB805691	HSB805691 Homo sapi	154	30	3.5	944	10	AF060872	AF060872 Mus muscu
82	31	3.6	36148	3	AC116100	AC116100 Dictyoste	155	30	3.5	952	9	HSB809308	HSB809308 Homo sapi
83	31	3.6	49306	3	AC115606	AC115606 Dictyoste	156	30	3.5	954	3	AY089222	AY089222 Drosophil
84	31	3.6	52867	2	AC021293	AC021293 Homo sapi	157	30	3.5	962	10	AF169157	AF169157 Mus muscu
85	31	3.6	137243	10	AL669902	AL669902 Mouse DNA	158	30	3.5	965	10	BC046674	BC046674 Homo sapi
86	31	3.6	159034	2	BK470154	BK470154 Datto rer	159	30	3.5	968	9	BC017116	BC017116 Homo sapi
87	31	3.6	160605	10	AC136101	AC136101 Rattus no	160	30	3.5	972	8	VURNACH14	VURNACH14 Homo sapi
88	31	3.6	161912	2	AC132314	AC132314 Mus muscu	161	30	3.5	983	10	BC064085	BC064085 Mus muscu
89	31	3.6	167539	2	AC141812	AC141812 Apis mell	162	30	3.5	988	8	AF154668	AF154668 Nicotiana
90	31	3.6	167539	2	AC141812	AC141812 Apis mell	163	30	3.5	990	6	BD078441	BD078441 101 human
91	31	3.6	169092	2	AC027572	AC027572 Homo sapi	164	30	3.5	990	6	BD078441	BD078441 101 human
92	31	3.6	177056	2	AC132579	AC132579 Mus muscu	165	30	3.5	1018	3	AK113894	AK113894 Clona int
93	31	3.6	182709	2	AC108403	AC108403 Mus muscu	166	30	3.5	1023	3	BC011708	BC011708 Homo sapi
94	31	3.6	182709	2	AC131772	AC131772 Mus muscu	167	30	3.5	1037	8	AY046929	AY046929 Oryza sat
95	31	3.6	191118	2	AC133170	AC133170 Mus muscu	168	30	3.5	1051	9	IR1034327	IR1034327 Homo sapi
96	31	3.6	197572	2	BK842704	BK842704 Datto rer	169	30	3.5	1058	9	HSB800817	HSB800817 Homo sapi
97	31	3.6	200031	2	AC104676	AC104676 Sus scrof	170	30	3.5	1060	9	HSB800823	HSB800823 Homo sapi
98	31	3.6	204652	2	PEFVAL13P6	PEFVAL13P6 Plasmodu	171	30	3.5	1068	9	AF002210	AF002210 Homo sapi
99	31	3.6	266115	2	AC122201	AC122201 Mus muscu	172	30	3.5	1074	3	HSB800078	HSB800078 Homo sapi
100	31	3.6	307166	10	AC116748	AC116748 Mus muscu	173	30	3.5	1076	3	MILEM1A	MILEM1A Homo sapi
101	31	3.5	79	6	AX494892	AX494892 Sequence	174	30	3.5	1080	6	AR035137	AR035137 Sequence
102	30	3.5	160	6	AX494834	AX494834 Sequence	175	30	3.5	1080	6	AR035137	AR035137 Sequence
103	30	3.5	166	6	AX494882	AX494882 Sequence	176	30	3.5	1080	6	BD140352	BD140352 Superoxid
104	30	3.5	169	6	AX494885	AX494885 Sequence	177	30	3.5	1080	6	BD140352	BD140352 Superoxid
105	30	3.5	197	6	AR425019	AR425019 Sequence	178	30	3.5	1082	9	BC020940	BC020940 Homo sapi
106	30	3.5	197	6	BD120572	BD120572 EST and e	179	30	3.5	1083	9	BC052605	BC052605 Homo sapi
107	30	3.5	198	6	AR425018	AR425018 Sequence	180	30	3.5	1089	9	BC006505	BC006505 Homo sapi
108	30	3.5	198	6	BD120571	BD120571 EST and e	181	30	3.5	1093	3	AF002571	AF002571 Homo sapi
109	30	3.5	217	6	AX182144	AX182144 Sequence	182	30	3.5	1096	3	AF006727	AF006727 Meloidogy
110	30	3.5	380	11	BT028857	BT028857 S208P378	183	30	3.5	1101	9	BC001720	BC001720 Homo sapi
111	30	3.5	412	5	LAU93207	LAU93207 Liza aurata	184	30	3.5	1108	9	S62028	S62028 recoverin l
112	30	3.5	415	6	BD271551	BD271551 49 human	185	30	3.5	1109	10	BC031711	BC031711 Mus muscu
113	30	3.5	416	9	AK024545	AK024545 Homo sapi	186	30	3.5	1135	9	BC026287	BC026287 Homo sapi
114	30	3.5	418	9	BC062215	BC062215 Homo sapi	187	30	3.5	1144	9	AF014404	AF014404 Homo sapi
115	30	3.5	421	11	G15951	G15951 human STR C	188	30	3.5	1178	9	BC014432	BC014432 Homo sapi
116	30	3.5	423	6	AX006054	AX006054 Sequence	189	30	3.5	1179	9	BC035797	BC035797 Homo sapi
117	30	3.5	434	5	AF503957	AF503957 Dp1nephel	190	30	3.5	1212	8	AY427801	AY427801 Arabidops
118	30	3.5	451	6	AR415101	AR415101 Sequence	191	30	3.5	1218	9	AF117959	AF117959 Homo sapi
119	30	3.5	451	6	BD110654	BD110654 EST and e	192	30	3.5	1226	9	AF052136	AF052136 Homo sapi
120	30	3.5	458	6	AX781005	AX781005 Sequence	193	30	3.5	1232	6	BD190855	BD190855 Secreted
121	30	3.5	508	6	AY190740	AY190740 Pagrus ma	194	30	3.5	1239	9	AK000852	AK000852 Homo sapi
122	30	3.5	520	6	AX386509	AX386509 Sequence	195	30	3.5	1246	8	BT009439	BT009439 Homo sapi
123	30	3.5	522	9	AK026629	AK026629 Homo sapi	196	30	3.5	1256	9	BC063557	BC063557 Homo sapi
124	30	3.5	529	9	BC003667	BC003667 Homo sapi	197	30	3.5	1258	9	BC001809	BC001809 Homo sapi
125	30	3.5	572	6	AR174092	AR174092 Sequence	198	30	3.5	1258	9	BC001824	BC001824 Homo sapi
126	30	3.5	572	6	BT009481	BT009481 Trilicium	199	30	3.5	1260	10	BC061808	BC061808 Rattus no
127	30	3.5	608	10	BC048521	BC048521 Mus muscu	200	30	3.5	1263	5	AF532312	AF532312 Opsanus b
128	30	3.5	609	9	BC020723	BC020723 Homo sapi	201	30	3.5	1274	8	AY171231	AY171231 Chlamydom
129	30	3.5	632	10	AB046449	AB046449 Rattus no	202	30	3.5	1289	9	BC019268	BC019268 Homo sapi
130	30	3.5	634	11	BY033759	BY033759 S212P578	203	30	3.5	1312	9	AY358200	AY358200 Homo sapi
131	30	3.5	669	6	AX523497	AX523497 Sequence	204	30	3.5	1318	9	AY358200	AY358200 Homo sapi
132	30	3.5	681	9	IROEST126	IROEST126 Homo sapi	205	30	3.5	1319	10	BC001990	BC001990 Mus muscu
133	30	3.5	685	9	AF293368	AF293368 Homo sapi	206	30	3.5	1330	10	BC062057	BC062057 Rattus no
134	30	3.5	710	9	BC063502	BC063502 Homo sapi	207	30	3.5	1331	9	BC015524	BC015524 Homo sapi
135	30	3.5	737	10	AB046448	AB046448 Mus muscu	208	30	3.5	1332	9	BC001055	BC001055 Homo sapi
136	30	3.5	742	9	AB046613	AB046613 Homo sapi	209	30	3.5	1337	9	BC033871	BC033871 Homo sapi
137	30	3.5	744	9	AK074237	AK074237 Homo sapi	210	30	3.5	1356	9	BC002543	BC002543 Homo sapi
138	30	3.5	751	9	AF229832	AF229832 Homo sapi	211	30	3.5	1356	10	AF203914	AF203914 Mus muscu

212	30	3.5	1373	5	SACHORION	X93306 Sparus aur	285	30	3.5	2102	10	BC029065	BC029065 Mus muscu
213	30	3.5	1374	5	HSMB01163	AL117627 Homo sapi	286	30	3.5	2116	9	BC050523	BC050523 Homo sapi
214	30	3.5	1381	4	AB047244	AB047244 Sorex ung	287	30	3.5	2131	9	BC034410	BC034410 Homo sapi
215	30	3.5	1383	9	BC016792	BC016792 Homo sapi	288	30	3.5	2132	9	AF258577	AF258577 Homo sapi
216	30	3.5	1390	10	BC015307	BC015307 Mus muscu	289	30	3.5	2132	9	AF258577	AF258577 Homo sapi
217	30	3.5	1400	8	AY063461	AY063461 Helianthu	290	30	3.5	2152	10	AB000113	AB000113 Rattus no
218	30	3.5	1411	6	AR177872	AR177872 Sequence	291	30	3.5	2199	9	AK074246	AK074246 Homo sapi
219	30	3.5	1411	6	AR340578	AR340578 Sequence	292	30	3.5	2199	9	BC021851	BC021851 Homo sapi
220	30	3.5	1414	6	AB5061	AB5061 Sequence 5	293	30	3.5	2202	3	AK116052	AK116052 Ciona int
221	30	3.5	1414	6	AR316377	AR316377 Sequence	294	30	3.5	2228	9	BC062614	BC062614 Homo sapi
222	30	3.5	1414	6	BD058038	BD058038 Plants wi	295	30	3.5	2240	9	AK000532	AK000532 Homo sapi
223	30	3.5	1438	6	BC009834	BC009834 Homo sapi	296	30	3.5	2265	6	AX376540	AX376540 Sequence
224	30	3.5	1439	10	BC022734	BC022734 Mus muscu	297	30	3.5	2265	6	AX454758	AX454758 Sequence
225	30	3.5	1451	9	BC017400	BC017400 Homo sapi	298	30	3.5	2265	6	AX491236	AX491236 Sequence
226	30	3.5	1457	10	RNCKR5	Y12009 R.norvegicu	299	30	3.5	2265	9	BC014923	BC014923 Homo sapi
227	30	3.5	1469	10	BC005631	BC005631 Mus muscu	300	30	3.5	2286	9	BC020211	BC020211 Homo sapi
228	30	3.5	1485	9	AF159141	AF159141 Homo sapi	301	30	3.5	2290	9	BC015738	BC015738 Homo sapi
229	30	3.5	1512	9	BC003417	BC003417 Homo sapi	302	30	3.5	2314	9	BC050454	BC050454 Homo sapi
230	30	3.5	1516	9	BC023662	BC023662 Homo sapi	303	30	3.5	2326	3	AY119078	AY119078 Drosophil
231	30	3.5	1552	9	AY358158	AY358158 Homo sapi	304	30	3.5	2353	8	AF502079	AF502079 Glycine m
232	30	3.5	1562	5	BC045880	BC045880 Dantio rer	305	30	3.5	2353	9	BC032645	BC032645 Homo sapi
233	30	3.5	1588	9	BC009879	BC009879 Homo sapi	306	30	3.5	2355	9	AF250859	AF250859 Homo sapi
234	30	3.5	1588	9	BC017012	BC017012 Homo sapi	307	30	3.5	2358	9	BC017169	BC017169 Homo sapi
235	30	3.5	1599	9	AF131792	AF131792 Homo sapi	308	30	3.5	2364	3	AY122239	AY122239 Drosophil
236	30	3.5	1600	9	HSMB04708	AL831335 Homo sapi	309	30	3.5	2379	6	AX239965	AX239965 Sequence
237	30	3.5	1606	9	BC051358	BC051358 Homo sapi	310	30	3.5	2396	6	AF020407	AF020407 Dictyoste
238	30	3.5	1611	10	AF242858	AF242858 Mus muscu	311	30	3.5	2405	9	BC002881	BC002881 Homo sapi
239	30	3.5	1636	9	AY299331	AY299331 Homo sapi	312	30	3.5	2446	17	AF119856	AF119856 Homo sapi
240	30	3.5	1643	9	BC016979	BC016979 Homo sapi	313	30	3.5	2452	8	AB058413	AB058413 Chlamydom
241	30	3.5	1650	9	BC036976	BC036976 Homo sapi	314	30	3.5	2591	5	AK026213	AK026213 Homo sapi
242	30	3.5	1651	9	AB060282	AB060282 Macaca fa	315	30	3.5	2605	5	BC044351	BC044351 Dantio rer
243	30	3.5	1668	9	BC026038	BC026038 Homo sapi	316	30	3.5	2613	6	AX746993	AX746993 Sequence
244	30	3.5	1674	9	HSMB01259	AL122102 Homo sapi	317	30	3.5	2613	6	AX091454	AX091454 Homo sapi
245	30	3.5	1680	10	BC010314	BC010314 Mus muscu	318	30	3.5	2627	6	AX676842	AX676842 Sequence
246	30	3.5	1684	9	BC034406	BC034406 Homo sapi	319	30	3.5	2718	6	BC008725	BC008725 Homo sapi
247	30	3.5	1684	10	BC055910	BC055910 Mus muscu	320	30	3.5	2725	6	AX055454	AX055454 Sequence
248	30	3.5	1686	9	BC029879	BC029879 Homo sapi	321	30	3.5	2725	6	AX089944	AX089944 Sequence
249	30	3.5	1690	6	AX534999	AX534999 Sequence	322	30	3.5	2725	6	AX464346	AX464346 Sequence
250	30	3.5	1715	9	BC035857	BC035857 Homo sapi	323	30	3.5	2725	6	AX697019	AX697019 Sequence
251	30	3.5	1732	9	HSMB06891	BX640874 Homo sapi	324	30	3.5	2725	9	AY358592	AY358592 Homo sapi
252	30	3.5	1747	5	BC057247	BC057247 Dantio rer	325	30	3.5	2731	10	BC037696	BC037696 Homo sapi
253	30	3.5	1749	9	AK026164	AK026164 Homo sapi	326	30	3.5	2749	9	HSMB02734	HSMB02734 Homo sapi
254	30	3.5	1765	9	BC012891	BC012891 Homo sapi	327	30	3.5	2772	5	AF357970	AF357970 Homo sapi
255	30	3.5	1788	9	HSMB06673	BX640627 Homo sapi	328	30	3.5	2796	5	AB070629	AB070629 Homo sapi
256	30	3.5	1805	9	BC026223	BC026223 Homo sapi	329	30	3.5	2815	9	BC023597	BC023597 Homo sapi
257	30	3.5	1821	5	AY095313	AY095313 Xenopus 1	330	30	3.5	2817	9	BC029104	BC029104 Homo sapi
258	30	3.5	1823	5	BC049889	BC049889 Mus muscu	331	30	3.5	2837	5	BC046834	BC046834 Xenopus 1
259	30	3.5	1840	10	AF182714	AF182714 Rattus no	332	30	3.5	2841	10	BC014295	BC014295 Mus muscu
260	30	3.5	1846	10	BC047211	BC047211 Mus muscu	333	30	3.5	2846	9	HSMB02834	HSMB02834 Homo sapi
261	30	3.5	1848	5	XLCTCLD2	Y10075 X.laevi's m	334	30	3.5	2848	6	AX092366	AX092366 Sequence
262	30	3.5	1848	9	BC046357	BC046357 Homo sapi	335	30	3.5	2848	6	AX358934	AX358934 Sequence
263	30	3.5	1853	9	AF177331	AF177331 Homo sapi	336	30	3.5	2848	6	AX362427	AX362427 Sequence
264	30	3.5	1856	9	BC044250	BC044250 Homo sapi	337	30	3.5	2848	6	AX697160	AX697160 Sequence
265	30	3.5	1861	9	AK026830	AK026830 Homo sapi	338	30	3.5	2848	9	AY358911	AY358911 Homo sapi
266	30	3.5	1863	9	BC018654	BC018654 Homo sapi	339	30	3.5	2852	6	126126	126126 Sequence 1
267	30	3.5	1863	9	BC018654	BC018657 Homo sapi	340	30	3.5	2852	10	S67465	S67465 angiofensin
268	30	3.5	1865	10	BC013463	BC013463 Mus muscu	341	30	3.5	2875	6	AX247632	AX247632 Sequence
269	30	3.5	1892	9	AB070011	AB070011 Macaca fa	342	30	3.5	2884	6	126127	126127 Sequence 5
270	30	3.5	1898	9	BC033207	BC033207 Homo sapi	343	30	3.5	2917	9	BC007609	BC007609 Homo sapi
271	30	3.5	1910	9	AF258548	AF258548 Homo sapi	344	30	3.5	2930	9	BC035395	BC035395 Homo sapi
272	30	3.5	1933	9	AB060850	AB060850 Macaca fa	345	30	3.5	2948	10	BC058100	BC058100 Mus muscu
273	30	3.5	1956	9	HSMB04748	AL333435 Homo sapi	346	30	3.5	2961	9	BC041128	BC041128 Homo sapi
274	30	3.5	1964	9	BC021799	BC021799 Homo sapi	347	30	3.5	2964	9	AK000622	AK000622 Homo sapi
275	30	3.5	1982	10	BC063088	BC063088 Mus muscu	348	30	3.5	3049	5	AK130506	AK130506 Homo sapi
276	30	3.5	1995	9	BC024685	BC024685 Mus muscu	349	30	3.5	3144	5	BC046266	BC046266 Xenopus 1
277	30	3.5	1997	9	BC007210	BC007210 Homo sapi	350	30	3.5	3200	6	A52563	A52563 Sequence 1
278	30	3.5	2004	17	AF119860	AF119860 Homo sapi	351	30	3.5	3200	6	126022	126022 CDNA of a t
279	30	3.5	2015	6	BD136416	BD136416 95 human	352	30	3.5	3200	6	126205	126205 Sequence 1
280	30	3.5	2021	10	AF188712	AF188712 Mus muscu	353	30	3.5	3200	6	126667	126667 Sequence 1
281	30	3.5	2036	8	HTU9756	AJ009756 Helianthu	354	30	3.5	3320	9	BC068884	BC068884 Homo sapi
282	30	3.5	2042	9	HSMB01184	AL117627 Homo sapi	355	30	3.5	3375	9	BC007129	BC007129 Mus muscu
283	30	3.5	2077	9	BC048271	BC048271 Homo sapi	356	30	3.5	3476	10	BC020166	BC020166 Homo sapi
284	30	3.5	2080	10	BC064006	BC064006 Mus muscu	357	30	3.5	3491	10	AF319949	AF319949 Mus muscu

358	3.5	3566	10	BC058990	BC058990 Mus muscu	431	3.5	145353	2	AC034177	AC034177 Homo sapi
359	3.5	3615	10	AF109143	AF109143 Mus muscu	432	3.5	145365	2	AC120216	AC120216 Mus muscu
360	3.5	3619	5	BC063897	BC063897 Siluana	433	3.5	146455	2	AC127512	AC127512 Homo sapi
361	3.5	3789	9	HSB0801485	AL133620 Homo sapi	434	3.5	146690	2	AC102254	AC102254 Mus muscu
362	3.5	3799	9	BC044907	BC044907 Homo sapi	435	3.5	146877	2	AC026487	AC026487 Homo sapi
363	3.5	3813	9	BC042906	BC042906 Homo sapi	436	3.5	147265	2	AC116806	AC116806 Mus muscu
364	3.5	3813	9	BC061883	BC061883 Homo sapi	437	3.5	147489	2	AP001926	AP001926 Homo sapi
365	3.5	4073	10	BC057371	BC057371 Mus muscu	438	3.5	150442	2	AC022782	AC022782 Mus muscu
366	3.5	4543	9	BC054518	BC054518 Homo sapi	439	3.5	150810	2	AL954570	AL954570 Dario rer
367	3.5	4547	10	BC050875	BC050875 Mus muscu	440	3.5	150986	2	AC023802	AC023802 Mus muscu
368	3.5	4659	10	AF507918	AF507918 Mus muscu	441	3.5	151751	10	EX088539	EX088539 Mouse DNA
369	3.5	4859	9	BC053676	BC053676 Homo sapi	442	3.5	152249	2	AC132874	AC132874 Mus muscu
370	3.5	4903	10	BC058105	BC058105 Mus muscu	443	3.5	152533	2	AC016506	AC016506 Homo sapi
371	3.5	5089	9	HSB0809093	EX648942 Homo sapi	444	3.5	154055	2	AL157774	AL157774 Human DNA
372	3.5	6003	10	AY428535	AY428535 Mus muscu	445	3.5	154495	2	AC127723	AC127723 Mus muscu
373	3.5	7200	3	AF030197	AF030197 Drosophila	446	3.5	154685	10	AL606511	AL606511 Mouse DNA
374	3.5	18166	2	PF05ALBP	AL929364 Plasmodiu	447	3.5	155586	2	AC115815	AC115815 Mus muscu
375	3.5	38181	2	AP005596	AP005596 Homo sapi	448	3.5	155752	10	EX539342	EX539342 Mouse DNA
376	3.5	38346	10	AL929497	AL929497 Mouse DNA	449	3.5	156441	2	AC122106	AC122106 Rattus no
377	3.5	42188	2	AC101010	AC101010 Mus muscu	450	3.5	157455	2	AC131994	AC131994 Mus muscu
378	3.5	55041	2	AC099912	AC099912 Mus muscu	451	3.5	157662	2	AC011574	AC011574 Homo sapi
379	3.5	57250	2	AC083997	AC083997 Homo sapi	452	3.5	157676	2	AC027358	AC027358 Homo sapi
380	3.5	59364	2	AC102347	AC102347 Mus muscu	453	3.5	157676	2	AC027358	AC027358 Homo sapi
381	3.5	64227	2	AC100013	AC100013 Mus muscu	454	3.5	158195	2	AC101830	AC101830 Homo sapi
382	3.5	65691	3	PF05ALBP1	Z97348 Plasmodiu	455	3.5	158382	2	AC016507	AC016507 Homo sapi
383	3.5	73190	2	AC130416	AC130416 Homo sapi	456	3.5	158548	3	PF05ALBP2	PF05ALBP2 Homo sapi
384	3.5	74586	2	AC060793	AC060793 Homo sapi	457	3.5	159505	2	AC023142	AC023142 Homo sapi
385	3.5	89128	8	NCB11823	AL669991 Neurospor	458	3.5	160149	2	AC118692	AC118692 Mus muscu
386	3.5	89251	9	HSB01826	AP001826 Homo sapi	459	3.5	161247	2	AC111052	AC111052 Homo sapi
387	3.5	92636	5	AC005251	AL121909 Human DNA	460	3.5	162061	2	AC068958	AC068958 Homo sapi
388	3.5	92636	5	AL603747	AL603747 Zebrafish	461	3.5	163216	2	AC122557	AC122557 Homo sapi
389	3.5	96095	4	BK640585	BK640585 Pig DNA s	462	3.5	163576	10	AL807744	AL807744 Mouse DNA
390	3.5	100061	2	AC016551	AC016551 Homo sapi	463	3.5	164639	2	AC122432	AC122432 Homo sapi
391	3.5	100418	9	AL355979	AL355979 Human DNA	464	3.5	167126	2	AC080108	AC080108 Homo sapi
392	3.5	106823	2	AC108692	AC108692 Homo sapi	465	3.5	167265	2	EX323810	EX323810 Dario rer
393	3.5	110000	2	AC111021	Continuation (2 of	466	3.5	167835	2	AC120501	AC120501 Gallus ga
394	3.5	110000	2	AC115630	Continuation (3 of	467	3.5	167835	2	AC128859	AC128859 Rattus no
395	3.5	110000	2	BK255276_04	Continuation (2 of	468	3.5	167858	2	EX555606	EX555606 Mus muscu
396	3.5	110000	2	BK323883_0	Continuation (5 of	469	3.5	167862	9	AC011966	AC011966 Homo sapi
397	3.5	110000	2	BK470178_0	BK470178 Dario rer	470	3.5	168447	2	AC115890	AC115890 Mus muscu
398	3.5	110000	2	BK470178_1	Continuation (2 of	471	3.5	168447	2	AC107676	AC107676 Mus muscu
399	3.5	110000	2	PF05ALBP1	Continuation (2 of	472	3.5	169804	2	AC009408	AC009408 Homo sapi
400	3.5	110000	2	PF05ALBP1	Continuation (2 of	473	3.5	170569	2	AC108109	AC108109 Homo sapi
401	3.5	110000	2	PF05ALBP1	Continuation (2 of	474	3.5	170569	2	AL228814	AL228814 Homo sapi
402	3.5	110000	2	PF05ALBP1	Continuation (2 of	475	3.5	170569	2	AP001263	AP001263 Homo sapi
403	3.5	110000	2	PF05ALBP1	Continuation (2 of	476	3.5	170569	2	AC119889	AC119889 Mus muscu
404	3.5	110000	2	PF05ALBP1	Continuation (2 of	477	3.5	171590	2	AC119889	AC119889 Mus muscu
405	3.5	110000	2	PF05ALBP1	Continuation (2 of	478	3.5	171590	2	HS215K18	HS215K18 Human DNA s
406	3.5	110000	2	PF05ALBP1	Continuation (2 of	479	3.5	171590	2	AC120031	AC120031 Homo sapi
407	3.5	110000	2	PF05ALBP1	Continuation (2 of	480	3.5	172332	2	AC132843	AC132843 Mus muscu
408	3.5	110000	2	PF05ALBP1	Continuation (2 of	481	3.5	172332	2	AC114342	AC114342 Mus muscu
409	3.5	110000	2	PF05ALBP1	Continuation (2 of	482	3.5	172332	2	AC099628	AC099628 Mus muscu
410	3.5	110000	2	PF05ALBP1	Continuation (2 of	483	3.5	172332	2	AC114820	AC114820 Mus muscu
411	3.5	110000	2	PF05ALBP1	Continuation (2 of	484	3.5	172332	2	AC069059	AC069059 Homo sapi
412	3.5	110000	2	PF05ALBP1	Continuation (2 of	485	3.5	172332	2	AC069059	AC069059 Homo sapi
413	3.5	110000	2	PF05ALBP1	Continuation (2 of	486	3.5	172332	2	AC122532	AC122532 Mus muscu
414	3.5	110000	2	PF05ALBP1	Continuation (2 of	487	3.5	172332	2	AL929086	AL929086 Zebrafish
415	3.5	110000	2	PF05ALBP1	Continuation (2 of	488	3.5	172332	2	AC124806	AC124806 Mus muscu
416	3.5	110000	2	PF05ALBP1	Continuation (2 of	489	3.5	172332	2	AC119361	AC119361 Rattus no
417	3.5	110000	2	PF05ALBP1	Continuation (2 of	490	3.5	172332	2	AC027119	AC027119 Homo sapi
418	3.5	110000	2	PF05ALBP1	Continuation (2 of	491	3.5	172332	2	AC102885	AC102885 Mus muscu
419	3.5	110000	2	PF05ALBP1	Continuation (2 of	492	3.5	172332	2	AC140566	AC140566 Didephis
420	3.5	110000	2	PF05ALBP1	Continuation (2 of	493	3.5	172332	2	AC019172	AC019172 Homo sapi
421	3.5	110000	2	PF05ALBP1	Continuation (2 of	494	3.5	172332	2	AC087844	AC087844 Homo sapi
422	3.5	110000	2	PF05ALBP1	Continuation (2 of	495	3.5	172332	2	AC091785	AC091785 Genomic s
423	3.5	110000	2	PF05ALBP1	Continuation (2 of	496	3.5	172332	2	AP001567	AP001567 Homo sapi
424	3.5	110000	2	PF05ALBP1	Continuation (2 of	497	3.5	172332	2	AC129489	AC129489 Homo sapi
425	3.5	110000	2	PF05ALBP1	Continuation (2 of	498	3.5	172332	2	AC129489	AC129489 Homo sapi
426	3.5	110000	2	PF05ALBP1	Continuation (2 of	499	3.5	172332	2	AC140335	AC140335 Mus muscu
427	3.5	110000	2	PF05ALBP1	Continuation (2 of	500	3.5	172332	2	AC019299	AC019299 Homo sapi
428	3.5	110000	2	PF05ALBP1	Continuation (2 of	501	3.5	172332	2	AC067861	AC067861 Homo sapi
429	3.5	110000	2	PF05ALBP1	Continuation (2 of	502	3.5	172332	2	AL161725	AL161725 Human DNA
430	3.5	110000	2	PF05ALBP1	Continuation (2 of	503	3.5	172332	2	AC132346	AC132346 Mus muscu

504	C	505	3.5	181597	9	AC090515	AC090515 Homo sapi	577	C	578	3.5	208315	2	EX323864	EX323864 Danio rer
505	C	506	3.5	181597	9	AC090515	AC090515 Mouse DNA	578	C	579	3.5	208342	2	AC105077	AC105077 Mus muscu
506	C	507	3.5	181805	10	AL670660	AL670660 Mus muscu	579	C	580	3.5	208367	2	EX682542	EX682542 Mus muscu
507	C	508	3.5	182631	2	AC117661	AC117661 Mus muscu	580	C	581	3.5	208725	2	AC113302	AC113302 Mus muscu
508	C	509	3.5	182741	2	AC117661	AC117661 Rattus no	581	C	582	3.5	210013	2	AC130672	AC130672 Mus muscu
509	C	510	3.5	182870	3	AC116960	AC116960 Dictyoste	582	C	583	3.5	210390	2	AC110247	AC110247 Mus muscu
510	C	511	3.5	183046	2	AC140775	AC140775 Mus muscu	583	C	584	3.5	210501	2	AC131708	AC131708 Mus muscu
511	C	512	3.5	183997	2	AC126420	AC126420 Mus muscu	584	C	585	3.5	211041	2	AC116413	AC116413 Mus muscu
512	C	513	3.5	184480	10	AL928623	AL928623 Mouse DNA	585	C	586	3.5	211897	2	AC118500	AC118500 Rattus no
513	C	514	3.5	185286	2	AC119901	AC119901 Mus muscu	586	C	587	3.5	212485	10	AC090122	AC090122 Mus muscu
514	C	515	3.5	186846	2	AC091046	AC091046 Homo sapi	587	C	588	3.5	212485	10	AL831986	AL831986 Mus muscu
515	C	516	3.5	187700	2	AC131061	AC131061 Mus muscu	588	C	589	3.5	213491	2	AC073473	AC073473 Homo sapi
516	C	517	3.5	187816	2	AC114404	AC114404 Mus muscu	589	C	590	3.5	213916	2	AC123354	AC123354 Mus muscu
517	C	518	3.5	188196	2	EX510911	EX510911 Danio rer	590	C	591	3.5	214062	2	AC109231	AC109231 Mus muscu
518	C	519	3.5	188648	2	AC091266	AC091266 Mus muscu	591	C	592	3.5	214315	2	AF027750	AF027750 Homo sapi
519	C	520	3.5	188717	2	CNS012PW	AL138478 Human chr	592	C	593	3.5	215392	2	AC124719	AC124719 Mus muscu
520	C	521	3.5	188768	9	AC023844	AC023844 Homo sapi	593	C	594	3.5	215379	2	AC124758	AC124758 Mus muscu
521	C	522	3.5	189384	2	AC124820	AC124820 Homo sapi	594	C	595	3.5	215941	2	AC121532	AC121532 Mus muscu
522	C	523	3.5	189334	2	AC005746	AC005746 Homo sapi	595	C	596	3.5	217002	2	AC117644	AC117644 Mus muscu
523	C	524	3.5	189356	9	AC005746	AC005746 Homo sapi	596	C	597	3.5	217015	10	AC103492	AC103492 Rattus no
524	C	525	3.5	189880	5	EX248330	EX248330 Zebrafish	597	C	598	3.5	217351	2	AC103492	AC103492 Rattus no
525	C	526	3.5	190440	10	AC068252	AC068252 Mus muscu	598	C	599	3.5	218161	2	AC120871	AC120871 Mus muscu
526	C	527	3.5	191109	2	AC123683	AC123683 Mus muscu	599	C	600	3.5	218553	2	AC079940	AC079940 Mus muscu
527	C	528	3.5	191111	9	AC010282	AC010282 Homo sapi	600	C	601	3.5	218593	2	AC131687	AC131687 Mus muscu
528	C	529	3.5	191358	9	AC012533	AC012533 Homo sapi	601	C	602	3.5	218993	2	AC111912	AC111912 Rattus no
529	C	530	3.5	191673	2	AL356743	AL356743 Homo sapi	602	C	603	3.5	219288	2	AC098309	AC098309 Rattus no
530	C	531	3.5	191723	2	AC123627	AC123627 Mus muscu	603	C	604	3.5	219952	2	AC084804	AC084804 Mus muscu
531	C	532	3.5	191775	2	AC074358	AC074358 Mus muscu	604	C	605	3.5	220298	2	AC104743	AC104743 Mus muscu
532	C	533	3.5	192501	2	AC093352	AC093352 Mus muscu	605	C	606	3.5	222205	2	AC125036	AC125036 Mus muscu
533	C	534	3.5	192368	2	AC093352	AC093352 Mus muscu	606	C	607	3.5	223089	2	AC129077	AC129077 Mus muscu
534	C	535	3.5	194138	2	AC131270	AC131270 Homo sapi	607	C	608	3.5	224031	10	AL844161	AL844161 Mouse DNA
535	C	536	3.5	194265	9	AC126365	AC126365 Homo sapi	608	C	609	3.5	224275	2	EX511189	EX511189 Danio rer
536	C	537	3.5	194274	2	AC147248	AC147248 Mus muscu	609	C	610	3.5	224513	2	AC090123	AC090123 Mus muscu
537	C	538	3.5	194303	2	AC115034	AC115034 Mus muscu	610	C	611	3.5	225320	2	AC114571	AC114571 Mus muscu
538	C	539	3.5	194449	2	AC103673	AC103673 Mus muscu	611	C	612	3.5	225383	2	AC108827	AC108827 Mus muscu
539	C	540	3.5	194695	2	AC026375	AC026375 Mus muscu	612	C	613	3.5	225883	2	AC099595	AC099595 Mus muscu
540	C	541	3.5	194871	9	CNS012PW	AL118558 Human chr	613	C	614	3.5	226010	2	AC130017	AC130017 Rattus no
541	C	542	3.5	194972	2	EX005377	EX005377 Danio rer	614	C	615	3.5	226010	2	AC120559	AC120559 Rattus no
542	C	543	3.5	195432	5	EX004992	EX004992 Zebrafish	615	C	616	3.5	226787	2	EX004886	EX004886 Danio rer
543	C	544	3.5	195460	2	EX005307	EX005307 Danio rer	616	C	617	3.5	226898	2	AC098510	AC098510 Rattus no
544	C	545	3.5	195802	2	AC139160	AC139160 Rattus no	617	C	618	3.5	227458	5	AC101337	AC101337 Rattus no
545	C	546	3.5	196682	2	EX571706	EX571706 Danio rer	618	C	619	3.5	228767	2	EX005261	EX005261 Zebrafish
546	C	547	3.5	196882	2	AC027054	AC027054 Homo sapi	619	C	620	3.5	229535	2	AC130110	AC130110 Rattus no
547	C	548	3.5	196890	2	AC137902	AC137902 Mus muscu	620	C	621	3.5	229762	2	AC102082	AC102082 Mus muscu
548	C	549	3.5	197430	2	AC140273	AC140273 Mus muscu	621	C	622	3.5	229904	2	AC110553	AC110553 Mus muscu
549	C	550	3.5	197450	2	AC140273	AC140273 Mus muscu	622	C	623	3.5	230188	2	AC091604	AC091604 Mus muscu
550	C	551	3.5	197662	2	AC024726	AC024726 Homo sapi	623	C	624	3.5	230254	2	AC074163	AC074163 Mus muscu
551	C	552	3.5	198687	2	EX813307	EX813307 Mus muscu	624	C	625	3.5	231177	2	AC121497	AC121497 Mus muscu
552	C	553	3.5	198767	2	AC116847	AC116847 Mus muscu	625	C	626	3.5	231546	2	EX784031	EX784031 Danio rer
553	C	554	3.5	198632	2	AC101885	AC101885 Mus muscu	626	C	627	3.5	231830	2	AC111010	AC111010 Mus muscu
554	C	555	3.5	199861	2	AC140419	AC140419 Mus muscu	627	C	628	3.5	232972	2	AC093991	AC093991 Rattus no
555	C	556	3.5	199919	2	EX547935	EX547935 Danio rer	628	C	629	3.5	233009	2	AC131686	AC131686 Mus muscu
556	C	557	3.5	200046	2	AC091161	AC091161 Homo sapi	629	C	630	3.5	233242	10	AL591070	AL591070 Mouse DNA
557	C	558	3.5	200148	2	AC115736	AC115736 Mus muscu	630	C	631	3.5	234287	2	AC134622	AC134622 Mus muscu
558	C	559	3.5	200292	2	AL929238	AL929238 Mus muscu	631	C	632	3.5	234810	2	AC105654	AC105654 Rattus no
559	C	560	3.5	201014	2	AC134595	AC134595 Mus muscu	632	C	633	3.5	234973	10	AC128850	AC128850 Rattus no
560	C	561	3.5	201143	2	HS150C2	AL022318 Human DNA	633	C	634	3.5	235054	2	AC114393	AC114393 Rattus no
561	C	562	3.5	201479	10	AL845495	AL845495 Mouse DNA	634	C	635	3.5	236068	2	AC121721	AC121721 Rattus no
562	C	563	3.5	202027	2	AC120156	AC120156 Gallus ga	635	C	636	3.5	237187	10	AC116463	AC116463 Mus muscu
563	C	564	3.5	202316	10	AC138134	AC138134 Mus muscu	636	C	637	3.5	237547	2	EX539339	EX539339 Mus muscu
564	C	565	3.5	202521	2	AC146953	AC146953 Pongo pyg	637	C	638	3.5	237566	2	AC140384	AC140384 Mus muscu
565	C	566	3.5	203765	2	AC139635	AC139635 Gallus ga	638	C	639	3.5	237785	2	AC113970	AC113970 Mus muscu
566	C	567	3.5	204057	10	AL592283	AL592283 Mouse DNA	639	C	640	3.5	237894	2	AC123616	AC123616 Mus muscu
567	C	568	3.5	204278	10	AC124507	AC124507 Mus muscu	640	C	641	3.5	238408	2	AC140402	AC140402 Mus muscu
568	C	569	3.5	204990	2	AC024914	AC024914 Mus muscu	641	C	642	3.5	239352	2	AC106294	AC106294 Rattus no
569	C	570	3.5	205379	2	EX548050	EX548050 Danio rer	642	C	643	3.5	240332	2	AC114846	AC114846 Rattus no
570	C	571	3.5	205784	10	AC122891	AC122891 Mus muscu	643	C	644	3.5	242727	2	AC126064	AC126064 Rattus no
571	C	572	3.5	205893	2	AC084324	AC084324 Mus muscu	644	C	645	3.5	242777	2	AC102363	AC102363 Mus muscu
572	C	573	3.5	206419	2	AC127551	AC127551 Mus muscu	645	C	646	3.5	242949	2	AC116255	AC116255 Rattus no
573	C	574	3.5	207418	9	AC090774	AC090774 Homo sapi	646	C	647	3.5	242955	5	EX005070	EX005070 Zebrafish
574	C	575	3.5	207428	2	AC068605	AC068605 Mus muscu	647	C	648	3.5	243177	2	AC137437	AC137437 Rattus no
575	C	576	3.5	207431	10	AL589596	AL589596 Mouse DNA	648	C	649	3.5	243948	2	AC141896	AC141896 Rattus no
576	C	577	3.5	208006	2	AC087877	AC087877 Mus muscu	649	C	650	3.5	245104	2	AC128348	AC128348 Rattus no

C 650	30	3.5	246140	2	AC139207	Mus muscu	723	29	3.3	366	3	AP323614	AP323614 Plasmodiu
C 651	30	3.5	246999	2	AC135656	Rattus no	C 724	29	3.3	380	6	AX400503	AX400503 Sequence
C 652	30	3.5	248527	2	AC107098	Rattus no	C 725	29	3.3	382	2	AX070352	AX070352 Sequence
C 653	30	3.5	248529	2	AC097592	Rattus no	C 726	29	3.3	389	6	AX069918	AX069918 Sequence
C 654	30	3.5	250029	3	AE014816	Plasmodiu	C 727	29	3.3	440	6	AX184953	AX184953 Sequence
C 655	30	3.5	253042	2	AC124839	Rattus no	C 728	29	3.3	479	6	AX099465	AX099465 Sequence
C 656	30	3.5	253146	2	AC128440	Rattus no	C 729	29	3.3	545	6	BD023176	BD023176 Secretary
C 657	30	3.5	254436	3	AE014827	Plasmodiu	C 730	29	3.3	479	6	BD275175	BD275175 48 Human
C 658	30	3.5	254449	3	AE014817	Plasmodiu	C 731	29	3.3	559	9	HSW800249	AT049644 Homo sapi
C 659	30	3.5	256647	2	AC109139	Mus muscu	C 732	29	3.3	588	6	AX677061	G72768
C 660	30	3.5	256801	2	AC133200	Mus muscu	C 733	29	3.3	598	6	AX067349	AX067349 Sequence
C 661	30	3.5	260665	2	AC113858	Rattus no	C 734	29	3.3	606	6	BC004324	BC004324 Homo sapi
C 662	30	3.5	266673	2	AC115671	Rattus no	C 735	29	3.3	607	3	AP257309	AP257309 Drosophil
C 663	30	3.5	267013	2	AC099348	Rattus no	C 736	29	3.3	625	6	AX523506	AX523506 Sequence
C 664	30	3.5	267464	2	AC114804	Mus muscu	C 737	29	3.3	638	9	BC040060	BC040060 Homo sapi
C 665	30	3.5	269294	2	AC135801	Rattus no	C 738	29	3.3	638	9	HSR333592	HSR333592 Homo sapi
C 666	30	3.5	270699	2	AC133821	Rattus no	C 739	29	3.3	638	9	BT001518	BT001518 Drosophil
C 667	30	3.5	271251	2	AC130969	Rattus no	C 740	29	3.3	640	3	BR374713	BR374713 Sequence
C 668	30	3.5	279520	2	AC098364	Rattus no	C 741	29	3.3	651	6	HSR341632	AJ341632 Homo sapi
C 669	30	3.5	282685	2	AC094597	Rattus no	C 742	29	3.3	657	10	BC035943	BC035943 Mus muscu
C 670	30	3.5	295883	2	AC139459	Mus muscu	C 743	29	3.3	666	6	AX430923	AX430923 Sequence
C 671	30	3.5	297984	2	AC099152	Rattus no	C 744	29	3.3	669	9	HSR337556	HSR337556 Homo sapi
C 672	30	3.5	314906	2	AC120788	Mus muscu	C 745	29	3.3	684	9	BC021118	BC021118 Homo sapi
C 673	30	3.5	314916	2	AC129089	Rattus no	C 746	29	3.3	684	9	AY118776	AY118776 Drosophil
C 674	30	3.5	315586	2	EX000708	Mus muscu	C 747	29	3.3	696	3	BC004498	BC004498 Homo sapi
C 675	30	3.5	326894	2	AC131688	Rattus no	C 748	29	3.3	698	9	BC028281	BC028281 Homo sapi
C 676	30	3.5	334051	2	AC123374	Rattus no	C 749	29	3.3	705	9	BD260773	BD260773 50 human
C 677	30	3.5	335050	2	PFH92935	Plasmodiu	C 750	29	3.3	708	6	AX430942	AX430942 Sequence
C 678	30	3.5	349751	3	PFH92935	Plasmodiu	C 751	29	3.3	719	8	AB089155	AB089155 Houttuyni
C 679	29	3.3	49	6	BE2856	Secretary P	C 752	29	3.3	719	8	BC006465	BC006465 Homo sapi
C 680	29	3.3	58	6	AX193328	Sequence	C 753	29	3.3	734	9	AB084102	AB084102 Prunus sa
C 681	29	3.3	58	6	AX381765	Sequence	C 754	29	3.3	748	8	AY249411	AY249411 Anguilla
C 682	29	3.3	64	6	AX381640	Sequence	C 755	29	3.3	753	5	BC059779	BC059779 Homo sapi
C 683	29	3.3	71	6	AR10275	Sequence	C 756	29	3.3	774	6	AX268837	AX268837 Sequence
C 684	29	3.3	71	6	BD143210	Screening	C 757	29	3.3	783	6	AX575617	AX575617 Sequence
C 685	29	3.3	74	6	AX494890	Sequence	C 758	29	3.3	786	3	AP329725	AP329725 Plasmodiu
C 686	29	3.3	76	6	AX381820	Sequence	C 759	29	3.3	795	3	AP102166	AP102166 Homo sapi
C 687	29	3.3	82	6	AR420937	Sequence	C 760	29	3.3	798	4	AB086138	AB086138 Oryctolag
C 688	29	3.3	82	6	BD116490	EST and e	C 761	29	3.3	798	4	AX06846	AX06846 Sequence
C 689	29	3.3	125	6	AX496152	Sequence	C 762	29	3.3	801	6	AX026018	AX026018 Homo sapi
C 690	29	3.3	132	6	AR236482	Sequence	C 763	29	3.3	811	9	HSW808731	HSW808731 Homo sapi
C 691	29	3.3	132	6	AX496057	Sequence	C 764	29	3.3	815	6	AR337568	AR337568 Sequence
C 692	29	3.3	167	6	AY5043	Sequence 72	C 765	29	3.3	840	6	BD130047	BD130047 Human ser
C 693	29	3.3	167	6	AY5043	Sequence 72	C 766	29	3.3	840	6	BD130047	BD130047 Human ser
C 694	29	3.3	176	6	AY592189	Sequence	C 767	29	3.3	840	6	AT574487	AT574487 Homo sapi
C 695	29	3.3	189	8	AR425017	Sequence	C 768	29	3.3	850	9	BC062665	BC062665 Homo sapi
C 696	29	3.3	193	6	AR425017	Sequence	C 769	29	3.3	860	9	BC038839	BC038839 Homo sapi
C 697	29	3.3	193	6	BD120570	EST and e	C 770	29	3.3	860	9	TCUJ2480	AJ002480 Trypanoso
C 698	29	3.3	213	11	HSU29031	Human chro	C 771	29	3.3	871	3	AY330624	AY330624 Galleria
C 699	29	3.3	231	6	AX284873	Sequence	C 772	29	3.3	881	9	BC012486	BC012486 Homo sapi
C 700	29	3.3	235	6	AX10988	Sequence	C 773	29	3.3	881	9	AY089390	AY089390 Drosophil
C 701	29	3.3	276	6	AX387447	Sequence	C 774	29	3.3	904	3	AF429973	AF429973 Spodopter
C 702	29	3.3	289	9	BC013933	Homo sapi	C 775	29	3.3	915	3	AR077212	AR077212 Sequence
C 703	29	3.3	290	6	AR280516	Sequence	C 776	29	3.3	917	6	AR105073	AR105073 Sequence
C 704	29	3.3	290	6	AR283012	Sequence	C 777	29	3.3	917	6	AP244682	AP244682 Zea mays
C 705	29	3.3	290	6	AR414785	Sequence	C 778	29	3.3	920	8	AP273708	AP273708 Drosophil
C 706	29	3.3	290	6	AR433780	Sequence	C 779	29	3.3	948	9	BC010076	BC010076 Homo sapi
C 707	29	3.3	290	6	AR350981	Sequence	C 780	29	3.3	961	8	AF434186	AF434186 Pimus pin
C 708	29	3.3	290	6	AR352747	Sequence	C 781	29	3.3	983	6	AR044575	AR044575 Homo sapi
C 709	29	3.3	290	6	AX302700	Sequence	C 782	29	3.3	983	6	AR157660	AR157660 Sequence
C 710	29	3.3	296	10	BC056228	Mus muscu	C 783	29	3.3	983	6	AR157660	AR157660 Sequence
C 711	29	3.3	312	6	AX185485	Sequence	C 784	29	3.3	988	6	BC023274	BC023274 Homo sapi
C 712	29	3.3	314	6	AR177282	Sequence	C 785	29	3.3	988	6	AX358774	AX358774 Sequence
C 713	29	3.3	314	6	BD332477	Secreted	C 786	29	3.3	991	6	AX362267	AX362267 Sequence
C 714	29	3.3	314	6	BD003137	Secretory	C 787	29	3.3	994	6	AY358387	AY358387 Homo sapi
C 715	29	3.3	314	6	BD086146	Secreted	C 788	29	3.3	1001	9	BC012202	BC012202 Homo sapi
C 716	29	3.3	323	6	AX186911	Sequence	C 789	29	3.3	1008	5	BC054321	BC054321 Xenopus l
C 717	29	3.3	328	6	AX067367	Sequence	C 790	29	3.3	1008	5	BC040729	BC040729 Homo sapi
C 718	29	3.3	335	9	HUMINSRMT	Sequence	C 791	29	3.3	1012	9	BC000367	BC000367 Homo sapi
C 719	29	3.3	355	9	BC005199	Homo sapi	C 792	29	3.3	1012	9	BC016170	BC016170 Homo sapi
C 720	29	3.3	357	9	AR329632	Plasmodiu	C 793	29	3.3	1014	6	EP02914	EP02914 CDNA encodi
C 721	29	3.3	357	9	AY255599	Echinococ	C 794	29	3.3	1029	8	AF488627	AF488627 Arabidops
C 722	29	3.3	357	9	AY255599	Echinococ	C 795	29	3.3	1029	8	AF488627	AF488627 Arabidops

796	29	3.3	1043	10	BC028852	BC028852 Mus muscu	869	29	3.3	1522	5	AY178797	AY178797 Dantio rer
797	29	3.3	1050	9	BC039529	BC039529 Homo sapi	870	29	3.3	1528	9	BC010660	BC010660 Homo sapi
798	29	3.3	1064	8	AT091509	U91509 Arabidopsi	871	29	3.3	1534	9	AF237772	AF237772 Homo sapi
799	29	3.3	1064	10	BC047212	BC047212 Mus muscu	872	29	3.3	1549	9	BC013614	BC013614 Homo sapi
800	29	3.3	1068	10	BC004682	BC004682 Mus muscu	873	29	3.3	1563	9	AK026353	AK026353 Homo sapi
801	29	3.3	1075	3	AK114882	AK114882 Cloma lnt	874	29	3.3	1564	9	AK024804	AK024804 Homo sapi
802	29	3.3	1076	3	BC008983	BC008983 Homo sapi	875	29	3.3	1567	9	BC014229	BC014229 Homo sapi
803	29	3.3	1123	6	196163	196163 Sequence 2	876	29	3.3	1570	6	AX012186	AX012186 Sequence
804	29	3.3	1126	9	AF278737	AF278737 Actus ara	877	29	3.3	1570	6	BD226376	BD226376 Pancreati
805	29	3.3	1128	9	BC048811	BC048811 Homo sapi	878	29	3.3	1570	9	BC047022	BC047022 Homo sapi
806	29	3.3	1139	10	BC058935	BC058935 Mus muscu	879	29	3.3	1574	10	BC026387	BC026387 Mus muscu
807	29	3.3	1145	10	BC039656	BC039656 Mus muscu	880	29	3.3	1575	9	BC002643	BC002643 Homo sapi
808	29	3.3	1146	9	HSW802966	AL713744 Homo sapi	881	29	3.3	1593	9	BC035716	BC035716 Homo sapi
809	29	3.3	1153	10	BC058112	BC058112 Mus muscu	882	29	3.3	1609	8	AB070757	AB070757 Vigna ang
810	29	3.3	1155	10	AY036116	AY036116 Mus muscu	883	29	3.3	1614	5	BC056793	BC056793 Dantio rer
811	29	3.3	1159	6	BD269309	BD269309 33 human	884	29	3.3	1620	8	AF049930	AF049930 Petunia x
812	29	3.3	1163	9	AB049910	AB049910 Macaca fa	885	29	3.3	1625	9	BC004314	BC004314 Homo sapi
813	29	3.3	1166	8	AF076985	AF076985 Zea mays	886	29	3.3	1627	10	BC011174	BC011174 Mus muscu
814	29	3.3	1174	10	BC049559	BC049559 Mus muscu	887	29	3.3	1641	9	AF051325	AF051325 Homo sapi
815	29	3.3	1195	8	AF185574	AF185574 Populus t	888	29	3.3	1641	9	BC011575	BC011575 Homo sapi
816	29	3.3	1200	6	BD269287	BD269287 33 human	889	29	3.3	1651	9	BC012107	BC012107 Homo sapi
817	29	3.3	1209	5	BC062526	BC062526 Dantio rer	890	29	3.3	1656	9	BC017379	BC017379 Homo sapi
818	29	3.3	1224	10	BC040081	BC040081 Mus muscu	891	29	3.3	1661	10	BC003872	BC003872 Mus muscu
819	29	3.3	1239	8	BC013668	BC013668 Homo sapi	892	29	3.3	1670	8	BPE490285	BPE490285 Betula pe
820	29	3.3	1240	8	AF055471	AF055471 Zea mays	893	29	3.3	1671	8	BPE490298	BPE490298 Betula pe
821	29	3.3	1248	6	AX011671	AX011671 Sequence	894	29	3.3	1672	8	BPE490290	BPE490290 Betula pe
822	29	3.3	1248	6	BD226282	BD226282 Pancreati	895	29	3.3	1672	8	BPE490293	BPE490293 Betula pe
823	29	3.3	1251	10	BC038552	BC038552 Mus muscu	896	29	3.3	1674	8	BPE490288	BPE490288 Betula pe
824	29	3.3	1256	5	BC053759	BC053759 Xenopus 1	897	29	3.3	1675	8	BPE490291	BPE490291 Betula pe
825	29	3.3	1274	9	BC035847	BC035847 Homo sapi	898	29	3.3	1677	8	BPE490176	BPE490176 Betula pe
826	29	3.3	1290	10	BC048938	BC048938 Mus muscu	899	29	3.3	1678	8	BPE490281	BPE490281 Betula pe
827	29	3.3	1303	10	BC024549	BC024549 Mus muscu	900	29	3.3	1678	8	BPE490297	BPE490297 Betula pe
828	29	3.3	1306	9	AF316359	AF316359 Homo sapi	901	29	3.3	1678	8	BPE491822	BPE491822 Betula pe
829	29	3.3	1304	10	BC027310	BC027310 Mus muscu	902	29	3.3	1679	8	BPE490284	BPE490284 Betula pe
830	29	3.3	1307	6	AX085856	AX085856 Sequence	903	29	3.3	1680	8	BPE490287	BPE490287 Betula pe
831	29	3.3	1316	10	BC018263	BC018263 Mus muscu	904	29	3.3	1680	8	BPE490292	BPE490292 Betula pe
832	29	3.3	1330	10	BC061713	BC061713 Rattus no	905	29	3.3	1680	8	BPE490295	BPE490295 Betula pe
833	29	3.3	1332	5	BSM601501	BSM601501 Xenopus 1	906	29	3.3	1681	8	BPE490289	BPE490289 Betula pe
834	29	3.3	1337	9	BSM601501	BSM601501 Homo sapi	907	29	3.3	1681	8	BPE490294	BPE490294 Betula pe
835	29	3.3	1341	9	BC037583	BC037583 Homo sapi	908	29	3.3	1681	8	BPE490284	BPE490284 Betula pe
836	29	3.3	1352	9	BC043573	BC043573 Homo sapi	909	29	3.3	1682	8	BPE490283	BPE490283 Betula pe
837	29	3.3	1353	9	BC013408	BC013408 Homo sapi	910	29	3.3	1683	8	BPE490286	BPE490286 Betula pe
838	29	3.3	1389	3	AF520591	AF520591 Paratitlio	911	29	3.3	1683	8	BPE490296	BPE490296 Betula pe
839	29	3.3	1394	10	BC011167	BC011167 Mus muscu	912	29	3.3	1686	10	BC040425	BC040425 Mus muscu
840	29	3.3	1395	10	BC002094	BC002094 Mus muscu	913	29	3.3	1711	8	AY061965	AY061965 Zea mays
841	29	3.3	1405	9	BC044934	BC044934 Homo sapi	914	29	3.3	1712	5	BC045320	BC045320 Dantio rer
842	29	3.3	1407	9	BC010409	BC010409 Homo sapi	915	29	3.3	1713	9	BC002798	BC002798 Homo sapi
843	29	3.3	1421	10	BC061257	BC061257 Mus muscu	916	29	3.3	1714	9	BC035655	BC035655 Homo sapi
844	29	3.3	1423	6	AX523512	AX523512 Sequence	917	29	3.3	1715	5	BC043784	BC043784 Xenopus 1
845	29	3.3	1429	9	BC008090	BC008090 Homo sapi	918	29	3.3	1731	3	AY118660	AY118660 Drosophi
846	29	3.3	1432	9	BC022088	BC022088 Homo sapi	919	29	3.3	1739	6	BD186888	BD186888 Drosophi
847	29	3.3	1439	9	BC004895	BC004895 Homo sapi	920	29	3.3	1743	10	BC055837	BC055837 Mus muscu
848	29	3.3	1453	9	BC002539	BC002539 Homo sapi	921	29	3.3	1745	6	AR203358	AR203358 Sequence
849	29	3.3	1454	10	BC043026	BC043026 Mus muscu	922	29	3.3	1745	9	AF453285	AF453285 Homo sapi
850	29	3.3	1450	9	BC004551	BC004551 Homo sapi	923	29	3.3	1750	9	AF461155	AF461155 Homo sapi
851	29	3.3	1450	9	BC027718	BC027718 Homo sapi	924	29	3.3	1754	3	AY069238	AY069238 Drosophi
852	29	3.3	1454	9	BC007082	BC007082 Homo sapi	925	29	3.3	1767	10	BC051163	BC051163 Mus muscu
853	29	3.3	1456	3	AF518767	AF518767 Manduca s	926	29	3.3	1768	8	BT009488	BT009488 Trilicium
854	29	3.3	1457	10	BC063163	BC063163 Rattus no	927	29	3.3	1768	10	BC057174	BC057174 Mus muscu
855	29	3.3	1458	9	BC011017	BC011017 Homo sapi	928	29	3.3	1771	9	BC014787	BC014787 Homo sapi
856	29	3.3	1459	9	AK026577	AK026577 Homo sapi	929	29	3.3	1774	5	BC045331	BC045331 Dantio rer
857	29	3.3	1459	9	BC041475	BC041475 Homo sapi	930	29	3.3	1783	3	AY070512	AY070512 Drosophi
858	29	3.3	1463	9	BC002572	BC002572 Homo sapi	931	29	3.3	1811	10	BC008612	BC008612 Mus muscu
859	29	3.3	1463	10	BC050896	BC050896 Mus muscu	932	29	3.3	1828	9	BC003610	BC003610 Homo sapi
860	29	3.3	1470	9	BC013436	BC013436 Homo sapi	933	29	3.3	1829	10	BC054468	BC054468 Mus muscu
861	29	3.3	1476	6	BD277281	BD277281 Secreted	934	29	3.3	1836	9	BC012136	BC012136 Homo sapi
862	29	3.3	1478	9	BC015888	BC015888 Homo sapi	935	29	3.3	1837	9	BC000716	BC000716 Homo sapi
863	29	3.3	1481	9	BC012880	BC012880 Homo sapi	936	29	3.3	1839	6	AR243053	AR243053 Sequence
864	29	3.3	1494	9	AF070535	AF070535 Homo sapi	937	29	3.3	1839	6	AR404234	AR404234 Sequence
865	29	3.3	1507	6	AX354366	AX354366 Sequence	938	29	3.3	1839	6	BD222419	BD222419 94 human
866	29	3.3	1507	6	AX354369	AX354369 Sequence	939	29	3.3	1842	8	AY062110	AY062110 Arabidopsi
867	29	3.3	1507	6	BD082413	BD082413 87 human	940	29	3.3	1844	10	MUSNACHRC	M30514 Mouse musci
868	29	3.3	1507	9	BC016800	BC016800 Homo sapi	941	29	3.3	1847	9	AF062481	AF062481 Homo sapi







REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 rosids; eucosids I; Rosales; Rosaceae; Maloideae; Malus.  
Yao, J., Dong, Y. and Morris, B.A.  
Parthenocarpic apple fruit production conferred by transposon  
insertion mutations in a MADS-box transcription factor  
Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)  
21107711  
11158635  
2 (bases 1 to 3130)  
Yao, J.L.  
Direct Submission  
Submitted (16-Oct-2000) Yao J.L., Plant Health and Development  
Group, Horticulture and Food Research Institute of New Zealand, 120  
Mt Albert Road, Auckland, Private Bag 92169, NEW ZEALAND  
Location/Qualifiers

## FEATURES

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1. 3130  
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/tissue\_type="leaf"  
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1916..1960,2783..3130)  
/gene="pi"  
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1916..1960,2783..3130)  
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/protein\_id="CAC28022.1"  
/db\_xref="GI:1266535"  
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/db\_xref="SPRMBL:O9AVU6"  
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1. 189  
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190..357  
/gene="pi"  
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424..1197  
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2783..3130  
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Query Match 37.2%; Score 323; DB 8; Length 3130;  
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Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 518 AAGAGATGTGAGAAACATGAGAAATGGGTATCATCAAGGAGCTGGGGAATCAACA 577  
DB 2808 AAGAGATGTGAGAAACATGAGAAATGGGTATCATCAAGGAGCTGGGGAATCAACA 2867  
QY 578 ACAACAGAGAGAGATACCTTTGGCTTCGGGRCAGCCTTATAGCCAAATCCACAG 637  
DB 2868 ACAACAGAGAGAGATACCTTTGGCTTCGGGRCAGCCTTATAGCCAAATCCACAG 2927  
QY 638 AGAGATCTAATAGATATATATCTTCATTTGCATGCTCTTTCTAACTAGTATATATCT 697  
DB 2928 AGAGATCTAATAGATATATATCTTCATTTGCATGCTCTTTCTAACTAGTATATATCT 2987  
QY 698 CTCACCTCTCTCTCTCTTTTTCATCTGCAAGAGATCTTATGATGAGATTCCA 757  
DB 2988 CTCACCTCTCTCTCTCTTTTTCATCTGCAAGAGATCTTATGATGAGATTCCA 3047  
QY 758 ATGGTTTGAATGAGATTAAGTCTTCTATAGAGCTTTGTGAACTTGAATATATTA 817  
DB 3048 ATGGTTTGAATGAGATTAAGTCTTCTATAGAGCTTTGTGAACTTGAATATATTA 3107  
QY 818 GGGGTGATGAAGACTGGTTGTG 840  
DB 3108 GGGGTGATGAAGACTGGTTGTG 3130

## RESULT 4

AX324675 121 bp DNA linear PAT 02-SEP-2002  
LOCUS  
DEFINITION  
Sequence 813 from Patent WO0192512.  
ACCESSION  
AX324675  
VERSION  
AX324675.1 GI:18095428  
KEYWORDS

SOURCE  
ORGANISM  
Malus x domestica (apple tree)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
UNIVERSITY OF DELAWARE (US)

1 Kmiec, E.B., Gampert, H.B., Rice, M.C. and Kim, J.  
Targeted chromosomal genomic alterations in plants using modified  
single stranded oligonucleotides  
Patent: WO 0192512-A 813 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)

## FEATURES

source  
1. 121  
/organism="Malus x domestica"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:3750"

## ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 1.1e-25;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGACCTA 62  
DB 1 GGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGACCTA 60  
QY 63 CTCGAGAGAGAGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGTGAGC 122  
DB 61 CTCGAGAGAGAGATGAGATTAATCAAGAGGCAAGAGATCACTGTTCTATGTGAGC 120

QY 123 T 123  
Db 121 T 121

## RESULT 5

AX324676/c 121 bp DNA linear PAT 02-SEP-2002  
LOCUS AX324676  
DEFINITION Sequence 814 from Patent WO0192512.  
ACCESSION AX324676  
VERSION AX324676.1 GI:18095429  
KEYWORDS  
SOURCE Malus x domestica (apple tree)  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1  
AUTHORS Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
Patent: WO 0192512-A 814 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES  
source Location/Qualifiers  
1. 121  
/organism="Malus x domestica"  
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/db\_xref="taxon:3750"

## ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 1,1e-25;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGAGCGGGAGGTTGATCAAGAGATTGAGACTCAAGTACAGGAGGTGACCTA 62  
Db 121 GGGAGCGGGAGGTTGATCAAGAGATTGAGACTCAAGTACAGGAGGTGACCTA 62  
QY 63 CTCGAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGC 122  
Db 61 CTCGAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGC 2  
QY 123 T 123  
Db 1 T 1

## RESULT 6

AX324679 121 bp DNA linear PAT 02-SEP-2002  
LOCUS AX324679  
DEFINITION Sequence 817 from Patent WO0192512.  
ACCESSION AX324679  
VERSION AX324679.1 GI:18095432  
KEYWORDS  
SOURCE Malus x domestica (apple tree)  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1  
AUTHORS Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
Patent: WO 0192512-A 817 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES  
source Location/Qualifiers  
1. 121  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:3750"

ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 1,1e-25;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAAGAGAGGTGACCTACTCC 66  
Db 1 CGTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAAGAGAGGTGACCTACTCC 60  
QY 67 AAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGATAA 126  
Db 61 TAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGATAA 120  
QY 127 G 127  
Db 121 G 121

## RESULT 7

AX324680/c 121 bp DNA linear PAT 02-SEP-2002  
LOCUS AX324680  
DEFINITION Sequence 818 from Patent WO0192512.  
ACCESSION AX324680  
VERSION AX324680.1 GI:18095433  
KEYWORDS  
SOURCE Malus x domestica (apple tree)  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1  
AUTHORS Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
Patent: WO 0192512-A 818 06-DEC-2001;  
UNIVERSITY OF DELAWARE (US)  
FEATURES  
source Location/Qualifiers  
1. 121  
/organism="Malus x domestica"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:3750"

## ORIGIN

Query Match 8.1%; Score 70; DB 6; Length 121;  
Best Local Similarity 99.2%; Pred. No. 1,1e-25;  
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAAGAGAGGTGACCTACTCC 66  
Db 121 CGTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAAGAGAGGTGACCTACTCC 62  
QY 67 AAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGATAA 126  
Db 61 TAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGATGATAA 2  
QY 127 G 127  
Db 1 G 1

## RESULT 8

AX324683 121 bp DNA linear PAT 02-SEP-2002  
LOCUS AX324683  
DEFINITION Sequence 821 from Patent WO0192512.  
ACCESSION AX324683  
VERSION AX324683.1 GI:18095436  
KEYWORDS  
SOURCE Malus x domestica (apple tree)  
ORGANISM Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE 1  
AUTHORS Kniec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.

TITLE	targeted chromosomal genomic alterations in plants using modified					
JOURNAL	single stranded oligonucleotides Patent: WO 0192512-A 821 06-DEC-2001; UNIVERSITY OF DELAWARE (US)					
FEATURES	Location/Qualifiers 1..121 /organism="Malus x domestica" /mol_type="unassigned DNA" /db_xref="taxon:3750"					
ORIGIN						
Query Match	8.1%;	Score 70;	DB 6;	Length 121;		
Best Local Similarity	99.2%;	Pred. No. 1.1e-25;				
Matches 120;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;		
Qy	28	AGGATTGGAACCTCAAGTAACAAGCGAGGTGACTTACTCCAAAGAGGAATGGGATTATC	87			
Dd	1	AGGATTGGAACCTCAAGTAACAAGCGAGGTGACTTACTCCAAAGAGGAATGGGATTATC	60			
Qy	88	AAGAAGCAAAGAGATCACTGTTCTATGTGATGCCTAAAGTATCTTTCATTATTATCT	147			
Dd	61	TGAAGGCAAAGAGATCACTGTTCTATGTGATGCCTAAAGTATCTTTCATTATTATCT	120			
Qy	148 A 148					
Dd	121 A 121					
RESULT 9						
AX324684/c						
LOCUS	AX324684	121 bp	DNA	linear	PAT 02-SEP-2002	
DEFINITION	Sequence 822 from Patent WO0192512.					
ACCESSION	AX324684					
VERSION	AX324684.1	GI:18095437				
KEYWORDS	Malus x domestica (apple tree)					
SOURCE	Malus x domestica					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.					
REFERENCE	Kmaec.E.B., Gamper.H.B., Rice.M.C. and Kim.J. Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 822 06-DEC-2001; UNIVERSITY OF DELAWARE (US)					
AUTHORS						
TITLE						
JOURNAL						
FEATURES	Location/Qualifiers 1..121 /organism="Malus x domestica" /mol_type="unassigned DNA" /db_xref="taxon:3750"					
ORIGIN						
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Best Local Similarity	99.2%;	Pred. No. 1.1e-25;				
Matches 120;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;		
Qy	28	AGGATTGGAACCTCAAGTAACAAGCGAGGTGACTTACTCCAAAGAGGAATGGGATTATC	87			
Dd	121	AGGATTGGAACCTCAAGTAACAAGCGAGGTGACTTACTCCAAAGAGGAATGGGATTATC	62			
Qy	88	AAGAAGCAAAGAGATCACTGTTCTATGTGATGCCTAAAGTATCTTTCATTATTATCT	147			
Dd	61	TGAAGGCAAAGAGATCACTGTTCTATGTGATGCCTAAAGTATCTTTCATTATTATCT	2			
Qy	148 A 148					
Dd	1 A 1					
RESULT 10						
AX324687						
LOCUS	AX324687	121 bp	DNA	linear	PAT 02-SEP-2002	

	DEFINITION	Sequence 825 from Patent WO0192512.
	ACCESSION	AX324687
	VERSION	AX324687.1 GI:18095440
	KEYWORDS	
	SOURCE	Malus x domestica (apple tree)
	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
	REFERENCE	1 Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J. Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 825 06-DEC-2001; UNIVERSITY OF DELAWARE (US) Location/Qualifiers 1..121 /organism="Malus x domestica" /mol_type="unassigned DNA" /db_xref="taxon:3750"
	JOURNAL	
	AUTHORS	
	TITLE	
	FEATURES	
	source	
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	Best Local Similarity	99.2%; Pred. No. 1.le-25;
	Matches	120; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Cy	31 ATTGAGAACTCAAGTACAGCAGCGAGGTGA CCTACTCCAAAGAGAGAATGGATTATCAAG	90
Dd	1 ATTGAGAACTCAAGTACAGCAGCGAGGTGA CCTACTCCAAAGAGAGAATGGATTATCAAG	60
Cy	91 AAGGCAAGAGAGATCATCTTTATGTATGTATGCTTAAGATATCTTTATCATTTATTCAGC	150
Dd	61 TAGGCAAGAGAGATCATCTTTATGTATGTATGCTTAAGATATCTTTATCATTTATTCAGC	120
Cy	151 T 151	
Dd	121 T 121	
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	LOCUS	AX324688 121 bp. DNA linear PAT 02-SEP-2002
	DEFINITION	Sequence 826 from Patent WO0192512.
	ACCESSION	AX324688
	VERSION	AX324688.1 GI:18095441
	KEYWORDS	
	SOURCE	Malus x domestica (apple tree)
	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
	REFERENCE	1 Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J. Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides Patent: WO 0192512-A 826 06-DEC-2001; UNIVERSITY OF DELAWARE (US) Location/Qualifiers 1..121 /organism="Malus x domestica" /mol_type="unassigned DNA" /db_xref="taxon:3750"
	JOURNAL	
	AUTHORS	
	TITLE	
	FEATURES	
	source	
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	Best Local Similarity	99.2%; Pred. No. 1.le-25;
	Matches	120; Conservative 0; Mismatches 1; Indels 0; Gaps 0,
Cy	31 ATTGAGAACTCAAGTACAGCAGCGAGGTGA CCTACTCCAAAGAGAGAATGGATTATCAAG	90
Dd	121 ATTGAGAACTCAAGTACAGCAGCGAGGTGA CCTACTCCAAAGAGAGAATGGATTATCAAG	62
Cy	91 AAGGCAAGAGAGATCATCTTTATGTATGTATGCTTAAGATATCTTTATCATTTATTCAGC	150

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Db      61 TAGGCAAGAGACTGTTCTATGATGATGATCAAAAGTATCTTATCACTTATCTAGC 2
Qy      151 T 151
Db      1 T 1

RESULT 12
BC043631
LOCUS   BC043631
DEFINITION 1811 bp mRNA linear VRT 13-JAN-2003
Xenopus laevis, similar to glycerol phosphate dehydrogenase 1,
cytoplasmic adult, clone IMAGE:488802, mRNA, partial cds.
ACCESSION BC043631
VERSION   BC043631.1 GI:27696704
KEYWORDS
SOURCE    Xenopus laevis (African clawed frog)
ORGANISM  Xenopus laevis
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
          Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 1811)
AUTHORS  Klein,S. and Strausberg,R.
TITLE     Direct Submission
JOURNAL   Submitted (09-JAN-2003) National Institutes of Health, Xenopus Gene
          Collection (XGC), National Institute of Child Health and Human
          Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
          20892-7510, USA
          NIH-MGC Project
REMARK    Contact: XGC help desk
          Email: gcaps-remail.nih.gov
          Tissue Procurement: Dr. Igor David
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
          BC Cancer Agency, Vancouver, BC, Canada
          info@bcgc.bc.ca
          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfield,
          Susanna Chan, Readman Chiu, Chris Fiehl, Erin Garland, Ran Guin,
          Letitia Hsiao, Martin Krzyminski, Reta Kutsche, Oliver Lee, Soo
          Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
          Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
          Scheil, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Scott,
          Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
          George Yang, Scott Zuyderduyn, Marco Marra.
          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LIML at: http://image.liml.gov
          Series: IRAX Plate: 95 Row: C Column: 2
          This clone was selected for full length sequencing because it
          passed the following selection criteria: Similarity but not
          identity to protein.
          location/Qualifiers
FEATURES
SOURCE
1..1811
/organism="Xenopus laevis"
/mol_type="mRNA"
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/product="similar to glycerol phosphate dehydrogenase 1,
cytoplasmic adult"
/protein_id="AAH3631.1"
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AIAKIVGNARLCPQNDIVAMVFEELIGKLTETLINSHEWKLPGHKLPAIVY
AVPDLASAGADILIFVPHQIGKCDLQKSHVKEAFGMSLKGVDGPGRLIL
SDIQRIGIOMSVLMGANTANEVADKPCETTIGCKNGKGLIKELFQTPNFRITV
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SATPESCGVADLTTCYGRNRKYGAFATGSGISIEGLEQENLNGOXTGQPSAEL
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ORIGIN
Query Match 4.1%; Score 36; DB 5; Length 1811;
Best Local Similarity 100.0%; Pred.No. 8e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      833 GGTTCGTGGCAAAAAAAAAAAAAAAAAAAAAA 868
Db      1764 GGTTCGTGGCAAAAAAAAAAAAAAAAAAAAAA 1799

RESULT 13
AB038462
LOCUS   AB038462
DEFINITION 967 bp mRNA linear PLN 07-NOV-2001
Rosa rugosa MASAKO BP mRNA for MADS-box protein, complete cds.
ACCESSION AB038462
VERSION   AB038462.1 GI:9857311
KEYWORDS
SOURCE    ROSA rugosa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE 1
AUTHORS  Kitahara,K., Hirai,S., Fukui,H. and Matsumoto,S.
TITLE     Rose MADS-box genes 'MASAKO BP and B3' homologous to class B floral
          identity genes
JOURNAL   Plant Sci. 161, 549-557 (2001)
REFERENCE 2 (bases 1 to 967)
AUTHORS  Matsumoto,S., Hirai,S. and Kitahara,K.
TITLE     Direct Submission
JOURNAL   Submitted (16-FEB-2000) Shogo Matsumoto, Gifu University,
          Department of Biology, Faculty of Education, 1-1, Yanagido, Gifu,
          Gifu 501-1193, Japan (E-mail:shmatsumo@gifu-u.ac.jp,
          Tel:+81-58-293-2257, Fax:+81-58-293-2207)
          Location/Qualifiers
FEATURES
SOURCE
1..967
/organism="Rosa rugosa"
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/db_xref="taxon:74645"
/tissue_type="Young floral parts"
/note="Rosa rugosa Thund. ex Murray"
1..967
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104..715
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/protein_id="BAB11939.1"
/db_xref="GI:9857312"
/translation="MGKRIEIKRIENSNROVTSKRNGLIKKAKEITVCDKAVS
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953
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polYA_site

ORIGIN
Query Match 3.9%; Score 34; DB 8; Length 967;
Best Local Similarity 100.0%; Pred.No. 9.7e-07;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      263 GCAATGAACTGATGATGCAAGAAAGCAATGA 296
Db      369 GCAATGAACTGATGATGCAAGAAAGCAATGA 402

RESULT 14
BC043508
LOCUS   BC043508
DEFINITION 1929 bp mRNA linear PRI 06-MAY-2003

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DEFINITION	Homo sapiens hypothetical protein LOC339166, mRNA (cDNA clone IMAGE:5163423), partial cds.
ACCESSION	BC043508
VERSION	BC043508.1
KEYWORDS	GI:27694155
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1929)
AUTHORS	Straussberg, R.L., Peigold, F.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldi, O.M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mulhany, S.U., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bonfield, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalski, U., Smalins, D.B., Scherter, A., Schein, J.E., Jones, S.J., and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 1929)
AUTHORS	Straussberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11N03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@bcsc.bc.ca">info@bcsc.bc.ca</a> Steven Jones, Jennifer Asano, Ian Bosdát, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice Mcleary, Steven Ness, Pawan Pandoh, Anna-Liisa Pabun, Parvaneh Saeedi, Jacqueline Schein, Diane Smilans, Michael Smith, Lorraine Spence, Jeff Strott, Michael Thorne, Miranada Teal, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRXK Place: 87 Row: e Column: 2. location/Qualifiers 1..1929 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5163423" /tissue_type="Brain, adult medulla" /clone_id="NTH MGC_119" /lab_host="DH10B" /note="Vector: pCMV-SPOXT6"
ORIGIN	

Query Match 3.9%; Score 34; DB 9; Length 1929;  
Best Local Similarity 100.0%; Pred. No. 9,1e-07;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 868  
|||||  
Db 1813 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 1846

RESULT 15  
AF059273  
LOCUS AF059273  
DEFINITION Rattus norvegicus glucocorticoid modulatory element binding protein  
ACCESSION AF059273  
VERSION AF059273.1 GI:3746540  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1964)  
Zeng,H., Jackson,D.A., Oshima,H. and Simons,S.S. Jr.  
Glucocorticoid modulatory element binding protein 2 (GMEB-2)  
Unpublished  
2 (bases 1 to 1964)  
Zeng,H., Jackson,D.A., Oshima,H. and Simons,S.S. Jr.  
Direct Submission  
Submitted (13-APR-1998) Steroid Hormones Sect., NIDDK/NIH, Bldg. 8,  
Room B2A-07, Bethesda, MD 20892, USA  
Location/Qualifiers  
1. 1964  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/cell\_line="Fus-5"  
/tissue\_type="liver"  
110..1699  
/note="GMEB-2"  
/codon\_start=1  
/product="glucocorticoid modulatory element binding  
protein 2"  
/protein\_id="AAC64001.1"  
/db\_xref="GI:3746541"  
/translation="MAPDVSVMEEVVVVTPDTAVDGSGEVEKTVLVTNNLAPHG  
GDLIEDMETENAAACAFAFASOLKEAVLVKAKEGENLEAIVPTGDSRANIL  
IMKRPVPGINVCVOYDEHVISKEKVLHAGSTLEMDKRAIMNIMIRKIMDSGE  
LDYOHKNGSNCNCRSKRIDLSGARVLSPTSEVYPIPLAADNUNGSPATITFC  
EDPDWTTTIGDPTFAFWRELKXAGLIDETVIOEQDLEETMKLCORVQDPPIQLD  
AVLLNNIVQNFMLDLVKVLAHRCMDRSREYASDIALAIDQCEHRRRAKELKKA  
KSHLSVLMFTLTPVSLPSPMKPRLRATSGPAAVMSQVLTQSAQALGEGMWSQL  
TSVPLGCVSTLSTVYLGKSPQAAAPASPSAPSLPGTIVLASGSTFPSTVEITHPDPT  
SSTVLTASTAMDGSTVYLKVSPLQTLTLPLGLPTLONVAQASPGASTIVTMPTAAT  
GPEHHTATIEVAVAEDHEQK"

ORIGIN  
Query Match 3.9%; Score 34; DB 10; Length 1964;  
Best Local Similarity 100.0%; Pred. No. 9,1e-07;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 835 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 868  
|||||  
Db 1930 TTGTGGGAAAAAAAAAAAAAAAAAAAAA 1963

Search completed: September 26, 2004, 01:07:34  
Job time : 3746.18 secs

Search completed: September 26, 2004, 01:07:34  
Job time : 3746.18 secs

## ORIGIN



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 15:45:02 ; Search time 2740.53 Seconds  
(without alignments)

9458.147 Million cell updates/sec

Title: US-10-069-527-1  
Perfect score: 868  
Sequence: 1 atggagacgtcggaaggttga.....aaaaaaaaaaaaaaaa 868

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST.\*  
1: em\_gesba:\*  
2: em\_esthm:\*  
3: em\_estlm:\*  
4: em\_estma:\*  
5: em\_estcv:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hnc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hnc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfm:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_inv:\*  
19: em\_ges\_pla:\*  
20: em\_ges\_vrt:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rod:\*  
26: em\_ges\_vrl:\*  
27: gb\_ges1:\*  
28: gb\_ges2:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	359.4	41.4	719	12	B1978968 zc06 Old
2	358	41.2	711	14	CB970125 CAB10003
3	346.8	40.0	723	12	B1978971 zc09 Old
4	336.8	38.8	642	13	B0879372 V059D02 P

	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																														
	318.6	312.4	306.0	296.2	295.8	285.6	280.4	279.4	279.4	279.4	279.4	279.4	279.4	278.8	278.8	278.8	278.8	278.4	275.6	275.6	275.6	275.6	271.8	270.4	269.8	268.4	266.6	266.4	266.2	265.6	264	263.8	259.2	257.8	249.4	242.6	242.6	242.6	242	241.6	241.6	240.8																													
	502	503	540	488	549	585	637	744	751	767	771	694	706	719	736	738	534	602	698	774	686	520	758	745	727	646	400	492	613	537	547	551	490	436	638	643	814	642	650	607																															
	B0104186	B0106062	B0107941	B0104054	CB073377	B0857987	B0012873	B0013785	B1932285	B1932302	B1932370	B0012106	B0991703	B0013737	B0013836	B0012321	B0994818	B0994330	B0851511	B0851511	B0853867	B0853123	CF373459	B0992097	CB971674	CF609891	B0105645	AI490968	BE807721	B0988714	AM922900	CB086405	BE805943	B0244728	B0246495	AJ568642	B0248831	B0247197	BE493790																																
	B0104186	g90294.e	B0106062	fc1436.e	B0104054	fc2302.e	B0857987	Q933C04.Y	B0012873	Q935U13.Y	B1932285	EST552174	B1932302	EST552191	B1931714	EST551603	BT932370	EST552259	B0012106	Q931A17.Y	B0991703	Q932309.Y	B0013737	Q935H11.Y	B0013836	Q935L18.Y	B0012321	Q931J19.Y	EM528650	sai159h08.	EM528650	Q938F07.Y	B0994330	Q936P01.Y	B0010787	Q9314H12.	B0851511	Q9B15118.	B0853867	Q9B1108.	B0853123	Q9B19005.	CF373459	CBRC5087G	B0992097	Q9R24105.	CB971674	CAB10005.	CF609891	INFT001_0	B0105645	Q90861.e	AI490968	EST241677	BE807721	s529e02.Y	B0988714	Q9F15K15.	AM922900	EST354170	CB086405	hj83h11.9	BE805943	ss51f05.Y	B0244728	B0246495	AJ568642	B0248831	B0247197	BE493790	WHR1275_E

## ALIGNMENTS

RESULT 1  
LOCUS B1978968 719 bp mRNA linear EST 29-OCT-2002  
DEFINITION zc06 Old Blush petal SMART library Rosa chinensis cDNA 5' similar to MADS-box protein, mRNA sequence.  
ACCESSION B1978968  
VERSION B1978968.1 GI:24420761  
KEYWORDS  
SOURCE  
ORGANISM Rosa chinensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids; I; Rosales; Rosaceae; Rosoideae; Rosa.  
REFERENCE  
AUTHORS 1 (bases 1 to 719)  
Channeliere,S., Riviere,S., Scalliet,G., Szczsl,J., Julien,F., Dolle,C., Verge,P., Dumas,C., Bendahmane,M., Hugueney,P. and Cock,J.M.  
TITLE Analysis of gene expression in rose petals using expressed sequence tags  
JOURNAL FEBS Lett. 515 (1-3), 35-38 (2002)  
MEDLINE 21940574  
PubMed 11943190  
COMMENT  
Contact: Cock JM  
RDP (UMR5667 INRA/CNRS/ENSG/UCBL)  
Ecole Normale Supérieure de Lyon  
46, Allée d'Italie, 69364 LYON Cedex 07, France  
Tel: 33472728611

Fax: 33472728600  
Email: Mark.Cockeans-Lyon.fr  
PCR Primers  
FORWARD: CTGGGAGAGGGCCATGCTGCTGCT  
BACKWARD: ATACGACTCACTATGAGGGCAATGGCC.  
Location/Qualifiers

1. 719  
/organism="Rosa chinensis"  
/mol\_type="mRNA"  
/strain="Botanical garden, Lyon"  
/cultivar="Old Blush"  
/db\_xref="taxon:74549"  
/sex="Hermaphrodite"  
/dev\_stage="Mixed (young bud, open bud, mature flower, senescing flower)"  
/lab\_host="Escherichia coli"  
/clone\_1lb="Old Blush petal SMART library"  
/note="Organ: Petal; Vector: pTriblEx2; Site\_1: SfiI; Site\_2: SfiI"

# ORIGIN

Query Match 41.4%; Score 359.4; DB 12; Length 719;  
Best Local Similarity 76.4%; Pred. No. 9.1e-45;  
Matches 498; Conservative 0; Mismatches 112; Indels 42; Gaps 3;

QY 1 ATGGAGCTGGAGAGGTTGATCAAGAGATTGAGAACTCAAGTAAAGGAGGAGTACC 60  
DB 83 ATGGAGAGGGGTAGATTGATTAGAGATTGAAACTCAAGCAAGAGGCGGTGACC 142  
QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGCAAGAGATGCTGCTGATGAT 120  
DB 143 TATTCTAGAGAGAGATGGATCATCAAGAGGCTAAGGAATCATCTTTGTGAT 202  
QY 121 GCTAAAGTATCTTATCATTTATTTAGCTTGGAGAGATGGTGAATATGCA--GC 177  
DB 203 GCTAAGGTTTCTTTATTCATTTAGCTTGGAGAGAAATGTTGAATATCGAGCGC 262  
QY 178 CTTCAACTGCTGCAAGAAATCTTGAACAATACCAAGCAATCTGGAGAGAGTTG 237  
DB 263 CTCGAGAGAGAGGAGTGAATCTTGAACATACCACTCAGCTCTGAAAGAGTTA 322  
QY 238 TGGAGTCTAAGATAGAGAACTCAGCAATGAAGTGAATAGTCAAGAGAGCAATGAC 297  
DB 323 TGGAGTCCAGAGATAGAACTCTCAATGAAGTGAATAGTCAAGAGAGCAATGAT 382  
QY 298 AGCATCAAGTAGAGCTCAGGAGCTGAGAGAGAGAGATATCAATCATTTGAACATGA 357  
DB 383 GGCATGCAATTTAGCTTGGCAATTTGAAGGGGAGAGACATATCATCTTGAACATG 442  
QY 358 GAGCTAGTGGCTTGAAGAGCACTTGAATGSCCTTACAGTATCCGGAGCAAGCAG 417  
DB 443 GACCTATGCGCTTGAAGAGCAATTTGAATGCGCTTGAAGTATCAGAGAGATG 502  
QY 418 TCGAAGTTGCTCAATGATGAGAGCAATGAGAGAGCACTGGAAGATGAGATAGGCG 477  
DB 503 TCGAAGTATGAGAGCGGTTAGAGAAATTAACAGAGCTCTGAGAGACAGATAGGCG 562  
QY 478 CTCATTTAGAGTGGAAAAACACAGAGATGAAAAATAAAGAGATGAGAAACATG 537  
DB 563 CTCGATACAGAGTGCACAAA-----ATGATGAATATGAAGAGATTTGAGGACATG 616  
QY 538 GAAAAAGGTATATCAGAGGAGCTGGGAACTACACACACACAGAGAGATACCT 597  
DB 617 -----AACTACACACACACAGAGATACCT 643  
QY 598 TTGGCTTCGAGGAGCTATTCAGCAATCTCAGAGAGAGATCTAAT 649  
DB 644 TTGGCTTACGTCTCAGGCTAATCAGCAATCTCAGAGAGAGATGAT 695

RESULT 2  
CB970125  
LOCUS CB970125 711 bp mRNA linear EST 30-APR-2003

DEFINITION CAB10003.1Ia\_Fa\_D04 Cabernet Sauvignon Flower Pre-bloom - CAB1  
Vitis vinifera cDNA clone CAB10003.1Ia\_Fa\_D04 5', mRNA sequence.  
ACCESSION CB970125  
VERSION CB970125.1 GI:30252574  
KEYWORDS EST.  
SOURCE Vitis vinifera  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Vitaceae; Vitis.  
1 (bases 1 to 711)  
Goes da Silva,F., Iandolo,A., Lim,H., Baek,J., Jones,K. and  
Cook,D.  
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon',  
berries at various developmental stages  
Unpublished (2003)  
Contact: Douglas Cook, PhD  
CARS Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcook@ucdavis.edu  
Seq primer: ACGGTACGGACATATGCC.  
Location/Qualifiers

# FEATURES

Source

1. 711  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="CAB10003.1Ia\_Fa\_D04"  
/sex="Hermaphrodite"  
/dev\_stage="Pre-bloom"  
/lab\_host="DMSalpha"  
/clone\_1lb="Cabernet Sauvignon flower Pre-bloom - CAB1"  
/note="Organ: Flower - Pre-bloom; Vector: pDNR; Site\_1: SfiI; Site\_2: SfiI; CAB1 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyptas or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:  
5'-AACGACGTGATCAAGAGTGAAGTGAAGTCAAGTAAAGCAGGAGTACC 60  
5'-ATTCTAAGGCCAGAGGCGGCGGACATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

# ORIGIN

Query Match 41.2%; Score 358; DB 14; Length 711;  
Best Local Similarity 73.2%; Pred. No. 1.5e-44;  
Matches 476; Conservative 0; Mismatches 165; Indels 9; Gaps 1;

QY 1 ATGGAGCTGGAGAGGTTGATCAAGAGATTGAGAACTCAAGTAAAGGAGGAGTACC 60  
DB 33 ATGGAGAGAGGAGAGATTGATCAAGAGATCGAAGACTCAAGCAGCAGGAGTACC 92  
QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGCAAGAGATCTGTTCTAATGAT 120  
DB 93 TACTCAAGAGAGAGATGGATCATGAGAGAGCCAGAGATCTGTTCTGCGAT 152  
QY 121 GCTAAAGTATCTTATCATTTATTTAGCTTGGAGAGATGGTGAATATGACAGCCT 180  
DB 153 GCTCATGCTCTCTGTTGATCTTGTAGCTGAGAGAAATGAGAGATGATACCCCT 212  
QY 181 TCAATACGCTGACAGAAATCTTGGCAATATACATGACATCTGGGAGAAAGTTGG 240  
DB 213 TCTAACAAGTTGATTATCTTGAATGATATCAAGAGCTGGGAGAGGCTCTGG 272  
QY 241 GATGCTAAGATGAGAACTCAGCATGAGATGAGATGAGTCAAGAGAGCAATGACAGC 300

Db 273 GATGCAAAACATGAAATCTCAGCAATGATAGATCAAAAAGAGAAATGATAGC 332

QY 301 ATGCAAGTACAGCTCAGGCAATCTGAGAGAGAGATTCACATCANTGAAACCTGTAAG 360

Db 333 ATGCAAGTACAGCTCAGGCAATCTGAGAGAGAGATTCACATCANTGAAACCTGTAAG 392

QY 361 CTGATGAGCTTGAAG 420

Db 393 CTGATGAGCTTGAAG 452

QY 421 AAGTTCGTGACATGATGAG 480

Db 453 GAATTCACAAAGATGCTCAAGAAAATCAAGAAATCTGAGAGAGAGAGAGAGAGAGAG 512

QY 481 ACTTATAGCTGCAAAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Db 513 AATTACATCGTGACCAACAG 572

QY 541 AATGGATATCATCAG 600

Db 573 AGTGGATATCATCAG 623

QY 601 GCCTTCGCGGTGACAGCTTATTCAGCCAAATCTCCAGAGAGAGAGAGAGAGAGAG 650

Db 624 GCCTTCGCGGTGACAGCCAAATTCAGCCAAATTCAGAGAGAGAGAGAGAGAGAG 673

RESULT 3

BI978971 723 bp mRNA linear EST 29-OCT-2002

LOCUS

DEFINITION

z009.Old Blush petal SMART library Rosa chinensis cDNA 5' similar to MADS-box protein, mRNA sequence.

ACCESSION

BI978971

VERSION

BI978971.1 GI:24420763

KEYWORDS

EST.

SOURCE

Rosa chinensis

ORGANISM

Rosa chinensis

REFERENCE

1. (bases 1 to 723)

Channeliere, S., Riviere, S., Scallier, G., Szecsi, J., Jullien, F., Dolle, C., Vergne, P., Dumas, C., Bendahmane, M., Hugueney, P. and Cock, J.M.

AUTHORS

Analysis of gene expression in rose petals using expressed sequence tags

TITLE

FEATUERS

source

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Cock JM

RDP (UMR5667 INRA/CNRS/ENSL/UCBL)

Ecole Normale Supérieure de Lyon

46, Allée d'Italie, 69364 LYON Cedex 07, France

Tel: 33472728611

Fax: 33472728600

Email: Mark.Cock@ens-lyon.fr

PCR Primers

FORWARD: CTGCGAAGCGCGCATTTGTTGCT

BACKWARD: ATACGACTCATATAGCGCAATGCGCC.

Location/Qualifiers

1. .723

/organism="Rosa chinensis"

/mol\_type="mRNA"

/strain="Botanical garden, Lyon"

/cultivar="Old Blush"

/db\_xref="taxon:74649"

/sex="Hermaphrodite"

/dev\_stage="Mixed (young bud, open bud, mature flower, senescing flower)"

/lab\_host="Escherichia coli"

/clone\_lib="Old Blush petal SMART library"

/note="Organ: Petal; Vector: pTipleX2; Site\_1: SfiI; Site\_2: SfiI"

ORIGIN

Query Match 40.0%; Score 346.8; DB 12; Length 723;

Best Local Similarity 76.1%; Pred. No. 76-43;

Matches 497; Conservative 0; Mismatches 113; Indels 43; Gaps 4;

QY 1 ATGGACGTGGAG 60

Db 83 ATGGACGTGGAG 142

QY 61 TACTCCAAAG 120

Db 143 TATTCTAAG 202

QY 121 GCTAAGATATCTTAT 177

Db 203 GCTAAGATATCTTAT 262

QY 178 CCTCAACTACAGCTGACAG 236

Db 263 CCTCAAG 322

QY 237 GTGGATGTGAG 296

Db 323 ATGGAGATGCAAG 382

QY 297 CAGCAGTCAAG 356

Db 383 TGCGATGCAAAATGAG 442

QY 357 AAGAGTGTAG 416

Db 443 GGAAGTGTAG 502

QY 417 GTCCAGTGTGAG 476

Db 503 GTCCAGTGTGAG 562

QY 477 CCTCACTTATGAG 536

Db 563 CCTCGATTCAG 616

QY 537 GGAAGTGTGAG 596

Db 617 G-----

QY 597 TTTTGCTTCGCGGTGACAGCTTATTCAGCAATCTCCAGAGAGAGAGAGAGAGAGAG 649

Db 644 TTTTGCTTCGCGGTGACAGCTTATTCAGCAATCTCCAGAGAGAGAGAGAGAGAGAG 696

RESULT 4

BU879372 642 bp mRNA linear EST 16-OCT-2002

LOCUS

DEFINITION

V059D02 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION

BU879372

VERSION

BU879372.1 GI:24070896

KEYWORDS

EST.

SOURCE

Populus balsamifera subsp. trichocarpa

ORGANISM

Populus balsamifera subsp. trichocarpa

REFERENCE

1. (bases 1 to 642)

Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.

AUTHORS

The Poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries

TITLE

JOURNAL

COMMENT

Contact: BHALERAO RUPALI R.

Umea Plant Science Center

Department of Plant Physiology

University of Umea, 901 87 Umea, Sweden

Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.unu.se.  
 Location/Qualifiers

# FEATURES

source

1. 642  
 /organism="Populus balsamifera subsp. trichocarpa"  
 /mol\_type="mRNA"  
 /sub\_species="trichocarpa"  
 /db\_xref="taxon:3694"  
 /tissue\_type="floral buds"  
 /clone\_lib="Populus flower cDNA library"  
 /note="Organ: flower"

## ORIGIN

Query Match 38.8%; Score 336.8; DB 13; Length 642;  
 Best Local Similarity 75.5%; Pred. No. 2,4e-41;  
 Matches 432; Conservative 0; Mismatches 137; Indels 3; Gaps 1;

## FEATURES

source

1. 502  
 /organism="Rosa hybrid cultivar"  
 /mol\_type="mRNA"  
 /strain="Golden Gate"  
 /db\_xref="taxon:128735"  
 /clone="990294.e"  
 /tissue\_type="petals"  
 /dev\_stage="young open flower at stage four"  
 /clone\_lib="Rose Petals (Golden Gate) Lambda Zap Express Library"  
 /note="Vector: pBKCMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 36.7%; Score 318.6; DB 13; Length 502;  
 Best Local Similarity 81.4%; Pred. No. 1.5e-38;  
 Matches 382; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

**AUTHORS**  
 Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weis, D.  
**TITLE**  
 Rose Scent: Genomics Approach to Discovering Novel Floral Fragrance-Related Genes  
**JOURNAL**  
 Plant Cell 14 (10), 2325-2338 (2002)  
**COMMENT**  
 Contact: Naama Menda  
 Petal Genomics  
 Faculty of Agricultural, Food and Environmental Quality Sciences,  
 The Hebrew University of Jerusalem  
 P.O. Box 12, Rehovot, 76100, Israel  
 Tel: 972 8 9489 683  
 Fax: 972 8 9468 265  
 Email: shaham@agri.huji.ac.il  
 Seq primer: T3 forward.  
 Location/Qualifiers

1 ATGGAGAGCTGGAGAGTTGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 60  
 74 ATGGAGAGAGTAAAGATTGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 133  
 61 TACTCCAAAGAGAGAAATGGATTATCAAGAGAGCAAGAGATCACTGTTCTATGTAT 120  
 134 TACTTAAAGAGAGAGAGTGGATCAATAAAAAAGAGAGATCAAGTTTATGCGAT 193  
 121 GCTAAAGTATCTTCTATCAATTTATTTAGCTCTGGAGAGATGTTGAATCTGAGCCCT 180  
 194 GCTCAAGTTTCTCTGATCTTCTGATTTCTGAGTTCTGAGAGAGATGATGATGACCCCT 253  
 181 TCAACTACGCTGACAGAAATCTTGAACAATACATGACATCTGGAGAGAGATTTGTG 240  
 254 TCCACTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 313  
 241 GATGCTAAGATGAGAACTCAAGATGAGAGATGAGATGAGATGAGATGAGATGAGATG 300  
 314 GATGCTAAGATGAGAACTCAAGATGAGAGATGAGATGAGATGAGATGAGATGAGATG 373  
 301 ATCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 360  
 374 ATCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 433  
 361 CTGATGCTTAAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 420  
 434 TTATATGCTTAAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 493  
 421 AAGTGTGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 480  
 494 GATGCTCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 553  
 481 ACTTATGAGCTGAGAAACCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 540  
 554 CAGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610  
 541 AATGGATATCATGAGAGCGAGCTGGGGAACTA 572  
 611 AATGCTTATCATCAAAAGGTTGAGAGACTTA 642

1 ATGGAGAGCTGGAGAGTTGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 60  
 34 ATGGAGAGAGTAAAGATTGATCAAGAGATGAGAACTCAAGTACAGAGCGGTGACC 93  
 61 TACTCCAAAGAGAGAAATGGATTATCAAGAGAGCAAGAGATCACTGTTCTATGTAT 120  
 94 TATCTTAAAGAGAGAGATGAGATGATCAAGAGAGCTTAAGAGAAATCACTGTTCTTGTAT 153  
 121 GCTAAAGTATCTTCTATCAATTTATTTAGCTCTGGAGAGATGTTGAATCTGCA---GC 177  
 154 GCTAAAGTATCTTCTATCAATTTATTTAGCTCTGGAGAGATGTTGAATCTGCAAGCGC 213  
 178 CCTCAACTACGCTGACAGAAATCTTGAACAATACATGACATCTGGAGAGAGATTTG 237  
 214 CTTAGAGAGAGCGGAGAGAAATCTTGAACAATACATGACATCTGAGAGAGATTTG 273  
 238 TGGATCTTAAAGATGAGAACTTCAAGATGAGATGAGATGAGATGAGATGAGATGAGATG 297  
 274 TGGATCTTAAAGATGAGAACTTCAAGATGAGATGAGATGAGATGAGATGAGATGAGATG 333  
 298 AGCATGAGATGAGAGCTCAAGGATCTGAGAGAGAGATGATGATGATGATGATGATGATG 357  
 334 GGCATGAGAAATTTGAGCTTCTGCAATTTGAAGGGGAGAGATGATGATGATGATGATGATG 393  
 358 GAGCTGATGAGCTTAAAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 417  
 394 GACCTGATGAGCTTAAAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 453  
 418 TCCAACTGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 466  
 454 TCGAAGTATCATGAGCGGCTTGAAGAAATTAACAGAGCTCTGAGAGAGC 502

**RESULT 5**  
 BQ104186 502 bp mRNA linear EST 16-APR-2002  
 LOCUS BQ104186  
 DEFINITION 990294.e Rose Petals (Golden Gate) Lambda Zap Express Library Rosa  
 hybrid cultivar cDNA clone 990294.e 5', mRNA sequence.  
 ACCESSION BQ104186  
 VERSION BQ104186.1 GI:20153848  
 KEYWORDS EST.  
 ORGANISM Rosa hybrid cultivar  
 SOURCE Rosa hybrid cultivar  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
 Rosids; eustosids I; Rosales; Rosaceae; Rosoideae; Rosa.  
 REFERENCE 1 (bases 1 to 502)

**RESULT 6**  
 BQ106062 503 bp mRNA linear EST 16-APR-2002  
 LOCUS BQ106062  
 DEFINITION fc1436.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library  
 Rosa hybrid cultivar cDNA clone fc1436.e 5', mRNA sequence.  
 ACCESSION BQ106062

VERSION BQ106062.1 GI:20155724  
 KEYWORDS EST.  
 SOURCE Rosa hybrid cultivar  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids I; Rosales; Rosaceae; Rosoideae; Rosa.  
 REFERENCE 1 (bases 1 to 503)  
 AUTHORS Guernan, I., Shalitz, M., Menda, N., Plestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weiss, D.  
 TITLE Rose Scent: Genomics Approach to Discovering Novel Floral Fragrance-Related Genes  
 JOURNAL Plant Cell 14 (10), 2325-2338 (2002)  
 COMMENT Contact: Naama Menda  
 Petal Genomics  
 Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem  
 P.O. Box 12, Rehovot, 76100, Israel  
 Tel: 572 8 9489 683  
 Fax: 572 8 9468 265  
 Email: shaham@agri.huji.ac.il  
 Seq primer: T3 forward.  
 FEATURES  
 source 1..503  
 Location/Qualifiers  
 /organism="Rosa hybrid cultivar"  
 /mol\_type="mRNA"  
 /strain="Fragrant Cloud"  
 /db\_xref="taxon:128735"  
 /clone="fc1436.e"  
 /tissue\_type="Petal"  
 /dev\_stage="Young open flower at stage four"  
 /clone\_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"  
 /note="Vector: pBKCMV; Site\_1: EcoRI; Site\_2: XhoI"  
 ORIGIN  
 Query Match 36.0%; Score 312.4; DB 13; Length 503;  
 Best Local Similarity 82.4%; Pred. No. 1.3e-37;  
 Matches 371; Conservative 0; Mismatches 76; Indels 3; Gaps 1;  
 1 ATGGACGTGGGAAGTTGAGATCAAGAGATTGAGAACTCACTAAACAGGAGTACC 60  
 51 ATGGGAGAGGGTAAGATTGAGATTAGAGATTGAAACTCAAGCAACAGGAGTACC 110  
 61 TACTCCAAAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTTTCTATGTGAT 120  
 111 TATCTTAAGAGAAAGATGGATCATCAAGAGGCTAAGGAAATCACTGTTCTTGTGAT 170  
 121 GCTAAGATCTCTTATCATTTATTTAGCTCTGGGAAGATGGTTGAATCTGCA---GC 177  
 171 GCTAAGTTTCTTATATCATTTGCTGTAAGCTCTGGAATAATGTTGAATCTGAGCGC 230  
 178 CCTTCAACTACGCTGACAGAAATCTTGGACAAATACCATGACATTTGGGAAGATTG 237  
 231 CCTAGAGAAAGCGAGATGAATATCTTGGACAAATACCATGACATTTGGGAAGATTG 290  
 238 TGGAGTGTAGAGTGAAGAACTCAGCAATGATGATGAGTCAAGCAAGAAAGCAATGAC 297  
 291 TGGATGTCAGAGCATGAGAACTCTGCAATGATGATGATGATGATGATGATGATGAT 350  
 298 AGCATGAGTAGAGCTCAGGCAATCTGAAGGAGAGATATCATCATTTGAACCATGTA 357  
 351 GGCATGCAATTTGAGCTTCGGCATTTGAAGGGGAGAAACATTAATCTTGAACCATGTG 410  
 358 GAGCGATAGGCTTAGAGAGAGCACTTGAATGCGCTTCAATATCCGGGACCAACAG 417  
 411 GACCTGATGCTTAGAGAGAGCAATTAATGCGCTTGAAGTATCAAGAGCAAGATG 470  
 418 TCCAGTTCTGTCAGATGATGAGACAT 447  
 471 TCGAAGTACATGAGCGCTTAGAGAAAT 500

RESULT 7  
 BU879741  
 LOCUS 540 bp mRNA linear EST 16-OCT-2002  
 DEFINITION V063H01 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.  
 ACCESSION BU879741  
 VERSION BU879741.1 GI:24071265  
 KEYWORDS EST.  
 SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)  
 ORGANISM Populus balsamifera subsp. trichocarpa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eustosids I; Malpighiales; Salicaceae; Saliceae; Populus.  
 REFERENCE 1 (bases 1 to 540)  
 AUTHORS Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.  
 TITLE The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: BHALERAO RUPALI R.  
 Umea Plant Science Center  
 Department of Plant Physiology  
 University of Umea, 901 87 Umea, Sweden  
 Tel: +46 90 786 5279  
 Fax: +46 90 786 6676  
 Email: rupali.bhalerao@plantphys.umu.se.  
 FEATURES  
 source 1..540  
 Location/Qualifiers  
 /organism="Populus balsamifera subsp. trichocarpa"  
 /mol\_type="mRNA"  
 /sub\_species="trichocarpa"  
 /db\_xref="taxon:3694"  
 /tissue\_type="floral buds"  
 /clone\_lib="Populus flower cDNA library"  
 /note="Organ: flower"  
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 Query Match 34.1%; Score 296.2; DB 13; Length 540;  
 Best Local Similarity 78.4%; Pred. No. 3.3e-35;  
 Matches 355; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
 1 ATGGACGTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGTACC 60  
 87 ATGGGAGAGGGTAAGATTGAGATTAGAGATTGAAACTCAAGCAACAGGAGTACC 146  
 147 TACTCCAAAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTTTCTATGTGAT 206  
 121 GCTAAGATCTCTTATCATTTATTTAGCTCTGGGAAGATGGTTGAATCTGAGCGCT 180  
 207 GCTCAAGTTTCTTGTCTATCTTTGCTGTAAGCTCTGGAAGATGATGATGATGATG 266  
 181 TCACTAGCGCTGACAGAAATCTTGGACAAATACCATGACATTTGGGAAGATTG 240  
 267 TCCACTACCGTGGTGGATGTTGGACAAATGATCAAGCAATCTGTTAAGGCGTGG 326  
 241 GATGCTAAGATGAGAACTCAGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300  
 327 GATGCTAAGATGAGAACTCAGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 386  
 387 ATGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 446  
 301 ATGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360  
 361 CTGATGCGCTTAGAGAGAGCACTTGAATGCGCTTCAATATCCGGGACCAACAGTCC 420  
 447 TGAATGCGCTTAGAGAGAGCACTTGAATGCGCTTCAATATCCGGGACCAACAGTCC 506  
 421 AAGTTCTGTCAGATGATGAGACATGGAAG 453  
 507 GAGTTCAAGATGATGAGACCAATGGAAG 539

RESULT 8  
LOCUS B0104054 488 bp mRNA linear EST 16-APR-2002  
DEFINITION fc2302.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library  
ACCESSION B0104054  
VERSION B0104054  
KEYWORDS B0104054.1 GI:20153716  
SOURCE EST.  
ORGANISM Rosa hybrid cultivar  
Rosa hybrid cultivar  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.  
1 (bases 1 to 488)  
Guterman, I., Shalit, M., Menda, N., Piestun, D., Dafny-Yelin, M.,  
Shalev, G., Bar, E., Dayadov, O., Ovadis, M., Emanuel, M., Wang, J.,  
Adam, Z., Pichersky, E., Lewinson, E., Zamir, D., Vainstein, A. and  
Weiss, D.  
Rose Scent: Genomics Approach to Discovering Novel Floral  
Fragrance-Related Genes  
Plant Cell 14 (10), 2325-2338 (2002)  
Contact: Naama Menda  
Petal Genomics  
Faculty of Agricultural, Food and Environmental Quality Sciences,  
The Hebrew University of Jerusalem  
P.O. Box 12, Rehovot, 76100, Israel  
Tel: 972 8 9489 683  
Fax: 972 8 9468 265  
Email: shahamagri.huji.ac.il  
Seq primer: T3 forward  
Location/Qualifiers  
1..488  
/organism="Rosa hybrid cultivar"  
/mol\_type="mRNA"  
/strain="Fragrant Cloud"  
/db\_xref="taxon:128735"  
/clone="fc2302.e"  
/issue\_type="Petals"  
/dev\_stage="Young open flower at stage four"  
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Express Library"  
/note="Vector: pBKCW; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 34.1%; Score 295.8; DB 13; Length 488;  
Best Local Similarity 79.0%; Pred. No. 4e-35;  
Matches 380; Conservative 0; Mismatches 92; Indels 9; Gaps 2;

62 ACTCCAGAGAGAGGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGATG 121  
|||  
3 ACCAGAGAGAGAGAGATGGATTCATCAAGAGCTTAAGAAATCACTGTTCTTGATG 62  
|||  
122 CTAAAGTATCTTTATCATTTATCTTCTGGAAGATGTTGAATACTGCA--GCC 178  
|||  
63 CTAAAGTCTTCTTATCATTTATCTTCTGGAAGATGTTGAATACTGAGCGGCC 122  
|||  
179 CTTCACATAGCTGAGCAAGAAATCTTGAGCAAAATACATGGAGCAATCGGAAGAGTTGT 238  
|||  
123 CTACAGAGAGAGCGAGTAAATCTTGAGCAAAATACATCTCACAGTCTGGAAGAGTTAT 182  
|||  
239 GGGATGCTTAAGCATGAGAACCTCGACATGATGATGATCAAGAAAGACATGACA 298  
|||  
183 GGGATGCTTAAGCATGAGAACCTCGACATGATGATGATCAAGAAAGACATGATG 242  
|||  
299 GCATGCAAGTAAAGCTTCAAGCATCTGAAGGAGAGATATCATATTTGAACCATGTG 358  
|||  
243 GCATGCAAAATTAAGCTTCAAGCATCTGAAGGAGAGATATCATATTTGAACCATGTG 302  
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359 AGCTGATGCTTGAAGAGAGCACTTGAAGATGGCTTCAAGTATCCGAGCAAGACAT 418  
|||  
303 ACCTGATGCTTGAAGAGAGCACTTGAAGATGGCTTCAAGTATCCGAGCAAGATGT 362  
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RESULT 9  
LOCUS CB077377 549 bp mRNA linear EST 24-JAN-2003  
DEFINITION h53a08.g1 Hedycotis terminalis flower - Stage 2 (NYBG) Hedycotis  
terminalis cDNA clone h53a08, mRNA sequence.  
ACCESSION CB077377  
VERSION CB077377.1 GI:27890814  
KEYWORDS EST.  
SOURCE Hedycotis terminalis  
ORGANISM Hedycotis terminalis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;  
Spermacoceae; Hedycotis.  
1 (bases 1 to 549)  
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,  
O'Shaughnessy, A.L., Ballie, V., Martienssen, R.A., McCombie, R.W.,  
Benfey, P. and Stevenson, D.  
Expressed tag sequences from Hedycotis terminalis flower - Stage 2  
(NYBG)  
Unpublished (2003)  
Contact: W. Richard McCombie  
Lila Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8874  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Plate: h53 row: a column: 08  
Seq primer: -21M13univRev  
High quality sequence stop: 549.  
Location/Qualifiers  
1..549  
/organism="Hedycotis terminalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:219667"  
/clone="h53a08"  
/dev\_stage="pre-anthesis; Stage 2"  
/clone\_lib="Hedycotis terminalis flower - Stage 2 (NYBG)"  
/note="Organ: flower; Vector: pBKCW; Site\_1: XhoI;  
Site\_2: Eco RI; Date: Completed 12/18/01. Submitted to  
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA  
Synthesis Kit. The library was size-fractionated to enrich  
for large inserts. Sample: collected on the island of  
Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN  
Query Match 32.9%; Score 285.6; DB 14; Length 549;  
Best Local Similarity 71.6%; Pred. No. 1.3e-33;  
Matches 375; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAACTCAAGTAACAGGCAAGTGACC 60  
|||  
26 ATGGGAGAGGTAAGATTGAGATCAAGAGATTGAACTCAAGTAACAGGCAAGTGACT 85  
|||  
61 TACTCCAGAGAGAGAAATGGATTATCAAGAGGCAAGAGATCACTGTTCTTATGAT 120  
|||  
86 TACTCGAAAGAGAAATCGGATCATGAAAAAGCTTAAGAAATCACTGTTCTTATGAT 145  
|||

QY 121 GCTAAGATATCTTATCATTTATTTAGCTCTGGAGAGTGTGTAATCTGACGCTT 180  
 Db 146 GCTAAGATATCTTATCATTTATTTAGCTCTGGAGAGTGTGTAATCTGACGCTT 205  
 QY 181 TCAACTACGCTGACAGAAATCTTGACAAATATCATGAGCAATCTGGAGAAAGTTGTG 240  
 Db 206 TCAACTATTTGTTCTATCTGATGCTTACCAAGAGTCTACTGGAGAAAGCTATGG 265  
 QY 241 GATCTAAGCATGAGAACTCTGCAATGATGATGATGATGATGATGATGATGATGATG 300  
 Db 266 GATTTTAAAGCATGAGAGTTTAAAGCAATGATGATGATGATGATGATGATGATGATG 325  
 QY 301 ATGAAGATGAGCTGAGGATCTGAGGAGGAGGATGATGATGATGATGATGATGATGATG 360  
 Db 326 ATGAAGATGAGCTGAGGATCTGAGGAGGAGGATGATGATGATGATGATGATGATGATG 385  
 QY 361 CTGATGAGCTTGAAGAGACATGTAATGCTTCAAGTATCCGAGCAAGCAAGTCC 420  
 Db 386 CTGATGAGCTTGAAGAGATTCATTTGAAATGCTTTCGTTTACTGACAAACAGAGT 445  
 QY 421 AAGTTCTGACATGATGAGACATGAGCACTGAGCAATGATGATGATGATGATGATGATG 480  
 Db 446 GAGATTTCTCAAGATGATGAGGAAATGATCAATGTTGAGGAGAGCTCAAGCAAGCTT 505  
 QY 481 ACTATGAGCTGCAAAAACAAGAGATGATGATGATGATGATGATGATGATGATGATG 524  
 Db 506 CAGTACATGTTGATCAGCAAGATATGCGCAGCATGAGAGGAAA 549

RESULT 10  
 B0857987 559 bp mRNA linear EST 14-AUG-2002  
 LOCUS QGB9A17.YG.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone  
 DEFINITION QGB9A17, mRNA sequence.  
 ACCESSION B0857987  
 VERSION B0857987.1 GI:22243452  
 KEYWORDS EST.  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asterales; Cichorioideae;  
 Cichorieae; Lactuca.  
 1 (bases 1 to 559)  
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
 Lai, Z., Church, S., Jackson, L. and Bradford, K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmndson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OG\_Ca\_Contig7827, see http://cgdb.ucdavis.edu/  
 for details.  
 Plate: QGB9 row: A column: 17.

## FEATURES

SOURCE

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultiVar="Salinas"  
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 /lab\_host="E.coli"  
 /clone\_lib="OG\_ABCDI lettuce salinas"  
 /note="Vector: pBRCDNA511ab. The library was constructed  
 from 10 different sources of RNA from a single genotype.  
 Separate cDNAs were generated using primers that

## ORIGIN

Query Match 32.3%; Score 280.4; DB 13; Length 559;  
 Best Local Similarity 72.7%; Pred. No. 7.5e-33;  
 Matches 362; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

incorporated unique 5' and 3' tags to distinguish each  
 source of RNA. cDNAs were then pooled, size-fractionated,  
 directionally cloned into a custom medium-copy vector and  
 transfections made with four size classes to minimize  
 size bias. Details of each source of RNA and library  
 construction can be obtained at http://cgdb.ucdavis.edu/  
 TNG\_TISSUE-flowers environmental stress  
 TNG\_LIB-OG ABCDI lettuce salinas  
 TNG\_SEQ=CGAATGCGG-

QY 1 ATGGAGCTGGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
 Db 23 ATGGAG 82  
 QY 61 TACTCGAAG 120  
 Db 83 TACTCGAAG 142  
 QY 121 GCTAAGATATCTTATCATTTATTTAGCTCTGGAGAGTGTGTAATCTGACGCTT 180  
 Db 143 GCTAAGATATCTTATCATTTATTTAGCTCTGGAGAGTGTGTAATCTGACGCTT 202  
 QY 181 TCAACTACGCTGACAGAAATCTTGACAAATATCATGAGCAATCTGGAGAAAGTTGTG 240  
 Db 203 AAAACCACTTATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 262  
 QY 241 GATG 300  
 Db 263 GATG 322  
 QY 301 ATGCAAGTGAAGCTGAGGATCTGAGAGAGAGATATCATTTGAAACCATGATGAG 360  
 Db 323 ATGCAAGTGAAGCTGAGGATCTGAGAGAGAGATATCATTTGAAACCATGATGAG 382  
 QY 361 CTGATGAGCTTGAAGAGACATGTAATGCTTCAAGTATCCGAGCAAGCAAGTCC 420  
 Db 383 CTGATGAGCTTGAAGAGATTCATTTGAAATGCTTTCGTTTACTGACAAACAGAGT 442  
 QY 421 AAGTTCTGACATGATGAGACATGAGCACTGAGCAATGATGATGATGATGATGATGATGATG 480  
 Db 443 GAAATCCCTAAATCATGAGAGATGAGCAATGATGATGATGATGATGATGATGATGATGATG 502  
 QY 481 ACTATGAGCTGCAAAAACAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 498  
 Db 503 ATGATATCTTGTGCAACAA 520

RESULT 11  
 B012873 685 bp mRNA linear EST 22-AUG-2002  
 LOCUS QGJ3C04.YG.ab1 OG EFGHJ lettuce serriola Lactuca sativa cDNA clone  
 DEFINITION QGJ3C04, mRNA sequence.  
 ACCESSION B012873  
 VERSION B012873.1 GI:22447268  
 KEYWORDS EST.  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; campanulids; Asterales; Asterales; Cichorioideae;  
 Cichorieae; Lactuca.  
 1 (bases 1 to 685)  
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
 Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
 Lai, Z., Church, S., Jackson, L. and Bradford, K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compgenomics.ucdavis.edu/

## TITLE



JOURNAL  
COMMENT

Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmoreveg@mail.ucdavis.edu]  
Belongs to contig Q5\_Ca\_contig7827, see <http://cgdb.ucdavis.edu/>  
for details.  
Plate: QGJ3 row: C column: 04.

# FEATURES

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Location/Qualifiers  
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/mol\_type="mRNA"  
/cultivar="L.serricola"  
/db\_xref="taxon:4236"  
/clone="QGJ3C04"  
/lab\_host="E.coli"  
/note="Vector: pBRCDNA51AB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>  
TAG\_SEQ=Not found"

## ORIGIN

Query Match 32.3%; Score 280.4; DB 13; Length 685;  
Best Local Similarity 72.7%; Pred. No. 6.6e-33;  
Matches 362; Conservative 0; Mismatches 136; Indels 0; Gaps 0;  
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DB 2 ATGGGAGAGAGAGAGATCAAGATTCAGAGATCAAGTAAAGGAGAGAGGAGC 61  
QY 61 TACTCCAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
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DB 242 GATGCAAAACATGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301  
QY 301 ATGCAAGTACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 302 ATGCAAAATGAGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361  
QY 361 CTGATGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
DB 362 CTATATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 421  
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DB 482 ATGATATCTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499

## RESULT 12

LOCUS B0013785 637 bp mRNA linear EST 22-AUG-2002  
DEFINITION QGJ5J13.yg.ab1 QG\_EFGHJ lettuce serricola Lactuca sativa cDNA clone  
QGJ5J13, mRNA sequence.  
B0013785  
ACCESSION B0013785.1 GI:22448160  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE

### AUTHORS

### TITLE

## JOURNAL

### COMMENT

Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Asmundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742  
Fax: 1-(530)-752-9659  
Email: akozik@ucdavis.edu [michelmoreveg@mail.ucdavis.edu]  
Belongs to contig Q5\_Ca\_contig7827, see <http://cgdb.ucdavis.edu/>  
for details.  
Plate: QGJ5 row: J column: 13.  
Location/Qualifiers  
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/lab\_host="E.coli"  
/note="Vector: pBRCDNA51AB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>  
TAG\_Lib=QG\_EFGHJ lettuce serricola  
TAG\_SEQ=GCTTACGAGG"

## FEATURES

### source

## ORIGIN

Query Match 32.2%; Score 279.4; DB 13; Length 637;  
Best Local Similarity 72.5%; Pred. No. 9.9e-33;  
Matches 361; Conservative 0; Mismatches 137; Indels 0; Gaps 0;  
QY 1 ATGGAGCTGGAGAGGTTGATCAAGATTCAGAGATTCAGAGATTCAGAGATTCAG 60  
DB 9 ATGGGAGAGAGAGAGATTCAGAGATTCAGAGATTCAGAGATTCAGAGATTCAG 68  
QY 61 TACTCCAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
DB 62 TACTCCAGAGAGAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 128  
QY 121 GCTAAGTATCTTATCATTTATTTAGCTCTGGAGAGAGAGAGAGAGAGAGAG 180  
DB 122 GCTAATGCTCTCTTGTATCTGTGCTCTTCTGGAGAGAGAGAGAGAGAGAG 188  
QY 181 TCAACTACGCTGACAGAAATCTTGAACAATACATGAGCAATCTGGAGAGAG 240

Db	189	AAACCACTTGATTCAGCATGCTGGATGCATTCAGAGCTTCTGTGAAATTAAGTTGG	248
Qy	241	GATGTTAAGCATGATAA CCTAGCACTAAGTGATATAGTCAATAAAGACAAATGACG	300
Db	249	GATGAAACATGAGAAATCTGCAGATGAATTTGATGATCAAGAAAGGACCAAAAG	308
Qy	301	ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGATATCACTCATTTGAACCATGTAG	360
Db	309	ATGCAAAATTGAGCTCAGGCATTTAAAGGGGAGATATATAACATCGTTAACTATAG	368
Qy	361	CTGATGGCTTGAAGAGAACCTTAAAAATGGCCTTAACAATCCGGGACAGAGTCC	420
Db	369	CTAAATGGGTATGAAGATGCACTTAAAAATGCACTCACACATTCGTGAGAAAAAG	428
Qy	421	AAATTGCTGACATATATAGAGACAAATGAAAAGCACTGGAAGATGAGAAATTAAGG	480
Db	429	GAAATCCCTAANATATATGAGGAAGCATGAAACAAATCTGAGGAAGAAATATG	488
Qy	481	ACTTATGAGCTCAAAAA	498
Db	489	ATGTATCTTGCAACAA	506

RESULT 13	BI932285	LOCUS	DEFINITION	BI932285	744 bp	mRNA	linear	EST 18-OCT-2001
				EST152174 tomato flower, 8 mm to preanthesis buds Lycopersicon				
				esculentum cDNA clone CTC0221A1 5' end, mRNA sequence.				

ACCESSION	BI9932285	
VERSION	BI9932285.1	GI:16246757
KEYWORDS	EST.	
SOURCE	Lycopersicon esculentum	
ORGANISM	Lycopersicon esculentum	(tomato)

REFERENCE  
AUTHORS

1 (bases 1 to 744)  
van der Hoeven, R.S., Bezzerides, J.L., Karmycheva, S.A., Tsai, J.,  
Uterbeck, T., Van Aken, S., Romling, C.M., Niemann, W., Friser, C.M.,

TITLE	Generation of ESTs from tomato flower tissue, buds 8 mm - preanthesis
JOURNAL	Unpublished (2001)
COMMENT	Contact: CUGI

100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics Institute  
Seq primer: 73  
Location/Qualifiers  
1..744  
FEATURES  
source

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/tissue_type="flower"
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/clone_id="tomato flower, 8 mm to preanthesis buds"
/notes="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research, flower buds and flowers
were taken from greenhouse plants (4-6 wks old, 1996).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

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Query Match	32.2%	Score 279.4	DB 12	Length 744
Best Local Similarity	66.2%	Pred. No. 8.9e-33		
Matches 419	Conservative	0	Mismatches 211	Indels 3
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Qy	91	AAGCAAAAGAGATCACTGTTCTATGTGATGCTAAATGATCTTTATCATTTATCTAC	150
Db	61	AAACCTAAAGAAATTAAGTTCTTTGTGAAGCTAAGGTTTCACTTATATCTTTGCTAGT	120
Qy	151	TCTTGGAAGATGTTGTGATACTGACGCCCTTCAACTACGCTGACAGAAATCTTGACAAA	210
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Qy	211	TACCATGACAACTGTGGAGAAATGTGGATGCTAAGCAATGGAACCTCAGAAATGAA	270
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Qy	271	GTGATAGAGTCAGAAAGAACATGACAGCATGCAATGAGCTCAAGCAATCTGAAGGA	330
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Qy	331	GAGGATATCACTATGTAACCATGTAGAGCTGATGAGCTTGAAGGAAAGCACTTGAAT	390
Db	301	GAAATTTCAATCAACTTACCCATAAAGAGCTTTAATATATGAAAGAAAGCTTACAAAT	360
Qy	391	GGCCTTCAAGATATCCGGAACAGCAGTCCAAGTTGTCGACATGATGAGACAAATGA	450
Db	361	GGACTTTCTAGTATCAGTGCACAGCAAGCTGTAATCTTGAGGAATGGTCAGGAAAAATCAT	420
Qy	451	AAGCACTGGAGATGAGAAATPAACGGCTCACTATGAGCTGCAAAAAACAACAGAGATG	510
Db	421	CAATTTCTGAGAGAGAAATATACCACTTCAATATGCTTTGC--ACAAAAAGAGATG	477
Qy	511	AAAAATTAAGAAATGTGAGAAACATGGAATAAGGATATCATGAGGCACTGGGAAC	570
Db	478	GGACCCATTTGTGAAATGGAATATAGAGAAATTCATGAAGAATGTATCATCAAGA	537
Qy	571	TACACACAACAACGACAGCAGATACCTTTTGCTTCGCGTGCAGCCTATTCAGCCAAAT	630
Db	538	GAAGGGATATATGATACCAATATCCATTTGGCTTACGAGATTCAGCCATCAGCCAAAT	597
Qy	631	CTCCAGAGAGAAATCTAATATGATATATCTTGC	663
Db	598	CTACATGAAAGATGTAAATTAATTAATATTC	630

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LOCUS	ES1551191	tomato flower, 8 mm to	linear EST 18-OCT-2001
DEFINITION	esculentum cDNA clone CTC022N23	5' end,	Lycopersicon
			mRNA sequence.

ACCESSION	B1932302
VERSION	B1932302.1
KEYWORDS	GI:16246774
SOURCE	EST.
ORGANISM	Lycopersicon esculentum (tomato)
	Lycopersicon esculentum

ORGANISM  
Eucarpisicon esculentum  
Lycariota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 751)  
REFERENCE  
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,  
AUTHORS

TITLE	Generation of ESTs from tomato flower tissue, buds 8 mm - preanthesis, unpublished (2001)
JOURNAL	
COMMENT	Contact: CUGI

100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics Institute  
Seq primer: T3.



Db 421 CAAATTCTGGAGGAGGAAAAATGAACAATTCAATATGCTTTGC--ACCAAAAGAGATG 477  
QY 511 AAAATTAAGAAGATGTGAGAAACATGGAATAATGGGTATCATCAGAGGCAGCTGGGAAAC 570  
Db 478 GGAGCCATTGTGTGAAGTGAATAATGAGAGAAATTCATGAGAGTGTATCATCAAGA 537  
QY 571 TACAACAACAACGACGACGATACCTTTGGCTTCCGCTGCAAGCTTATTCAGCAAT 630  
Db 538 GAAAGGATTATGATGACCAATGTCATTGGCTTACAGGTGACCAATGACCAAAAT 597  
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Db 598 CTACATGAAGAAGTGTAAATTAATTAATTCC 630

Search completed: September 25, 2004, 22:02:24  
Job time : 2746.53 secs



Mon Sep 27 09:56:00 2004

us-10-069-527-1.rmpb

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 16:09:57 / Search time 476.696 Seconds  
(without alignments)  
9222.595 Million cell updates/sec

Title: US-10-069-527-1  
Perfect score: 868  
Sequence: 1 atggagacgtggagagtgta.....aaaaaaaaaaaaaaaaaaaa 868

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329.4	37.9	951	US-10-767-795-2121	Sequence 2121, Ap
2	308.2	35.5	900	US-10-425-114-10295	Sequence 10295, A
3	308.2	35.5	933	US-10-424-599-32218	Sequence 32218, A
4	307	35.4	535	US-09-732-627A-3282	Sequence 3282, A
5	303.2	34.9	649	US-10-021-323-8689	Sequence 8689, Ap
6	302.2	34.8	1007	US-10-425-114-14870	Sequence 14870, A
7	302.2	34.8	1021	US-10-424-599-65326	Sequence 65326, A
8	301.2	34.7	474	US-09-732-627A-4667	Sequence 4667, Ap
9	296.6	34.2	601	US-10-021-323-13542	Sequence 13542, A
10	296.6	34.2	639	US-10-021-323-8682	Sequence 8682, Ap
11	265.2	30.6	896	US-10-278-536-238	Sequence 238, App
12	265.2	30.6	914	US-10-412-6998-55	Sequence 55, App1
13	233.6	26.9	1148	US-10-435-114-26809	Sequence 26809, A
14	217.8	23.1	3265	US-10-437-963-9922	Sequence 9922, Ap

15	216.8	25.0	657	US-10-425-114-4580	Sequence 4580, Ap
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17	188.8	21.8	306	US-09-732-627A-3518	Sequence 3518, Ap
18	187.2	21.6	310	US-09-732-627A-3967	Sequence 3967, Ap
19	175	20.2	1242	US-10-260-238-499	Sequence 499, App
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21	148.4	17.1	1536	US-10-425-114-21316	Sequence 21316, A
22	148.2	17.1	681	US-10-104-580-3	Sequence 3, Appl1
23	148.2	17.1	946	US-10-104-580-2	Sequence 2, Appl1
24	141	16.2	1036	US-10-424-599-120794	Sequence 120794, A
25	140.6	16.2	2718	US-10-424-599-120795	Sequence 120795, A
26	138.4	15.9	390	US-09-922-293-1337	Sequence 3337, Ap
27	138.2	15.9	871	US-10-425-114-10670	Sequence 10670, A
28	136.8	15.8	498	US-09-732-627A-4479	Sequence 4479, Ap
29	136.8	15.8	644	US-10-021-323-8631	Sequence 8631, Ap
30	136.6	15.7	407	US-09-922-293-3294	Sequence 3294, Ap
31	133.6	15.4	320	US-09-922-293-1	Sequence 1, Appl1
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33	130	15.0	2237	US-10-425-114-13120	Sequence 13190, A
34	129	14.9	258	US-09-922-293-1947	Sequence 1947, Ap
35	127	14.6	348	US-09-922-293-1197	Sequence 1197, Ap
36	127	14.6	730	US-10-767-701-7879	Sequence 7879, Ap
37	122.6	14.1	1212	US-10-425-114-11957	Sequence 11957, A
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39	120.4	13.9	266	US-09-922-293-1948	Sequence 1948, Ap
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42	119.6	13.8	425	US-09-922-293-14	Sequence 14, Appl
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# ALIGNMENTS

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Sequence 2121, Application US/10767795  
Publication No. US20040181830A1  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Cao, Yongwei  
APPLICANT: Zhou, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21 (53534) B  
CURRENT APPLICATION NUMBER: US/10/767,795  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 117596  
SEQ ID NO 2121  
LENGTH: 951  
TYPE: DNA  
ORGANISM: Gossypium hirsutum  
OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C37363\_1  
US-10-767-795-2121

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Qy	121	GCTAAGATATCTTATCATTTATTTAGCTCTGGAGAGATGTTGATATCTGACCCCT	180	
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 Db 341 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTGAAACATGTAGAG 400  
 QY 361 CTGATGCTTGAAGAGAGCACTTGAATAATGCTTCAAGTATCCGAGCAAGACATCC 420  
 Db 401 CTGATGCTTGAAGAGAGCACTTGAATAATGCTTCAAGTATCCGAGCAAGACATCC 460  
 QY 421 AGTGTGCTGACATGATGAGACATGAGAAAGCACTGAAAGATGAGATAGAGCCCTC 480  
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 QY 481 ACTATGAGCTGCAAAAACAAGAGATGAAATGAAAGATGAGAAACATGAGAA 540  
 Db 521 AGTTTCATCTGATCAACACACA--AGTGGCTTATGAAAGTGCAGAGAG--CAGATGAT 577  
 QY 541 AATGGGATATATGAGAGAGCTGGGGAACTACAAACAACAGACAGATACCTTT 600  
 Db 578 CATGGATACCGAGAGCCCG-----GACTTCAACTCAGAGATGCTTCC 622  
 QY 601 GCCTTCGCTGAGGCTTATTCAGCCAAATCTCCAGAGAGATCTATTAGA 653  
 Db 623 ACCTTCAGTGAAGCAATGACGCAACTTACAGAGAGATGTATTAACA 675

RESULT 2  
 US-10-425-114-10295  
 ; Sequence 10295, Application US/10425114  
 ; Publication No. US2004003488A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(5313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 10295  
 ; LENGTH: 900  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700903463\_FLI  
 US-10-425-114-10295

Query Match 35.5%; Score 308.2; DB 13; Length 900;  
 Best Local Similarity 75.6%; Pred. No. 3.1e-77;  
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 QY 1 ATGGAGCTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGTGAC 60  
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 Db 134 TACTCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGAGATTAATGTTCTATGTAT 193  
 QY 121 GCTAAAGTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 180

Db 194 GCTCAAGTTCCCTTATCATCTTGTGTCTCTGGAGATGATGATCATCAGCCCC 253  
 QY 181 TCAACTACGCTGACAGAAATCTTGGACAAATACCATGACAACTCTGGAGAAAGTTGTGG 240  
 Db 254 TCACTAGTTGATGATGATTTTGGACCAATATCAAGAAACTCTGGAGAAAGTTATG 313  
 QY 241 GATGCTAAGCATGAACTCTGACGATGAAAGTGAATGAGTCAAGAAAGCAATGACAC 300  
 Db 314 GATGCTAAGCATGAACTCTGACGATGAAAGTGAATGAGTCAAGAAAGCAATGATAC 373  
 QY 301 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTGAAACATGTAGAG 360  
 Db 374 ATGCAATGAGCTCAGGACATCTGAAAGGAGAGATATCAATCATTGAAACATGTAGAG 433  
 QY 361 CTGATGCTTGAAGAGAGCACTTGAATAATGCTTCAAGTATCCGAGCAAGACATCC 420  
 Db 434 CTGATGCTTGAAGAGAGCACTTGAATAATGCTTCAAGTATCCGAGCAAGACATCC 493  
 QY 421 AGTGTGCTGACATGATGAGACATGAGAAAGCACTGAAAGATGAGATAGAGCCCTC 480  
 Db 494 GATGCTTGAATGAGATGAGAAATATCCAAATCTCTGAGAGAGCACTCAAGACGCTC 553  
 QY 481 ACTATGAGCTGCAAAAACAAGAGATGAAATGAAAGATGAGAAACATGAGAA 540  
 Db 554 AATTCTCTTCTGCAACACATTTGG 578

RESULT 3  
 US-10-424-599-32218  
 ; Sequence 32218, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J  
 ; APPLICANT: Kovalic, David K  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 32218  
 ; LENGTH: 933  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_129098C.1  
 US-10-424-599-32218

Query Match 35.5%; Score 308.2; DB 13; Length 933;  
 Best Local Similarity 75.6%; Pred. No. 3.1e-77;  
 Matches 382; Conservative 0; Mismatches 123; Indels 0; Gaps 0;  
 QY 1 ATGGAGCTGGAGAGTTGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGTGACC 60  
 Db 107 ATGGAGAGGGGTAAAGATTGATCAAAAGATTGAGAACTCAAGCAACGGAAGTTACC 166  
 QY 61 TACTCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGATCACTGTTCTATGTAT 120  
 Db 167 TACTCCAAAGAGAGAGATGAGATTAATCAAGAGAGAGAGATTAATGTTCTATGTAT 226  
 QY 121 GCTAAAGTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 180  
 Db 227 GCTCAAGTTCCCTTATCATCTTGTGTCTCTGGAGAGATGATGATGATGATGATGAT 286  
 QY 181 TCAACTACGCTGACAGAAATCTTGAACAATACCATGACATTCGAGAGAGAGAGAGAG 240  
 Db 287 TCAACTACGCTGACAGAAATCTTGAACAATACCATGACATTCGAGAGAGAGAGAGAG 346  
 QY 241 GATGCTAAGCATGAACTCTGACGATGAAAGTGAATGAGTCAAGAAAGCAATGACAC 300  
 Db 347 GATGCTAAGCATGAACTCTGACGATGAAATGATGATGATGATGATGATGATGATGAT 406



QY 301 ATGCAAGTAGAGCTCAGGACATCTGAAGGAGAGATATCATCATTTGAAACATGTAGAG 360  
| | | | |  
Db 407 ATGCAATTTAGAGCTCAGGACCTTGAAGGAGAGACATCACTGATTAACAGGAA 466  
| | | | |  
QY 361 CTGATGGCTTTAAGAGAGACATTTGAAATGCGCTTCAAGTATCCGGACAAAGCATGCC 420  
| | | | |  
Db 467 CTGATGGCTTTAAGAGAGAGCTTGAATGCGCTTCAAGTATCCGGACAAAGAGAG 526  
| | | | |  
QY 421 AAGTGGTGCAGATGATGAGAGCAATGGAAGGACATGGAATGAGAAATTAAGCGCTC 480  
| | | | |  
Db 527 GAAGTGCACAGATGTTCAAGAGAAATGACAAATTTGGAGAGAGCAAAATTAAGAACTC 586  
| | | | |  
QY 481 ACTTATGAGCTGCAAAAACAACAGG 505  
| | | | |  
Db 587 AATTCTCTTCTGCAACACATTTGG 611  
| | | | |

RESULT 4  
US-09-732-627A-3282

/ Sequence 3282, Application US/09732627A  
/ Publication No. US2004012338A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Fincher, Karen L.  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
/ TITLE OF INVENTION: Plants  
/ FILE REFERENCE: 38-21(51770)B  
/ CURRENT APPLICATION NUMBER: US/09/732,627A  
/ CURRENT FILING DATE: 2000-12-08  
/ NUMBER OF SEQ ID NOS: 4930  
/ SEQ ID NO 3282  
/ LENGTH: 535  
/ TYPE: DNA  
/ ORGANISM: Gossypium hirsutum  
/ FEATURE:  
/ OTHER INFORMATION: Clone ID: LIB3493-014-P1-M1-C8  
US-09-732-627A-3282

Query Match 35.4%; Score 307; DB 12; Length 535;  
Best Local Similarity 75.7%; Pred. No. 4.9e-77;  
Matches 393; Conservative 0; Mismatches 125; Indels 1; Gaps 1;

QY 10 GGGAGGTTGAGTCAAGAGATTTGAGAACTCAAGTCAAGGACGAGTGAACCTTCACTCAAG 69  
| | | | |  
Db 1 GGGCAAGTTGAGTCAAGAGATTTGAGAACTCAAGTCAAGGACGAGTGAACCTTCACTCAAG 60  
| | | | |  
QY 70 AGAGGAATGGGATTTATCAAGAGGCAAGGAGATCTGTTCTATGTATGCTAAAGTA 129  
| | | | |  
Db 61 AGAGGAATGGGATTTATCAAGAGGCAAGGAGATCTGTTCTATGTATGCTAAAGTA 120  
| | | | |  
QY 130 TCTCTTATCATTTTATTTAGCTCTGGAGATGGTTGATTAATCTGACAGCCCTTCACTAG 189  
| | | | |  
Db 121 TCTCTTATCATTTTATTTGCTAGTTCTGGAGATGGTTGATTAATCTGACAGCCCTTCACTAG 180  
| | | | |  
QY 190 CTGACAGAAATCTTGGACAAATACATGAGACATCTGGAGAAAGTTGGGATGCTAG 249  
| | | | |  
Db 181 TTGATGATATTTTGGACCAATATCA-GAAAATCTTGGAGAAAGTTGGGATGCTAAA 239  
| | | | |  
QY 250 CATAGAAACCTCAGCAATGAGTGAATGAGTCAAGAAAGCATGACAGATGCAAGTA 309  
| | | | |  
Db 240 CATAGAAATCTCAGCAATGAGTGAATGAGTCAAGAAAGCATGAGTGAAGTGAAGT 299  
| | | | |  
QY 310 GAGCTCAGCATCTGAAGGAGAGATATCAATCATTTGAAACATGTAGAGCTGATGCC 369  
| | | | |  
Db 300 GAGCTCAGCATTTGAAAGGAGAGATATCAATCATTTGCTTCAAGAGAGCTGATGCC 359  
| | | | |  
QY 370 TTAGAGAGAGCACTTGAATGCGCTTCAAGTATCCGGACAAAGCATGCAATTTGCTC 429  
| | | | |  
Db 360 TTAGAGAGAGCACTTGAATGCGCTTCAAGTATCCGGACAAAGCATGCAATTTGCTC 419  
| | | | |  
QY 430 GACATGATGAGAGCAATGAGAGAGCACTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 489  
| | | | |  
Db 420 GATATGAG 479  
| | | | |

QY 490 CTGCAAAAACAACAGAGATGAAATTAAGAGATGTC 528  
| | | | |  
Db 480 GTGAATCAACAGCAACTGATTTATGAAATGTGAGAGAG 518  
| | | | |

RESULT 5  
US-10-021-323-8899

/ Sequence 8899, Application US/10021323  
/ Publication No. US20040123340A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Deikman, Jill  
/ APPLICANT: Peng, Paul C.C.  
/ APPLICANT: Fincher, Karen L.  
/ APPLICANT: Ziegler, Todd E.  
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
/ TITLE OF INVENTION: Plants  
/ FILE REFERENCE: 38-21(52274)B  
/ CURRENT APPLICATION NUMBER: US/10/021,323  
/ CURRENT FILING DATE: 2001-12-12  
/ PRIOR APPLICATION NUMBER: US 60/255, 619  
/ PRIOR FILING DATE: 2000-12-14  
/ NUMBER OF SEQ ID NOS: 17880  
/ SEQ ID NO 8899  
/ LENGTH: 649  
/ TYPE: DNA  
/ ORGANISM: Gossypium hirsutum  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: (1)..(649)  
/ OTHER INFORMATION: unsure at all n locations  
/ OTHER INFORMATION: Clone ID: LIB3828-021-Q1-K6-C2  
US-10-021-323-8899

Query Match 34.9%; Score 303.2; DB 17; Length 649;  
Best Local Similarity 70.4%; Pred. No. 6.7e-76;  
Matches 455; Conservative 0; Mismatches 173; Indels 18; Gaps 3;

QY 8 GTGGAGGTTGAGTCAAGAGATTTGAGAACTCAAGTCAAGGACGAGTGAACCTTCACTCA 67  
| | | | |  
Db 3 GGGGAGGTTGAGTCAAGAGATTTGAGAACTCAAGTCAAGGACGAGTGAACCTTCACTCA 62  
| | | | |  
QY 68 AGAGGAATGGGATTTATCAAGAGGCAAGGAGATCACTGTTTATGTAGTCTAAAG 127  
| | | | |  
Db 63 AGAGGAATGGGATTTATCAAGAGGCAAGGAGATCACTGTTTATGTAGTCTAAAG 122  
| | | | |  
QY 128 TATCTTATCATTTTATTTAGCTCTGGAGATGGTTGATTAATGCAAGCCCTTCACTCA 187  
| | | | |  
Db 123 TTTCTTATCATTTTATTTGATGTTCTGGCAAGTGAAGATGCAAGCCCTTCACTCA 182  
| | | | |  
QY 188 CCGTGCAGAAATCTTGGACAAATACATGACAAATCTGGGAGAAAGTTGGGATGCTA 247  
| | | | |  
Db 183 ATTGTGATATTTTGGACCAATATCAGAAAGCTTCGGGAGAAAGTTATGGGATGCTA 242  
| | | | |  
QY 248 AGCATGAGAACTCAGCAATGAGTGAATGAGTGAAGAAACATATGACAGATGCAAG 307  
| | | | |  
Db 243 AACATGAGAACTCAGCAATGAGTGAATGAGTGAAGAAACATATGACAGATGCAAG 302  
| | | | |  
QY 308 TAGAGCTCAGCATCTGAAGGAGAGATATCAATCATTTGAAACATGTAGAGCTGATGG 367  
| | | | |  
Db 303 TTGAACTGAGCATTTGAAAGGAGAGATATCACTCTTGTGCTTCAAGAGAGCTGATGG 362  
| | | | |  
QY 368 CTTTGAAGAGACATTTGAATGCGCTTCAAGATTCGGGACAAAGCATGCAAGTTCC 427  
| | | | |  
Db 363 CATATGAGATGCGCTTGAATGCGCTTCAAGATTCGGGACAAAGCATGCAAGTTCC 422  
| | | | |  
QY 428 TCGACATGATGAGAGCAATGGAAGGACCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 487  
| | | | |  
Db 423 TTGATTAAGACATGAGAAATTAACAAATTCCTGGAAGAGACATCAAGAGAGCTCAAGTTCA 482  
| | | | |  
QY 488 AGCTGCAAAAACAACAGAGATGAAATTAAGAGATGGAAGATGGAAGATGGAAGATGGAAG 547  
| | | | |  
Db 483 TTCTGATTAACAACA-AGTGCCTTATGAAGTGAAGAGAG-CAGATGATCATGAT 539  
| | | | |



```

RESULT 9
US-10-021-323-13542
; Sequence 13542, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Ull

```

```

RESULT 10
US-10-021-323-8682
; Sequence 8682, Application US/10021323
; Publication No. US2004012340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21 (52274)B  
CURRENT APPLICATION NUMBER: US/10/021,323  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255, 619  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 17880  
SEQ ID NO 8682  
LENGTH: 639  
TYPE: DNA  
ORGANISM: *Gossypium hirsutum*  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(639)  
OTHER INFORMATION: unsure at all n locations  
OTHER INFORMATION: Clone ID: LIB828-014-Q1-K6-G9  
US-10-021-323-8682

Query Match 34.2%; Score 296.6; DB 17; Length 639;  
Best Local Similarity 74.4%; Pred. No. 5.2e-74;  
Matches 374; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 3 GGGACGTGGGAAGCTTGAATCAAGAGATTGGAATCAAGTAAACGACAGTGAACCTA 62  
DB 25 GGGAGAGGGGAGATTTGAGTCAAGAGATTGGAATCAAGTAAACGACAGTGAACCTA 84  
QY 63 CTCGAAGAGAGAGATTTGATTAACAAGAGCAAGAGATCACTGTTCTATGTGATGC 122  
DB 85 TTCAGAGAGAGAGATTTGATTAACAAGAGCAAGAGATCACTGTTCTATGTGATGC 144  
QY 123 TAAAGTATCTCTTATCATTTATCTAGCTCTGGGAAGATGTTGAATATCTGACCCCTTC 182  
DB 145 TAAAGTATCTCTTATCATTTATCTAGCTCTGGGAAGATGTTGAATATCTGACCCCTTC 204  
QY 183 AACTAGCTGACAGAAATCTTGACCAATATCAATGACATCTGGGAAGATTTGGA 242  
DB 205 TACTAATTTGGTGGATTTTGGACCAATATCAAGAGATTTCCGGGAAGATTTGGA 264  
QY 243 TGTAAAGCATGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGAT 302  
DB 265 TGTAAAGCATGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGAT 324  
QY 303 GCAAGAGAGAGCTGAGCATCTGGAAGGAGAGATTCATCATTTGAACCATGTAAGCT 362  
DB 325 GCAAGATTTGAGATTTGGAAGGAGAGATTCATCATTTGCTTTGCTTTACAGAGCT 384  
QY 363 GATGCTTTAGAGAGAACTTGAATGAGCTTCAAGTATCCGGAACAGAGCTCA 422  
DB 385 GATGCTTTAGAGAGAACTTGAATGAGCTTCAAGTATCCGGAACAGAGCTCA 444  
QY 423 GTTCGTGAGATGATGAGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 482  
DB 445 GTTCGTGAGATGATGAGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 504  
QY 483 TTATGAGCTGCAAAAACACAG 505  
DB 505 TTTCATTTGAAATCAACACAG 527

RESULT 11  
US-10-278-536-238  
Sequence 238, Application US/10278536  
Publication No. US2003013186A1

GENERAL INFORMATION:  
APPLICANT: Samaha, Raymond  
APPLICANT: Heard, Jacqueline  
APPLICANT: Uiang, Cal-Zhong  
APPLICANT: Pineda, Omaira  
APPLICANT: Reuber, Lynne  
APPLICANT: Riechmann, Jose-Luis  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Keddie, James  
APPLICANT: Ratcliffe, Oliver

APPLICANT: Pigirim, Marsha  
APPLICANT: Adam, Luc  
APPLICANT: Broun, Pierre  
TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES  
FILE REFERENCE: NBI-011  
CURRENT APPLICATION NUMBER: US/10/278,536  
CURRENT FILING DATE: 2002-10-22  
PRIOR APPLICATION NUMBER: 60/125,814  
PRIOR FILING DATE: 1999-03-23  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 238  
LENGTH: 896  
TYPE: DNA  
ORGANISM: *Arabidopsis thaliana*  
FEATURE:  
OTHER INFORMATION: G134  
US-10-278-536-238

Query Match 30.6%; Score 265.2; DB 15; Length 896;  
Best Local Similarity 68.0%; Pred. No. 6.1e-65;  
Matches 385; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

QY 1 ATGGACGTGGGAAGCTTGAATCAAGAGATTGGAATCAAGTAAACGACAGTGAACCTA 60  
DB 24 ATGGGTAGAGAGAAAGATCGATTAAGAGATGAGAACGCAACAGAGTGTGAGC 83  
QY 61 TACTCCAGAGAGAGATTTGATTAACAAGAGCAAGAGATCACTGTTCTATGTGATGC 120  
DB 84 TTCTCAAGAGAGAGATTTGATTAACAAGAGCAAGAGATCACTGTTCTATGTGATGC 143  
QY 121 GCTAAGTATCTTTATCATTTATTTAGCTCTGGGAAGATGTTGAATATCTGACCCCTTC 180  
DB 144 GCAAAAGTTCCTCTATTAATCTTTGCAAGTAAATGATGATGATGATGATGATGATGAT 203  
QY 181 TCAACTAGCTGACAGAAATCTTGACCAATATCAATGACATCTGGGAAGATTTGGA 240  
DB 204 TCAATGATTTGGTGGATTTTGGACCAATATCAAGAGATTTCCGGGAAGATTTGGA 263  
QY 241 GATGCTTTAGAGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGAT 300  
DB 264 GATGCTTTAGAGAGAACTTCAAGCATGATGATGATGATGATGATGATGATGATGAT 323  
QY 301 ATGCAAGTAAAGCTGAGCATCTGGAAGGAGAGATTCATCATTTGAACCATGTAAGCT 360  
DB 324 TTACAACTGAGAGCTGAGCATTTGGAAGGAGAGATTCATCATTTGCTTTGCTTTACAGAGCT 383  
QY 361 CTATGAGCTTTAGAGAGAACTTGAATGAGCTTCAAGTATCCGGAACAGAGCTCA 420  
DB 384 CTATGAGCTTTAGAGAGAACTTGAATGAGCTTCAAGTATCCGGAACAGAGCTCA 443  
QY 421 AAGTGTGAGATGATGAGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 480  
DB 444 AAGTGTGAGATGATGAGAGCAATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 503  
QY 481 ACTTATGAGCTGCAAAAACACAGAGATGAAATTAAGAGATGAGTGAAGAAACATGGA 540  
DB 504 ACTTATGAGCTGCAAAAACACAGAGATGAAATTAAGAGATGAGTGAAGAAACATGGA 560  
QY 541 AATGGTATCATGAGAGAGCTGGG 566  
DB 561 ATGAGAGATCATGAGAGAGCTGGG 586

RESULT 12  
US-10-412-699B-55  
Sequence 55, Application US/10412699B  
Publication No. US20040045049A1

GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.

```

APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc J.
APPLICANT: Broun, Pierre E.
APPLICANT: Pineda, Omayra
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddle, James S.
APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samana, Raymond R.
APPLICANT: Pilgrim, Marsha L.
APPLICANT: Creelman, Robert A.
APPLICANT: Dubell, Arnold N.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: WBI-0048CIP
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/489,376
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 09/533,030
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/532,591
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/819,142
PRIOR FILING DATE: 2001-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55
LENGTH: 914
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G134
US-10-412-699B-55

```

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Query Match 30.6%; Score 265.2; DB 13; Length 914;
Best Local Similarity 68.0%; Pred. No. 6.1e-65;
Matches 385; Conservative 0; Mismatches 178; Indels 3; Gaps 1;

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QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCACTTAACAGGAGGTGACC 60
DB 36 ATGGGAGGAGGAGATGAGATTAAGAGATAGAGACGAAACACAGAGTGTACG 95
QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
DB 96 TTCTCAAGAGAGAGATGAGATTGTGTAAGAGGCTAAAGAGATCACAGTTCTTTGTGAT 155
QY 121 GCTAAAGATCTCTTATGATTTATCTAGCTCTGGGAAAGATGGTGAATATCGAGCCCT 180
DB 156 GCAAAAGTTGCCCTCATATCTTTGCAAGTAAAGTGAATGATGATGATTTACTGTTGCTT 215
QY 181 TCAACTAGCTGACAGAAATCTTGGACAATATCCATGGACAATCTGGAGAAAGTTGTG 240
DB 216 TCCATGAGATCTTGGGTATGTTGACCAATACCAAGATTATCTGGGCAAGAACTATGG 275
QY 241 GATGCTAAGCATGAGAACTCTGACGAAAGATGAGATAGAGTCAAGAAAGACATGACAGC 300
DB 276 GATGCTAAGCATGAGAACTCTTGAAGATGATGATGATGATGATGATGATGATGATGATG 335

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QY 301 ATGCAAGTAGAGCTCAGGATCTGAGAGAGAGATATCAATCATTTGAAACATGTAGAG 360
DB 336 TTACAGCTGAGGCTCAGGATTTTAAAGAGAAATATATAGCTCTCTCAACTTGAATAAT 395
QY 361 CTGATGCTTAAAGAGAGACCTTGAATAATGCTTACAGTATCCGGGCAACAGACTGCC 420
DB 396 CTGATGCTGTCGAGACGCGCATTGAACATGCTTCACAAAGTCCGAGACCAAGATG 455
QY 421 AAGTTCGTCGACATGATGAGAGACATGAGAAAGGCACTGGAAGATGAGAAATPAAGCGCTC 480
DB 456 GAGATCTTATATCAAGAGAGAGAAATGAGAAATGATGGCGGAGAGCAACGCACTC 515
QY 481 ACTTATGAGCTGCAAAAACAGAGATGAAATTAAGAGAAATGAGAAATGAGAAATGAGAA 540
DB 516 ACTTCCAGCTGC--AACCAAGAGATGGCTATAGCAACCAACGCAAGAGAAATGATG 572
QY 541 AATGCTATCATCTGAGGCAAGCTGGG 566
DB 573 ATGAGAGATCATGATGGGCAAGTTGG 598

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RESULT 13
US-10-425-114-26809
Sequence 26809, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(533.3)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26809
LENGTH: 1148
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4606-002-H7_FLI
US-10-425-114-26809

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Query Match 26.9%; Score 233.6; DB 13; Length 1148;
Best Local Similarity 62.7%; Pred. No. 7.7e-56;
Matches 400; Conservative 0; Mismatches 229; Indels 9; Gaps 2;

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QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCACTTAACAGGAGGTGACC 60
DB 287 ATGGGAGGAGGAGATGAGATTAAGAGATGAGAACTCTAACAACCGGAGGTGACC 346
QY 61 TACTCCAGAGAGAGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
DB 347 TTCTCAAGAGAGAGATGAGATTGTGTAAGAGGCTAAAGAGATCACAGTTCTTTGTGAT 155
QY 121 GCTAAAGATCTCTTATGATTTATCTAGCTCTGGGAAAGATGGTGAATATCGAGCCCT 180
DB 407 GCCGAGTGGCGCTCTCATCTTTCTTCAAGCGGCGCAACCTCTAGACATCTGCTGCC 466
QY 481 TCAACTAGCTGACAGAAATCTTGGACAATATCCATGGACAATCTGGGAAAGTTGTG 240
DB 467 AGGACCTCGCTGTCAGAGATCTTGGAGAGTACCAACCACTCCGGGAAGATTCTGTG 526
QY 241 GATGCTAAGCATGAGAACTCTGACGAAAGATGAGATAGAGTCAAGAAAGACATGACAGC 300
DB 527 GGTGAAGAGCAAGAACTCTGAGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATG 586
QY 301 ATGCAAGTAGAGCTCAGGATCTGAGAGAGAGATATCAATCATTTGAAACATGTAGAG 360

```

Db 587 ATGCAAGATTACGCTCAGGATCTGAAAGCGAGGACCTGAACTTCCTCGACCCGAGGAG 646  
Qy 361 CTGATGCGCTTAGAGAGGACCTTGAATAATGCGCTTACAGTATCCGGGACCAAGCATGCC 420  
Db 647 CTGATCGCTATTGAAGAGGCGCTCCAGATATGGGACAGCAACATGGCGAGGAGGAGATG 706  
Qy 421 AAGTTCGTCCAGATGAGAGAGCAATGAGAAAGCACTGGAAGATGAGATTAAGCGCTTC 480  
Db 707 GACTACTGAGAGATGACCAAGAGATGGAAAGATGCTGGAGAGCAACCAAGATATCTG 766  
Qy 481 ACTTATGAGCTGCAAAAAACAAGAGATGAAATAAAGAGATGAGAAACATGGA 540  
Db 767 ACTTTAGATGTC---ACCAACAGGCTGTGATCTGACGGCGGCATGAGGGAGCTGGAG 823  
Qy 541 AATGGGATATATCAGAGGCGAGCTGGGGAATTAACAACAACAGCAGATATCTTTT 600  
Db 824 ACCGATACCATCATGAGTCCAGC-----ACGACAGGATTTCAITTCAGATGCCGCTTC 877  
Qy 601 GCCTTCGCGTGACGCTTATTCAGCCCAATCTCCAGGA 638  
Db 878 ACCTTCGGGTGACAGCCCAACCAACCCCACTTCAGGA 915

## RESULT 14

US-10-437-963-9922  
; Sequence 9922, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 9922  
; LENGTH: 3265  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_16293C.1  
US-10-437-963-9922

Query Match 25.1%; Score 217.8; DB 17; Length 3265;  
Best Local Similarity 61.3%; Pred. No. 4,8e-51;  
Matches 392; Conservative 0; Mismatches 232; Indels 15; Gaps 2;

Qy 1 ATGGAGCTGGGAAAGGTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGGTGACC 60  
Db 120 ATGGGGCGCGCAAGATCAAGATCAAGAGATCGAATTCACGACCGGAGGTGACG 179  
Qy 61 TACTCCAGAGAGAGAGATGATTAACAAGAGCAAGAGATCACTGTTCTATGTGAT 120  
Db 180 TTCTCGAAGCGCGCTCCGGGATCTCAAGAGAGCCCGGAGATGGGCTGCTCGGAC 239  
Qy 121 GCTAAGATCTCTTATCATCTTATCTAGCTCTGGGAGAGTGTTGATATCTGACGCC 180  
Db 240 CCGGAGGTGGGGGTGCTATCTTCTCAGCGCGGCAAGCTCTCGACTTATGACGCC 299  
Qy 181 TCACTACGCTGACAGAAATCTTGAACAATACATGACATCTGGAGAAAGTTGGG 240  
Db 300 AAGACCAAGCTGTCAAGATCTTGAAGATACCAAGACCACTCCGGGAAATACTCTGG 359  
Qy 241 GATGCTAAGCATGAGAACTTACGCAATGAATGATAGTCAAGAAAGCAATGACAC 300  
Db 360 GATGAGAAAGCAAGAGCTCAGCGCAGAGATCATGCTGTCTCAAGAGAGAAAGCAAGAC 419

Qy 301 ATGCAAGTAGAGCTCAGGATCTGAGAGGAGAGATTCACATCATTTGAACATGTAGAG 360  
Db 420 ATGCAAGATCGAGCTCAGGATATGAGAGAGAGATGTGAATCTCCCTCGACCCAAAGAG 479  
Qy 361 CTGATGCGCTTAGAGAGGACCTTGAATAATGCGCTTACAGTATCCGGGACCAAGCATGCC 420  
Db 480 CTGATCGGATCGAGAGGCGCTCCAAACAACGCGCCCAATCTGCGGAGCAAGATATGAT 539  
Qy 421 AAGTTCGTCCAGATGAGAGACATGGAAGGACATGGAAGATGAGATTAAGCGGCTTC 480  
Db 540 GACCACTGAGAGATGATTAAGAAATGAGAGATGCTGGAGAGACAGCAACAGATGTTG 599  
Qy 481 ACTTATGAGCTGCAAAAAACAAGAGATGAAATAAAGAGATGAGAAACATGGA 540  
Db 600 GCTTTAGGGTGC---ACGACAGAGGTGAGCTGACGGCGGCATTAAGGAGCTGGAG 656  
Qy 541 AATGGGATATATCAGAGGCGAGCTGGGGAATTAACAACAACAGCAGATATCTTTT 600  
Db 657 CTGGCTACCAACA-----CGAGACAGGGAATTTGGGGCTCTGATGCGCTTC 704  
Qy 601 GCCTTCGCGTGACGCTTATTCAGCCCAATCTCCAGGAG 639  
Db 705 ACCTTCAGGGGTGACAGCCCAACCAACCCCACTTCAGGAG 743

## RESULT 15

US-10-425-114-4580  
; Sequence 4580, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 4580  
; LENGTH: 657  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700382572\_FLI  
US-10-425-114-4580

Query Match 25.0%; Score 216.8; DB 13; Length 657;  
Best Local Similarity 64.6%; Pred. No. 3.5e-51;  
Matches 323; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 1 ATGGAGCTGGGAAAGGTGAGATCAAGAGATTGAGAACTCAAGTAACAGGAGGTGACC 60  
Db 136 ATGGGGCGCGGAAAGATCAAGATCAAGAGATCGAATCTTAACAACCGGAGGTGACC 195  
Qy 61 TACTCCAGAGAGAGATGATTAACAAGAGCAAGAGATCACTGTTCTATGTGAT 120  
Db 196 TTCTCGAAGCGCGGCGGAGCTGTCAGAGAGGACCGGAAATGCGCTGCTCGGAC 255  
Qy 121 GCTAAGATCTCTTATCATCTTATCTAGCTCTGGGAGAGTGTTGATATCTGACGCC 180  
Db 256 GCCGAGTGGGGGTGCTATCTTCTCAGCGCGGCAAGCTCTAGAGATGCTCGGCC 315  
Qy 181 TCACTACGCTGACAGAAATCTTGAACAATACATGACATCTGGGAAAGTTGGG 240  
Db 316 AAGACCTGCTGTCAAGATCTTGAAGATACCAAGACCACTCCGGGAAATACTCTGG 375  
Qy 241 GATGCTAAGCATGAGAACTTACGCAATGAATGATAGTCAAGAAAGCAATGACAC 300

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Db      376  GGTGAGAAACACAAGAACTGAGTGCAGAGATCGACAGAGTCAGAGAGAGAAAGCAAC 435
Qy      301  ATGCAAGTAGAGCTCAGGCACTGAAAGGAGAGATATCATCATTGAAACCATGTAGAG 360
Db      436  ATGCAAGATTCAAGCTCAGGCACTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
Qy      361  CTGATGACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db      496  CTGATGACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Qy      421  AAGTTCGTCCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db      556  GACTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
Qy      481  ACTTATGAGCTGCAGAAACA 500
Db      616  ACTTTAGATGCACCAACA 635

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Search completed: September 25, 2004, 22:22:17  
 Job time : 478.636 secs





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 15:55:57 ; Search time 75.535 Seconds  
(without alignments)  
6376.765 Million cell updates/sec

Title: US-10-069-527-1

Sequence: 1 atgggacgtgggaagcttga.....aaaaaaa 866

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%

. Listing first 45 summaries

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3: /cgn2_6/prodata/2/ina/6A_COMB_seg.*
4: /cgn2_6/prodata/2/ina/6B_COMB_seg.*
5: /cgn2_6/prodata/2/ina/POTUS_COMB_seg.*
6: /cgn2_6/prodata/2/ina/backfile1_seg.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	148.2	17.1	681	4	US-09-410-464-3	Sequence 3, Appl1
2	148.2	17.1	946	4	US-09-410-464-2	Sequence 2, Appl1
3	109	12.6	4285	4	US-09-410-464-1	Sequence 1, Appl1
4	105.6	12.2	1070	3	US-08-904-284-1	Sequence 1, Appl1
5	93.6	10.8	2437	3	US-08-904-284-6	Sequence 6, Appl1
6	93.4	10.8	1043	2	US-08-867-087B-12	Sequence 12, Appl1
7	92.2	10.6	945	2	US-08-485-961-9	Sequence 9, Appl1
8	92.2	10.6	945	2	US-08-867-087B-10	Sequence 10, Appl1
9	92	10.6	1345	1	US-08-592-214A-7	Sequence 7, Appl1
10	92	10.6	1345	3	US-08-659-188-7	Sequence 7, Appl1
11	92	10.6	1345	3	US-08-655-227-7	Sequence 7, Appl1
12	92	10.6	1345	3	US-08-655-241-7	Sequence 7, Appl1
13	92	10.6	1345	3	US-09-149-976-7	Sequence 7, Appl1
14	92	10.6	1345	4	US-09-398-326-7	Sequence 7, Appl1
15	91	10.5	795	3	US-08-904-284-2	Sequence 2, Appl1
16	90.6	10.4	1180	2	US-08-867-087B-16	Sequence 16, Appl1
17	90.4	10.4	2679	3	US-08-904-284-4	Sequence 4, Appl1
18	88.2	10.2	1457	1	US-08-460-512-1	Sequence 1, Appl1
19	87.8	10.1	1059	2	US-08-867-087B-14	Sequence 14, Appl1
20	87.6	10.1	299	4	US-09-313-294A-3385	Sequence 685, Appl1
21	87.6	10.1	1062	3	US-09-067-800-1	Sequence 1, Appl1
22	87.6	10.1	1062	3	US-09-105-652-1	Sequence 1, Appl1
23	87.6	10.1	1062	3	US-09-349-677-1	Sequence 1, Appl1
24	87.6	10.1	1062	4	US-09-708-584-1	Sequence 1, Appl1
25	87.4	10.1	794	1	US-08-592-214A-3	Sequence 3, Appl1
26	87.4	10.1	794	3	US-08-659-188-3	Sequence 3, Appl1
27	87.4	10.1	794	3	US-08-655-227-3	Sequence 3, Appl1

28	87.4	10.1	794	3	US-08-655-241-3	Sequence 3, Appl.1
29	87.4	10.1	794	3	US-09-149-976-3	Sequence 3, Appl.1
30	87.4	10.1	794	4	US-09-339-326-3	Sequence 3, Appl.1
31	85.8	9.9	1054	2	US-08-537-156-1	Sequence 1, Appl.1
32	85.8	9.9	1057	3	US-08-655-188-1	Sequence 1, Appl.1
33	85.8	9.9	1057	3	US-08-655-227-1	Sequence 1, Appl.1
34	85.8	9.9	1057	3	US-08-655-241-1	Sequence 1, Appl.1
35	85.8	9.9	1057	4	US-09-339-326-1	Sequence 1, Appl.1
36	85	9.8	723	4	US-09-410-464-1.1	Sequence 11, Appl.1
37	85	9.8	768	1	US-08-537-214A-5	Sequence 5, Appl.1
38	85	9.8	768	3	US-08-655-188-5	Sequence 5, Appl.1
39	85	9.8	768	3	US-08-655-227-5	Sequence 5, Appl.1
40	85	9.8	768	3	US-08-655-241-5	Sequence 5, Appl.1
41	85	9.8	768	4	US-09-149-976-5	Sequence 5, Appl.1
42	85	9.8	768	4	US-09-339-326-5	Sequence 5, Appl.1
43	85	9.8	1219	4	US-09-410-464-10	Sequence 10, Appl.1
44	84.4	9.7	779	1	US-08-539-214A-9	Sequence 9, Appl.1
45	84.4	9.7	779	3	US-08-655-188-9	Sequence 9, Appl.1

## ALIGNMENTS

	RESULT	1
	US-09-410-464-3	
	/ Sequence 3, Application US/09410464	
	/ Patent No. 635892	
	GENERAL INFORMATION:	
	APPLICANT: Strauss et al.	
	TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in	
	TITLE OF INVENTION: poplar and other plant species.	
	FILE REFERENCE: 53375	
	CURRENT APPLICATION NUMBER: US/09/410.464	
	CURRENT FILING DATE: 1999-10-01	
	EARLIER APPLICATION NUMBER: 09/287,700	
	EARLIER FILING DATE: 1999-04-06	
	EARLIER APPLICATION NUMBER: 60/080,851	
	EARLIER FILING DATE: 1998-04-06	
	NUMBER OF SEQ ID NOS: 24	
	SOFTWARE: Patentin Ver. 2.0	
	SEQ ID NO 3	
	LENGTH: 681	
	TYPE: DNA	
	ORGANISM: Populus balsamifera subsp. trichocarpa	
	FEATURE:	
	NAME/KEY: CDS	
	LOCATION: (1)..(681)	
	US-09-410-464-3	
Qy	Query Match	17.1%; Score 148.2; DB 4; Length 681;
	Best Local Similarity	58.9%; Pred.No. 8.3e-33;
Matches	255; Conservative	0; Mismatches 178; Indels 0; Gaps 0
Dd	1 ATGGGACGTGGGAAGGTGGATGAGTCAAGAAGATTGGAACCTCAACTTAACAGCAGTGACC	60
	1 ATGGGTGTGGAAAGTTGTAATCAAGAAAGTCGAAAACCCACAAGCGAAGTCACC	60
Qy	61 TACTCCAAGAGAGAGATGAGATTATCAAGAAAGCAAAGAGATCATCTGTTCTATGGAT	120
Dd	61 TACTCGAAGAGAAAGATATGTTTTTCAAGAAAGCCCAGAAGCATCACGTGATCTTGAT	120
Qy	121 GCATAAGTATCTTTATCTGATTTATCTGAGCTCTGGGAAGATGGTTGAATCTGCAGCCCT	180
Dd	121 GCATAGGTCTCTTTATCTGATTTATCTGAGCTCTGGGAAGATGGTTGAATCTGCAGCCCT	180
Qy	181 TCACCTACGCTGCACAAAACTTTGGACAAATGCCATGACATCTGGAGAACGTTTGG	240
Dd	181 TCACATCGACAAGAAAGATCTACGATCATATCGAAACGTTTAGGATATGATCTGTGG	240
Qy	241 GATGCTAGATGATGAAGAACCTCAGCATGATGAGTATGAGTCAAGAAACATGACAGC	3000
Dd	241 GGACCTAATATCGAAGAAATGCAAGACACTTGAGAAAGCTGATGATGATCATATTAAG	3000



ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 960296.94193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1070 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-904-284-1

Query Match 12.2% Score 105.6; DB 3; Length 1070;  
Best Local Similarity 55.9%; Pred. No. 1.7e-20;  
Matches 229; Conservative 0; Mismatches 169; Indels 12; Gaps 1;

QY 1 ATGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGTGACC 60  
DB 19 ATGGCTGTGGAAAAATCGAGATAAAGAGATCGAAGATCGAATAGCAGACAGTCACT 78  
QY 61 TACTCCAAAGAGAGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGAT 120  
DB 79 TTTTCAAGAGGGGCTTCTGCTTACTTAAAGAGCTGTGAGCTCTCTGTTCTTGTGAT 138  
QY 121 GCTAAAGTATCTCTTATCATTTTATCTAGCTCTGGAGATGGTTGATTAATCTGACGCC 180  
DB 139 GCTGAAGTCTGTGATCGTCTTCTCTTAAGTCTGGAGCTCTTCAAGTATCTCACTACT 198  
QY 181 TCAACTACGCTGACAGAAATCTTGACAAATACCATGACCAATCTGGAGAGAGTTGGG 240  
DB 199 GGAATGAGCAACACTTTCAGATACGATACCA-----CCAGATTCTTCA 246  
QY 241 GATGCTAAGATGAGAACTCAGCAATGAGTGAATGATGATCAAGAAAGCATGACAGC 300  
DB 247 GCTTCTAAGCAGAGAGATTTGTCAGAGTGTGATTTTAAAGATCAACTTCAAG 306  
QY 301 ATGCAAGTAGAGCTCAGGCACTTGAGAGGAGAGATATCATCATTTGAACATGTAGAG 360  
DB 307 CTTCAGAGAAACATTACAACTGACGGGCAAGGCTTGATCTCTGACCTTTAAAGAG 366  
QY 361 CTGATGCTTAAAGAGAGCACTTGAAGAGGCTTACAGATCCGCGGA 410  
DB 367 CTGCAAGCCTTGAGCAGCACTATATCATGATGATTTACTGTCAGAGA 416

## RESULT 5

US-08-904-284-6  
Sequence 6, Application US/08904284  
Patent No. 613935  
GENERAL INFORMATION:  
APPLICANT: Fernandez, Donna E.  
APPLICANT: Heck, Gregory R.  
TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN  
TITLE OF INVENTION: TRANSGENIC PLANTS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/904,284

FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
REFERENCE/DOCKET NUMBER: 960296.94193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2437 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-904-284-6

Query Match 10.8% Score 93.6; DB 3; Length 2437;  
Best Local Similarity 70.0%; Pred. No. 7.5e-17;  
Matches 126; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1 ATGGAGCTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGTGACC 60  
DB 527 ATGGCTGTGGAAAAATCGAGATAAAGAGATCGAAGATCGAATAGCAGACAGTCACT 586  
QY 61 TACTCCAAAGAGAGATGGATTATCAAGAGCAAGAGATCACTGTTCTATGTGAT 120  
DB 587 TTTTCAAGAGGGCTTCTGCTTACTTAAAGAGCTGTGAGCTCTCTGTTCTTGTGAT 646  
QY 121 GCTAAAGTATCTCTTATCATTTTATCTAGCTCTGGAGATGGTTGATTAATCTGACGCC 180  
DB 647 GCTGAAGTCTGTGATGCTTCTCTTAAGTCTGGCAAGCTCTTGAAGTATCTCACTACT 706

## RESULT 6

US-08-867-087B-12  
Sequence 12, Application US/08867087B  
Patent No. 5990386  
GENERAL INFORMATION:  
APPLICANT: An, Gynheung  
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT  
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klarquist Sparkman Campbell Leigh &  
STREET: Whinston, LLP  
STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,087B  
FILING DATE: June 2, 1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/323,449  
FILING DATE: October 14, 1994  
APPLICATION NUMBER: U.S. 08/485,981  
FILING DATE: June 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan E.  
REGISTRATION NUMBER: 35,123  
REFERENCE/DOCKET NUMBER: 4630-47071  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1043 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-867-087B-12

Query Match 10.8%; Score 93.4; DB 2; Length 1043;  
Best Local Similarity 53.8%; Pred. No. 5.4e-17;  
Matches 218; Conservative 0; Mismatches 181; Indels 6; Gaps 1;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGATCAAGTAACTAAGGACGAGGTGACC 60  
DB 34 ATGGGGAGGGGAGAGAGTTGAGCTGAAGCGCATGAGAGACAAGATCAACAGGACAGGTGACC 93  
QY 61 TACTCCAGAGAGAGAAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120  
DB 94 TTCTCCAGAGGCGGCAACGCGCTCTCAAGAGGCTTACGAGCTGTCCGTTCTCTGCGAC 153  
QY 121 GCTAAGTATCTTATTCATTTATTTAGCTGAGAGATGTTGAATATGACAGCCCT 180  
DB 154 GCGGAGTCCGCGCTCATCTCTTCCAGCCGCGGCAAGCTTACGAGTTCGCGAGCC 213  
QY 181 TCAACTACGCTGACAGAAATCTTGAACAATACATGACAAATCTGGGAGAGATTGG 240  
DB 214 GGCATACCAAGACCTTTAGAAAGGTACCAACATTTGCTACAAATCTCAATATTCAC 273  
QY 241 GATGTAAGATGAGAACCTCAG-----CAATGAAGTGAATAGAGTCAAGAAACAAAT 294  
DB 274 AATGCACTTTCTGAACCTCAGAGTGTGTCATGAATGTCAAGTTGAAGCAAAATTT 333  
QY 295 GACAGATGCAAGTAGAGTCAAGCATCTGAAGGAGAGATATCAATCATTTGAACCAT 354  
DB 334 GAAGCTTTCAGGCGCACTCAAGGCACTTCTGGGAGAGATCTTGACCACTGACCGTC 393  
QY 355 GTAGAGCTGATGCGCTTAAAGAGAGACCTTGAATAATGGCTTACA 399  
DB 394 AAGGAATTGAGAGCTGAGAAACGTTGAATGTGACTATCA 438

## RESULT 7

US-08-485-981-9  
Sequence 9, Application US/08485981  
Patent No. 5861542  
GENERAL INFORMATION:  
APPLICANT: At. Gynheung  
TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND  
TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klarguist Sparkman Campbell Leigh &  
ADDRESSEE: Whinston  
STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,981  
FILING DATE: June 7, 1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/323,449

FILING DATE: October 14, 1994  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan. E.  
REGISTRATION NUMBER: 35,123  
REFERENCE/DOCKET NUMBER: 4630-42933  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 945 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-485-981-9

Query Match 10.6%; Score 92.2; DB 2; Length 945;  
Best Local Similarity 67.4%; Pred. No. 1.1e-16;  
Matches 130; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAACTGAGGAGGTGACC 60  
DB 16 ATGGGAGGGGTAGGGTTGAGCTTAAGAGAAATGAGAAACAAGTCAACAGGCAAGTAC 75  
QY 61 TACTCCAGAGAGAGAAATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120  
DB 76 TTGCTTAAGAGAGAAATGACCTTTGAAGAAAGCTTAATGAGCTTCTGTTCTTGTGAT 135  
QY 121 GCTAAGTATCTTATTCATTTATTTAGCTGAGAGATGTTGAATATGACAGCCCT 180  
DB 136 GCTGAGGTGCTCTCATCTTCTTCCATATGAGGAGAACTGTAAGAGTTGCAATGAC 195  
QY 181 TCAACTACGCTGA 193  
DB 196 TCTAGATGCTCA 208

## RESULT 8

US-08-867-087B-10  
Sequence 10, Application US/08867087B  
Patent No. 5990386  
GENERAL INFORMATION:  
APPLICANT: At. Gynheung  
TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT  
TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klarguist Sparkman Campbell Leigh &  
ADDRESSEE: Whinston, LLP  
STREET: One World Trade Center  
STREET: 121 S.W. Salmon Street  
STREET: Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America  
ZIP: 97204  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,087B  
FILING DATE: June 2, 1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/323,449  
FILING DATE: October 14, 1994  
APPLICATION NUMBER: U.S. 08/485,981  
FILING DATE: June 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Alan. E.